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(57) Abstract

This invention relates to newly identified tissue specific cancer associated polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "cancer antigens", and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such tissue specific cancer antigens for detection, prevention and treatment of tissue specific disorders, particularly the presence of cancer. This invention relates to the cancer antigens as well as vectors, host cells, antibodies directed to cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing tissue specific disorders, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.

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Human Cancer Associated Gene Sequences and Polypeptides

Field of the Invention

This invention relates to newly identified tissue specific cancer associated polynucleotides and the polypeptides encoded by these polynucleotides herein collectively known as "cancer antigens," and to the complete gene sequences associated therewith and to the expression products thereof, as well as the use of such cancer antigens for detection, prevention and treatment of tissue specific diseases, particularly cancers. This invention relates to the cancer antigens as well as vectors, host cells, antibodies directed to cancer antigens and recombinant and synthetic methods for producing the same. Also provided are diagnostic methods for diagnosing and treating, preventing and/or prognosing disorders related to tissue specific diseases, including cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention. The present invention further relates to methods and/or compositions for inhibiting the production and/or function of the polypeptides of the present invention.

Background of the Invention

Cell growth is a carefully regulated process which responds to specific needs of the body. Occassionally, the intricate, and highly regulated controls dictating the rules for cellular division break down. When this occurs, the cell begins to grow and divide independently of its homeostatic regulation resulting in a condition commonly referred to as cancer. In fact, cancer is the second leading cause of death among Americans aged 25-44.

Cancers or malignant tumors are characterized by continuous cell proliferation and cell death. Cancer cells have been shown to exhibit unique gene expression, and dozens of cancer-specific genetic markers, tumor antigens, have been identified. P35B, a tumor rejection antigen, was first identified in mouse. A point mutation in the P35B gene elicits a cytolytic T lymphocyte response but no detectable antibody response (Szikora, J. P. et al. (1990) EMBO J. 9:1041-1050). A human homolog of P35B, FX, is a homodimeric

NADP(H)-binding protein of 68 kDa. FX acts as a combined epimerase and NADPH-dependent reductase in converting GDP-4-keto-6-D-deoxymannose to GDP-L-fucose (Tonetti, M. et al. (1996) J. Biol. Chem. 271: 27274-27279). GDP-L-fucose is the substrate of several facosyl-transferases involved in the biosysthesis of blood group ABH antigenic determinants. GDP-L-fucose is also utilized in synthesizing fucosylated glycoproteins and glycolipids which function in cell adhesion and recognition (Springer, T. A. and Lasky, L. A. (1991) Nature 329: 196-197; Brandley, B. K. et al. (1990) Cell 63: 861-863; and Feizi, T. and Childs, R. A. (1987) Biochem. J. 245: 1-11).

Thus, there is a need for the identification and characterization of novel tissue specific polynucleotides and polypeptides which modulate activation and differentiation of cells, both normally and in disease states. In particular, there is a need to isolate and characterize additional molecules that mediate apoptosis, DNA repair, tumor-mediated angiogenesis, genetic imprinting, immune responses to tumors and tumor antigens and, among other things, that can play a role in detecting, preventing, ameliorating or correcting dysfunctions or diseases.

Summary of the Invention

The present invention includes isolated nucleic acid molecules comprising, or alternatively, consisting of, a cancer associated polynucleotide sequence disclosed in the sequence listing (as SEQ ID NOs:1 to 842) and/or contained in a human cDNA clone described in Tables 1, 2 and 5 and deposited with the American Type Culture Collection ("ATCC"). Fragments, variant, and derivatives of these nucleic acid molecules are also encompassed by the invention. The present invention also includes isolated nucleic acid molecules comprising, or alternatively consisting of, a polynucleotide encoding a cancer polypeptide. The present invention further includes cancer polypeptides encoded by these polynucleotides. Further provided for are amino acid sequences comprising, or alternatively consisting of, cancer polypeptides as disclosed in the sequence listing (as SEQ ID Nos: 843 to 1684) and/or encoded by a human cDNA clone described in Tables 1, 2 and 5 and deposited with the ATCC. Antibodies that bind these polypeptides are also encompassed by the invention. Polypeptide fragments, variants, and derivatives of these amino acid sequences are also encompassed by the invention, as are polynucleotides encoding these polypeptides and antibodies that bind these polypeptides. Also provided are diagnostic methods for diagnosing

and treating, preventing, and/or prognosing disorders related to cancer, and therapeutic methods for treating such disorders. The invention further relates to screening methods for identifying agonists and antagonists of cancer antigens of the invention.

Detailed Description

Tables

Table 1 summarizes some of the cancer antigens encompassed by the invention (including contig sequences (SEQ ID NO:X) and the cDNA clone related to the contig sequence) and further summarizes certain characteristics of the cancer polynucleotides and the polypeptides encoded thereby. The first column shows the "SEQ ID NO:" for each of the 842 cancer antigen polynucleotide sequences of the invention. The second column provides a unique "Sequence/Contig ID" identification for each cancer associated sequence. The third column, "Gene Name," and the fourth column, "Overlap," provide a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database and the database accession no. for the database sequence having similarity, respectively. The fifth and sixth columns provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity), respectively, observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence. The ninth column provides a unique "Clone ID" for a cDNA clone related to each contig sequence. The tenth column shows the tissue in which each SEQ ID NO:X is predominantly expressed.

Table 2 summarizes ATCC Deposits, Deposit dates, and ATCC designation numbers of deposits made with the ATCC in connection with the present application.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, fifteen or more of any one or more of these public EST sequences are optionally excluded from certain embodiments of the invention.

Table 4 lists residues comprising antigenic epitopes of antigenic epitope-bearing fragments present in most of the cancer associated polynucleotides described in Table 1 as predicted by the inventors using the algorithm of Jameson and Wolf, (1988) Comp. Appl.

Biosci. 4:181-186. The Jameson-Wolf antigenic analysis was performed using the computer program PROTEAN (Version 3.11 for the Power MacIntosh, DNASTAR, Inc., 1228 South Park Street Madison, WI). Cancer associated polypeptides (e.g., SEQ ID NO:Y, polypeptides encoded by SEQ ID NO:X, or polypeptides encoded by the cDNA in the referenced cDNA clone) may possess one or more antigenic epitopes comprising residues described in Table 4. It will be appreciated that depending on the analytical criteria used to predict antigenic determinants, the exact address of the determinant may vary slightly. The residues and locations shown in column two of Table 4 correspond to the amino acid sequences for most cancer associated polypeptide sequence shown in the Sequence Listing.

Table 5 shows the cDNA libraries sequenced, and ATCC designation numbers and vector information relating to these cDNA libraries.

Definitions

The following definitions are provided to facilitate understanding of certain terms used throughout this specification.

In the present invention, "isolated" refers to material removed from its original environment (e.g., the natural environment if it is naturally occurring), and thus is altered "by the hand of man" from its natural state. For example, an isolated polynucleotide could be part of a vector or a composition of matter, or could be contained within a cell, and still be "isolated" because that vector, composition of matter, or particular cell is not the original environment of the polynucleotide. The term "isolated" does not refer to genomic or cDNA libraries, whole cell total or mRNA preparations, genomic DNA preparations (including those separated by electrophoresis and transferred onto blots), sheared whole cell genomic DNA preparations or other compositions where the art demonstrates no distinguishing features of the polynucleotide/sequences of the present invention.

As used herein, a "polynucleotide" refers to a molecule having a nucleic acid sequence contained in SEQ ID NO:X (as described in column 1 of Table 1) or the related cDNA clone (as described in column 9 of Table 1 and contained within a library deposited with the ATCC). For example, the polynucleotide can contain the nucleotide sequence of the full length cDNA sequence, including the 5' and 3' untranslated sequences, the coding region, as well as fragments, epitopes, domains, and variants of the nucleic acid sequence.

Moreover, as used herein, a "polypeptide" refers to a molecule having an amino acid sequence encoded by a polynucleotide of the invention as broadly defined (obviously excluding poly-Phenylalanine or poly-Lysine peptide sequences which result from translation of a polyA tail of a sequence corresponding to a cDNA).

In the present invention, "SEQ ID NO:X" was often generated by overlapping sequences contained in multiple clones (contig analysis). A representative clone containing all or most of the sequence for SEQ ID NO:X is deposited at Human Genome Sciences, Inc. (HGS) in a catalogued and archived library. As shown in column 9 of Table 1, each clone is identified by a cDNA Clone ID. Each Clone ID is unique to an individual clone and the Clone ID is all the information needed to retrieve a given clone from the HGS library. In addition to the individual cDNA clone deposits, most of the cDNA libraries from which the clones were derived were deposited at the American Type Culture Collection (hereinafter "ATCC"). Table 5 provides a list of the deposited cDNA libraries. One can use the Clone ID to determine the library source by reference to Tables 2 and 5. Table 5 lists the deposited cDNA libraries by name and links each library to an ATCC Deposit. Library names contain four characters, for example, "HTWE." The name of a cDNA clone ("Clone ID") isolated from that library begins with the same four characters, for example "HTWEP07". As mentioned below, Table 1 correlates the Clone ID names with SEQ ID NOs. Thus, starting with a SEQ ID NO, one can use Tables 1, 2 and 5 to determine the corresponding Clone ID, from which library it came and in which ATCC deposit the library is contained. Furthermore, it is possible to retrieve a given cDNA clone from the source library by techniques known in the art and described elsewhere herein. The ATCC is located at 10801 University Boulevard, Manassas, Virginia 20110-2209, USA. The ATCC deposits were made persuant to the terms of the Budapest Treaty on the international recognition of the deposit of microorganisms for the purposes of patent procedure.

A "polynucleotide" of the present invention also includes those polynucleotides capable of hybridizing, under stringent hybridization conditions, to sequences contained in SEQ ID NO:X, or the complement thereof (e.g., the complement of any one, two, three, four, or more of the polynucleotide fragments described herein), and/or sequences contained in the related cDNA clone within a library deposited with the ATCC. "Stringent hybridization conditions" refers to an overnight incubation at 42 degree C in a solution comprising 50% formamide, 5x SSC (750 mM NaCl, 75 mM trisodium citrate), 50 mM sodium phosphate (pH

7.6), 5x Denhardt's solution, 10% dextran sulfate, and 20 μg/ml denatured, sheared salmon sperm DNA, followed by washing the filters in 0.1x SSC at about 65 degree C.

Also included within "polynucleotides" of the present invention are nucleic acid molecules that hybridize to the polynucleotides of the present invention at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation of formamide concentration (lower percentages of formamide result in lowered stringency); salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37 degree C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH_2PO_4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 ug/ml salmon sperm blocking DNA; followed by washes at 50 degree C with 1XSSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5X SSC).

Note that variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. Typical blocking reagents include Denhardt's reagent, BLOTTO, heparin, denatured salmon sperm DNA, and commercially available proprietary formulations. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

Of course, a polynucleotide which hybridizes only to polyA+ sequences (such as any 3' terminal polyA+ tract of a cDNA shown in the sequence listing), or to a complementary stretch of T (or U) residues, would not be included in the definition of "polynucleotide," since such a polynucleotide would hybridize to any nucleic acid molecule containing a poly (A) stretch or the complement thereof (e.g., practically any double-stranded cDNA clone generated using oligo dT as a primer).

The polynucleotides of the present invention can be composed of any polyribonucleotide or polydeoxribonucleotide, which may be unmodified RNA or DNA or modified RNA or DNA. For example, polynucleotides can be composed of single- and double-stranded DNA, DNA that is a mixture of single- and double-stranded regions, single- and double-stranded RNA, and RNA that is mixture of single- and double-stranded regions, hybrid molecules comprising DNA and RNA that may be single-stranded or, more typically, double-stranded or a mixture of single- and double-stranded regions. In addition, the

polynucleotide can be composed of triple-stranded regions comprising RNA or DNA or both RNA and DNA. A polynucleotide may also contain one or more modified bases or DNA or RNA backbones modified for stability or for other reasons. "Modified" bases include, for example, tritylated bases and unusual bases such as inosine. A variety of modifications can be made to DNA and RNA; thus, "polynucleotide" embraces chemically, enzymatically, or metabolically modified forms.

In specific embodiments, the polynucleotides of the invention are at least 15, at least 30, at least 50, at least 100, at least 125, at least 500, or at least 1000 continuous nucleotides but are less than or equal to 300 kb, 200 kb, 100 kb, 50 kb, 15 kb, 10 kb, 7.5kb, 5 kb, 2.5 kb, 2.0 kb, or 1 kb, in length. In a further embodiment, polynucleotides of the invention comprise a portion of the coding sequences, as disclosed herein, but do not comprise all or a portion of any intron. In another embodiment, the polynucleotides comprising coding sequences do not contain coding sequences of a genomic flanking gene (i.e., 5' or 3' to the gene of interest in the genome). In other embodiments, the polynucleotides of the invention do not contain the coding sequence of more than 1000, 500, 250, 100, 50, 25, 20, 15, 10, 5, 4, 3, 2, or 1 genomic flanking gene(s).

"SEQ ID NO:X" refers to a tissue specific cancer antigen polynucleotide sequence described in Table 1. SEQ ID NO:X is identified by an integer specified in column 1 of Table 1. The polypeptide sequence SEQ ID NO:Y is a translated open reading frame (ORF) encoded by polynucleotide SEQ ID NO:X. There are 842 cancer antigen polynucleotide sequences described in Table 1 and shown in the sequence listing (SEQ ID NO:1 through SEQ ID NO:842). Likewise there are 842 polypeptide sequences shown in the sequence listing, one polypeptide sequence for each of the polynucleotide sequences (SEQ ID NO:843 through SEQ ID NO:1684). The polynucleotide sequences are shown in the sequence listing immediately followed by all of the polypeptide sequences. Thus, a polypeptide sequence corresponding to polynucleotide sequence SEQ ID NO:1 is the first polypeptide sequence shown in the sequence listing. The second polypeptide sequence corresponds to the polynucleotide sequence shown as SEQ ID NO:2, and so on. In otherwords, since there are842 polynucleotide sequences, for any polynucleotide sequence SEQ ID NO:X, a corresponding polypeptide SEQ ID NO:Y can be determined by the formula X + 842 = Y. In addition, any of the unique "Sequence/Contig ID" defined in column 2 of Table 1, can be linked to the corresponding polypeptide SEQ ID NO:Y by reference to Table 4.

The polypeptides of the present invention can be composed of amino acids joined to each other by peptide bonds or modified peptide bonds, i.e., peptide isosteres, and may contain amino acids other than the 20 gene-encoded amino acids. The polypeptides may be modified by either natural processes, such as posttranslational processing, or by chemical modification techniques which are well known in the art. Such modifications are well described in basic texts and in more detailed monographs, as well as in a voluminous research literature. Modifications can occur anywhere in a polypeptide, including the peptide backbone, the amino acid side-chains and the amino or carboxyl termini. It will be appreciated that the same type of modification may be present in the same or varying degrees at several sites in a given polypeptide. Also, a given polypeptide may contain many types of modifications. Polypeptides may be branched, for example, as a result of ubiquitination, and they may be cyclic, with or without branching. Cyclic, branched, and branched cyclic polypeptides may result from posttranslation natural processes or may be made by synthetic methods. Modifications include acetylation, acylation, ADP-ribosylation, amidation, covalent attachment of flavin, covalent attachment of a heme moiety, covalent attachment of a nucleotide or nucleotide derivative, covalent attachment of a lipid or lipid derivative, covalent attachment of phosphotidylinositol, cross-linking, cyclization, disulfide bond formation, demethylation, formation of covalent cross-links, formation of cysteine, formation of pyroglutamate, formylation, gamma-carboxylation, glycosylation, GPI anchor formation, hydroxylation, iodination, methylation, myristoylation, oxidation, pegylation, proteolytic processing, phosphorylation, prenylation, racemization, selenoylation, sulfation, transfer-RNA mediated addition of amino acids to proteins such as arginylation, and ubiquitination. (See, for instance, PROTEINS - STRUCTURE AND MOLECULAR PROPERTIES, 2nd Ed., T. E. Creighton, W. H. Freeman and Company, New York (1993); POSTTRANSLATIONAL COVALENT MODIFICATION OF PROTEINS, B. C. Johnson, Ed., Academic Press, New York, pgs. 1-12 (1983); Seifter et al., Meth Enzymol 182:626-646 (1990); Rattan et al., Ann NY Acad Sci 663:48-62 (1992).)

The cancer polypeptides of the invention can be prepared in any suitable manner. Such polypeptides include isolated naturally occurring polypeptides, recombinantly produced polypeptides, synthetically produced polypeptides, or polypeptides produced by a combination of these methods. Means for preparing such polypeptides are well understood in the art.

The polypeptides may be in the form of the secreted protein, including the mature form, or may be a part of a larger protein, such as a fusion protein (see below). It is often advantageous to include an additional amino acid sequence which contains secretory or leader sequences, pro-sequences, sequences which aid in purification, such as multiple histidine residues, or an additional sequence for stability during recombinant production.

The cancer polypeptides of the present invention are preferably provided in an isolated form, and preferably are substantially purified. A recombinantly produced version of a polypeptide, including the secreted polypeptide, can be substantially purified using techniques described herein or otherwise known in the art, such as, for example, by the one-step method described in Smith and Johnson, Gene 67:31-40 (1988). Polypeptides of the invention also can be purified from natural, synthetic or recombinant sources using techniques described herein or otherwise known in the art, such as, for example, antibodies of the invention raised against the polypeptides of the present invention in methods which are well known in the art.

By a polypeptide demonstrating a "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

"A polypeptide having functional activity" refers to polypeptides exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular assay, such as, for example, a biological assay, with or without dose dependency. In the case where dose dependency does exist, it need not be identical to that of the polypeptide, but rather substantially similar to the dose-dependence in a given activity as compared to the polypeptide of the present invention (i.e., the candidate polypeptide will exhibit greater activity or not more than about 25-fold less and, preferably, not more than about tenfold less activity, and most preferably, not more than about three-fold less activity relative to the polypeptide of the present invention).

The functional activity of the cancer antigen polypeptides, and fragments, variants derivatives, and analogs thereof, can be assayed by various methods.

For example, in one embodiment where one is assaying for the ability to bind or compete with full-length polypeptide of the present invention for binding to an antibody to the full length polypeptide antibody, various immunoassays known in the art can be used, including but not limited to, competitive and non-competitive assay systems using techniques such as radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoradiometric assays, gel diffusion precipitation reactions, immunodiffusion assays, in situ immunoassays (using colloidal gold, enzyme or radioisotope labels, for example), western blots, precipitation reactions, agglutination assays (e.g., gel agglutination assays, hemagglutination assays), complement fixation assays, immunofluorescence assays, protein A assays, and immunoelectrophoresis assays, etc. In one embodiment, antibody binding is detected by detecting a label on the primary antibody. In another embodiment, the primary antibody is detected by detecting binding of a secondary antibody or reagent to the primary antibody. In a further embodiment, the secondary antibody is labeled. Many means are known in the art for detecting binding in an immunoassay and are within the scope of the present invention.

In another embodiment, where a ligand is identified, or the ability of a polypeptide fragment, variant or derivative of the invention to multimerize is being evaluated, binding can be assayed, e.g., by means well-known in the art, such as, for example, reducing and non-reducing gel chromatography, protein affinity chromatography, and affinity blotting. See generally, Phizicky, E., et al., Microbiol. Rev. 59:94-123 (1995). In another embodiment, physiological correlates polypeptide of the present invention binding to its substrates (signal transduction) can be assayed.

In addition, assays described herein (see Examples) and otherwise known in the art may routinely be applied to measure the ability of polypeptides of the present invention and fragments, variants derivatives and analogs thereof to elicit polypeptide related biological activity (either in vitro or in vivo). Other methods will be known to the skilled artisan and are within the scope of the invention.

<u>Cancer Associated Polynucleotides and Polypeptides of the Invention</u>

It has been discovered herein that the polynucleotides described in Table 1 are expressed at significantly enhanced levels in human cancer tissues as shown in column 10 of

Table 1. Accordingly, such polynucleotides, polypeptides encoded by such polynucleotides, and antibodies specific for such polypeptides find use in the prediction, diagnosis, prevention and treatment of tissue specific disorders, including cancer as more fully described below.

Table 1 summarizes some of the polynucleotides encompassed by the invention (including contig sequences (SEQ ID NO:X) and the related cDNA clones) and further summarizes certain characteristics of these tissue specific cancer associated polynucleotides and the polypeptides encoded thereby.

Table 1

Seq ID No.	Sequence/ Contig ID	Gene Name	Overlap	HGS Nucleotide Start	End	% Identity	% Similarity	Clone ID	Tissue(s)
1	507291	uvomorulin [Homo sapiens] >sp|Q15855|Q15855 UVOMORULIN PRECURSOR (E-CADHERIN) (ARC-1/UVOMORULIN). >gi|930046 uvomorulin (140 AA) [Homo sapiens] {SUB 168-307} Length = 878	gi|340185	2	475	100	100	HCHAU23	Pancreas, Breast/Ovarian
2	508000	HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >gi|179345 HLA-B-associated transcript 2 (BAT2) [Homo sapiens] >pir|B35098|B35098 MHC class III histocompatibility antigen HLA-B-associated transcript 2 - human >sp|P48634|BAT2_HUMAN LARGE PROLINE-RICH P	gi|179339	100	1902	86	87	HWAAK56	Lung, Breast/Ovarian
3	518325			110	310			HHFCP36	Lung, Pancreas, Colon, Breast/Ovarian
4	523111	Sm D2 [Homo sapiens] >pir|I38861|I38861 small nuclear ribonucleoprotein chain D2 - human Length = 118	gi|600748	233	670	88	88	HATAE67	Lung, Breast/Ovarian
5	526869	(AC002291) Similar ATP-dependent RNA Helicase [Arabidopsis thaliana] >sp|O49289|O49289 SIMILAR ATP-DEPENDENT RNA HELICASE. Length = 845	gi|2829912	1	552	67	77	HT4FP57	Pancreas, Breast/Ovarian
6	532211	retinoic acid-binding protein [Bos taurus] Length = 138	gi|162906	2	481	95	98	HHGCV63	Lung, Breast/Ovarian

7	532247			160	384			HEBCC47	Pancreas, Breast/Ovarian
8	537932	alcohol dehydrogenase [Homo sapiens] >gi|178134 alcohol dehydrogenase 3 [Homo sapiens] >pir|JH0789|DEHUC2 alcohol dehydrogenase (EC 1.1.1.1) 5 - human >sp|P11766|ADHX_HUMAN ALCOHOL DEHYDROGENASE CLASS III CHI CHAIN (EC 1.1.1.1) (GLUTATHIONE-DEPENDENT FOR	gi|178130	1	1149	92	92	HUSIB86	Lung, Breast/Ovarian
9	540117			174	635			HRGBU25	Lung, Breast/Ovarian
10	547710	transketolase [Homo sapiens] Length = 623	gi|1297297	2	1189	92	92	HMUAZ27	Lung, Pancreas
11	551747	rtvp-1 [Homo sapiens] >pir|JC5308|JC5308 testis-specific, vespid, and pathogenesis-related protein 1 - human >sp|P48060|GLIP_HUMAN GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEIN). Length = 266	gi|1030053	26	931	91	91	HTDAE10	Lung, Pancreas
12	552799	delta- aminolevulinate synthase (housekeeping) [Homo sapiens] >pir|S13682|SYHUAL 5-aminolevulinate synthase (EC 2.3.1.37) 1 precursor - human >sp|P13196|HEM1_HUMAN 5-AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA-AM	gi|28583	104	814	100	100	HHECX90	Lung, Pancreas, Breast/Ovarian

13	553243	RING7 [Homo sapiens] >gi|557702 HLA-DMB [Homo sapiens] >gi|512472 HLA-DMB [Homo sapiens] >gi|1054742 DMB [Homo sapiens] >pir|I37533|I37533 MHC class II histocompatibility antigen HLA-DM beta chain precursor - human Length = 263	gi|313002	202	1017	93	93	HUKDI44	Lung, Pancreas
14	553368	(AF053944) aortic carboxypeptidase-like protein ACLP [Homo sapiens] >sp|G3288916|G3288916 AORTIC CARBOXYPEPTIDASE-LIKE PROTEIN ACLP. >gnl|PID|d1013781 AEBP1 [Homo sapiens] {SUB 314-1158} Length = 1158	gi|3288916	1	459	96	96	HADGE84	Lung, Pancreas
15	554349			3	776			HUSGK19	Lung, Pancreas
16	558491	immunoglobulin heavy chain [Homo sapiens] Length = 152	gi|567128	1	429	98	100	HUFCN61	Lung, Pancreas, Colon
17	558983	dJ68O2.2 [Homo sapiens] >sp|P35579|MYSN_HUMAN MYOSIN HEAVY CHAIN, NONMUSCLE TYPE A (CELLULAR MYOSIN HEAVY CHAIN, TYPE A) (NMMHC-A). >gi|553596 cellular myosin heavy chain [Homo sapiens] {SUB 1-1337} Length = 1960	gnl|PID|e1294465	219	623	100	100	HOHBM82	Pancreas, Breast/Ovarian
18	572943			367	522			HBAMC47	Pancreas, Breast/Ovarian
19	585892	epithelial tumor antigen precursor, membrane-bound form - human Length = 515	pir|S10572|S10572	3	965	89	89	HUKAL69	Lung, Pancreas, Colon, Breast/Ovarian

20	589390	C1 inhibitor [Homo sapiens] >gi|29535 C1 inhibitor [Homo sapiens] >pir|S15386|ITHUC1 complement C1 inhibitor precursor - human >sp|P05155|IC1_HUMAN PLASMA PROTEASE C1 INHIBITOR PRECURSOR (C1 INH). >gnl|PID|e3783 C1 inhibitor (AA 155-478) (1 is 2nd base i	gnl|PID|e222400	3	983	96	96	HSRAB10	Lung, Pancreas
21	596882			800	1057			HMCEP91	Lung, Pancreas, Colon
22	616289	nucleoporin p58 [Rattus norvegicus] >sp|P70581|P70581 NUCLEOPORIN P58. Length = 585	gi|1537068	1	390	67	70	HAJCB44	Lung, Pancreas
23	622140	selenophosphate synthetase 2 [Homo sapiens] >sp|Q99611|Q99611 SELENOPHOSPHATE SYNTHETASE 2. Length = 448	gi|1815622	92	325	97	97	HEONC67	Pancreas, Breast/Ovarian
24	623566	karyopherin alhph 3 [Homo sapiens] >sp|O00505|IMA3_HUMAN IMPORTIN ALPHA-3 SUBUNIT (KARYOPHERIN ALPHA-3 SUBUNIT). Length = 521	gnl|PID|d1021210	66	1652	99	99	HDPPP20	Lung, Breast/Ovarian
25	647714			1	711			HSSEH29	Pancreas, Breast/Ovarian
26	647752	ubiquitin conjugating-protein [Oryctolagus cuniculus] >gi|184046 HHR6B (Human homologue of yeast RAD 6); putative [Homo sapiens] >gi|30954 E2 protein [Homo sapiens] >gi|207555 ubiquitin conjugating-protein [Rattus norvegicus] >gnl|PID|e233515 HR6B gene pr	gi|165780	3	590	100	100	HDTDH46	Lung, Colon

27	651774	P58 [Homo sapiens] >pir|S68363|S68363 protein disulfide-isomerase (EC 5.3.4.1) ER60 precursor - human >sp|P30101|ER60_HUMAN PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (GRP58) (ERP57). Length	gi|1147739	1	1632	96	96	HDPAA15	Lung, Pancreas, Breast/Ovarian
28	651995	collagen [Mus musculus] >pir|S23779|S23779 collagen alpha 1(VIII) chain - mouse >sp|Q00780|CA18_MOUSE COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR. >bbs|134935 alpha 1-VIII collagen [rats, mesangial cell, Peptide Partial, 172 aa] [Rattus sp.] {SUB 399-570} Leng	gnl|PID|e245912	3	335	90	95	HBTAD44	Lung, Pancreas
29	652156	phospholipid hydroperoxide glutathione peroxidase [Homo sapiens] >sp|O43381|O43381 GSHH_HUMAN (EC 1.11.1.9) (GLUTATHIONE PEROXIDASE). >gi|3399677 (AC005390) GSSH_HUMAN, partial CDS [Homo sapiens] {SUB 149-197} Length = 197	gi|825667	262	633	94	94	HOEBK80	Lung, Breast/Ovarian
30	653010			79	183			HSRAA58	Lung, Pancreas
31	655904	von Willebrand factor [Homo sapiens] >pir|A34480|VWHU von Willebrand factor precursor - human >gi|553810 von Willebrand factor [Homo sapiens] {SUB 990-1947} >gnl|PID|e222518 von Willebrand factor [Homo sapiens] {SUB 1-178} >gi|340316 von Willebrand antige	gi|340356	632	1891	96	96	HSEBB94	Lung, Breast/Ovarian
32	657852			70	522			HCHAL14	Colon, Breast/Ovarian
33	666414			1	285			HOSFG18	Lung, Pancreas

34	667847	ribosomal protein S9 [Rattus norvegicus] >pir|JN0587|S21497 ribosomal protein S9 - rat Length = 194	gi|57143	1	714	98	98	HCFLJ62	Lung, Pancreas, Breast/Ovarian
35	670188	G protein gamma-10 subunit [Homo sapiens] >pir|I39158|I39158 GTP-binding regulatory protein gamma-10 chain - human >sp|P50151|GBGA_HUMAN GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-10 SUBUNIT. Length = 68	gi|995919	2	238	100	100	HWADR30	Lung, Pancreas
36	670279	ribosomal protein S24 [Homo sapiens] >gi|517222 ribosomal protein S24 [Homo sapiens] >gi|49652 ribosomal protein S19 (AA 1 - 133) [Mesocricetus auratus] >gi|57858 ribosomal protein S24 [Rattus norvegicus] >gi|57722 ribosomal protein S24 (AA 1-133) [Rattus	gi|337506	96	503	87	87	HSAYG46	Lung, Pancreas, Breast/Ovarian
37	670729	acidic ribosomal phosphoprotein (P1) [Homo sapiens] >pir|B27125|R6HUP1 acidic ribosomal protein P1 - human Length = 114	gi|190234	74	496	100	100	H2CBM17	Lung, Pancreas, Colon, Breast/Ovarian
38	674123			40	438			HYACJ55	Lung, Pancreas
39	676496	collagen type VI, alpha 3 chain [Homo sapiens] >sp|E1292418|E1292418 COLLAGEN TYPE VI, ALPHA 3 CHAIN. Length = 3176	gnl|PID|e1292418	250	1029	98	98	HSLIC82	Lung, Pancreas
40	678162	TAXREB107 [Homo sapiens] >pir|I51803|I51803 TAXREB107 - human Length = 288	gnl|PID|d1005017	528	974	100	100	HBJJA02	Lung, Pancreas, Breast/Ovarian

41	678248	dolichol-phosphate-mannose synthase [Homo sapiens] >sp|O60762|O60762 DOLICHOL-PHOSPHATE-MANNOSE SYNTHASE. >gnl|PID|d1026578 dolichol-phosphate-mannose synthase [Homo sapiens] {SUB 1-120} Length = 260	gnl|PID|d1026577	3	770	100	100	HMTAK71	Lung, Pancreas
42	683668	alpha 1 (I) chain propeptide [Homo sapiens] >gi|180380 alpha-1 type I collagen [Homo sapiens] {SUB 64-201} Length = 1040	gi|180392	566	1912	94	94	HWHGV07	Lung, Pancreas, Breast/Ovarian
43	693172	Q1Z 7F5 [Homo sapiens] >gi|189266 may code for Wilm's tumor-related protein [Homo sapiens] >gi|190814 Wilm's tumor-related protein [Homo sapiens] >gi|1203971 QM gene product [Homo sapiens] >bbs|135740 QM [human, nontumorigenic Wilms' microcell hybrid c	gi|184407	23	214	97	100	HNHIW05	Lung, Pancreas, Breast/Ovarian
44	694303			2824	3219			HOGAV47	Lung, Breast/Ovarian
45	695042	Description: KRAB zinc finger protein; this is a splicing variant that contains a stop codon and frame shift between the KRAB box and the zinc finger region; Method: conceptual translation supplied by author [Homo sapiens] >sp|Q13359|Q13359 KRAB ZINC FING	gi|1049295	471	680	74	91	HISBX26	Pancreas, Breast/Ovarian
46	699799	lipocortin (AA 1-346) [Homo sapiens] >pir|A03080|LUHU annexin I - human >sp|P04083|ANX1_HUMAN ANNEXIN I (LIPOCORTIN I) (CALPACTIN II) (CHROMOBINDIN 9) (P35) (PHOSPHOLIPASE A2 INHIBITORY PROTEIN). {SUB 2-346} Length = 346	gi|34388	3	1121	100	100	HNDAA51	Lung, Breast/Ovarian

47	702216	dihydrodiol dehydrogenase [Homo sapiens] >gi|487135 hepatic dihydrodiol dehydrogenase [Homo sapiens] >gi|181549 dihydrodiol dehydrogenase [Homo sapiens] >pir|A53436|A53436 3-alpha-hydroxysteroid/dihydrodiol dehydrogenase (EC 1.1.1.-) - human >sp|Q04828|DB	gi|452484	41	1048	95	95	HNALC11	Lung, Pancreas
48	703015	latent transforming growth factor-beta-binding protein - human Length = 1820	pir|A55494|A55494	3	587	100	100	HGCOX28	Lung, Pancreas
49	706391	vacuolar H+ ATPase proton channel subunit [Homo sapiens] >pir|A39367|A39367 H+-transporting ATPase (EC 3.6.1.35) chain PKD1 - human Length = 155	gi|189676	29	622	85	85	HMABL73	Lung, Breast/Ovarian
50	706892	copper transport protein HAH1 [Homo sapiens] >sp|O00244|O00244 COPPER TRANSPORT PROTEIN HAH1. Length = 68	gi|1945365	3	287	82	82	HUFDS83	Lung, Breast/Ovarian
51	706924			2847	3215			HRAEB20	Lung, Breast/Ovarian
52	707642	ribosomal protein L8 [Homo sapiens] >gi|57704 ribosomal protein L8 [Rattus rattus] >gi|1527178 ribosomal protein L8 [Mus musculus] >pir|JU0177|R5RTL8 ribosomal protein L8, cytosolic - rat >pir|JN0923|JN0923 ribosomal protein L8, cytosolic - human >gi|3851	gi|433899	1	516	94	94	HSRDJ44	Lung, Pancreas, Colon, Breast/Ovarian
53	710369			99	611			HSPAI81	Lung, Pancreas, Breast/Ovarian
54	718826			581	877			HSIFK68	Lung, Breast/Ovarian

55	719790	lipocortin II [Homo sapiens] >pir|A23942|LUHU36 annexin II - human >sp|P07355|ANX2_HUMAN ANNEXIN II (LIPOCORTIN II) (CALPACTIN I HEAVY CHAIN) (CHROMOBINDIN 8) (P36) (PROTEIN I) (PLACENTAL ANTICOAGULANT PROTEIN IV) (PAP-IV). {SUB 2-339} >sp|G545587|G545587	gnl|PID|d1000439	3	869	98	98	HKABK62	Lung, Pancreas
56	720222	homology with 16.7 KD putative viral protein YUB1_NPVAC [Caenorhabditis elegans] Length = 250	gnl|PID|e1346018	34	729	45	60	HSKEP04	Lung, Pancreas, Breast/Ovarian
57	724033			1	654			HPJBV92	Lung, Pancreas, Breast/Ovarian
58	724767	epsilon isoform of 61kDa regulatory subunit of PP2A [Homo sapiens] >gi|1478070 protein phosphatase B56-epsilon [Homo sapiens] >sp|Q16537|Q16537 EPSILON ISOFORM OF 61KDA REGULATORY SUBUNIT OF PP2A. >gi|1022892 protein phosphatase PP2A0 B' subunit delta is	gnl|PID|e220196	71	526	100	100	HKABH59	Lung, Breast/Ovarian
59	727065	ATPase [Homo sapiens] Length = 617	gi|291868	228	1010	99	99	HELGY15	Lung, Pancreas
60	727246	(AB009282) cytochrome b5 [Homo sapiens] >sp|O43169|O43169 CYTOCHROME B5 (FRAGMENT). Length = 146	gnl|PID|d1024640	3	509	96	98	HCFMH52	Lung, Colon
61	727932			41	199			HLJDO53	Lung, Breast/Ovarian
62	731167	Sec23 protein [Homo sapiens] Length = 765	gnl|PID|e236013	1	987	99	99	HDTEM51	Lung, Pancreas

63	732514	lysophosphatidic acid acyltransferase-alpha [Homo sapiens] >gi|2253613 putative lysophospholipid acyltransferase [Homo sapiens] >gnl|PID|e286645 1-acylglycerol-3-phosphate O-acyltransferase [Homo sapiens] >sp|Q99943|PLCA_HUMAN 1-ACYL-SN-GLYCEROL-3-PHOSPHA	gi|2155238	3	794	99	99	HLDBX26	Pancreas, Prostate
64	734080			1	567			HFIBK44	Lung, Breast/Ovarian
65	734288	cysteinyl-tRNA synthetase [Homo sapiens] Length = 595	gi|927229	154	2067	99	99	HKABU01	Lung, Pancreas
66	739448	Nascent polypeptide associated complex alpha subunit [Homo sapiens] >gi|4092060 (AF054187) alpha NAC [Homo sapiens] >pir|S49326|S49326 Nascent polypeptide associated complex alpha chain - human >sp|Q13765|Q13765 NASCENT POLYPEPTIDE ASSOCIATED COMPLEX ALPH	gi|556642	441	1184	82	82	HKGAT31	Lung, Breast/Ovarian
67	739668			2	484			HAPTL07	Lung, Pancreas
68	740060	Diff33 gene product [Homo sapiens] >sp|Q13530|Q13530 PLACENTAL PROTEIN DIFF33. Length = 494	gi|1293563	76	1536	94	94	HMEGB82	Lung, Pancreas
69	741560			3	296			HCGMI12	Lung, Colon
70	742543	human gamma-glutamyl hydrolase [Homo sapiens] >sp|Q92820|Q92820 HUMAN GAMMA-GLUTAMYL HYDROLASE (EC 3.4.22.12). Length = 318	gi|2951931	187	804	99	100	HE2BG62	Lung, Colon, Breast/Ovarian
71	742831			25	297			HCDAL47	Pancreas, Colon

72	745327	channel-like integral membrane protein [Homo sapiens] >gi|1314304 channel-like integral membrane protein [Homo sapiens] >pir|A41616|A41616 erythrocyte integral membrane protein 28K - human >sp|P29972|AQP1_HUMAN AQUAPORIN-CHIP (WATER CHANNEL PROTEIN FOR RE	gi|180501	1	534	98	98	HWHPM73	Lung, Pancreas
73	745695	Mac-2 binding protein [Homo sapiens] >gi|483474 90K gene product [Homo sapiens] >pir|A47161|A47161 Mac-2-binding glycoprotein precursor - human >sp|Q08380|Q08380 MAC-2 BINDING PROTEIN PRECURSOR. Length = 585	gi|307153	886	2016	98	98	HOPBN02	Lung, Pancreas
74	750316	(AF029890) hepatitis B virus X interacting protein [Homo sapiens] >sp|O43504|O43504 HEPATITIS B VIRUS X INTERACTING PROTEIN. Length = 91	gi|2745883	99	398	100	100	HKMLD65	Lung, Pancreas, Breast/Ovarian
75	750522			172	906			HUKFI58	Lung, Pancreas, Colon, Breast/Ovarian
76	750583			58	189			HBJJB66	Lung, Breast/Ovarian
77	751020			1	480			HEBAE80	Lung, Breast/Ovarian
78	752196			1	120			HLIAL67	Pancreas, Prostate
79	753084	UGTrel1 [Homo sapiens] >pir|JC5024|JC5024 UDP-galactose transporter related isozyme 1 - human >sp|P78383|P78383 UGTREL1. Length = 322	gi|1669560	53	1168	87	87	HDPKG74	Lung, Pancreas
80	754957	The ha1237 gene product is related to S.pombe rad21 gene product. [Homo sapiens] Length = 631	gnl|PID|d1008135	242	1330	94	94	HWBGB01	Lung, Pancreas

81	756557	myosin I heavy chain [Rattus norvegicus] >pir|A45439|A45439 myosin I heavy chain - rat >sp|Q05096|Q05096 MYOSIN HEAVY CHAIN I. Length = 1136	gi|56733	1	888	94	94	HE8AF67	Lung, Pancreas, Colon, Breast/Ovarian
82	756712			1457	1729			HSYBW76	Lung, Pancreas
83	757414	5-lipoxygenase activating protein [Homo sapiens] >pir|A39824|A39824 5-lipoxygenase-activating protein - human >sp|P20292|FLAP_HUMAN 5-LIPOXYGENASE ACTIVATING PROTEIN (FLAP) (MK-886-BINDING PROTEIN). Length = 161	gi|182658	1	477	99	100	HCABA08	Lung, Colon
84	757614	tetratricopeptide repeat protein [Homo sapiens] >sp|Q99614|Q99614 TETRATRICOPEPTIDE REPEAT PROTEIN. Length = 292	gi|1688074	83	991	100	100	HMEJS13	Lung, Pancreas, Breast/Ovarian
85	757815	(AF038604) contains similarity to Drosophila ovarian tumor locus protein (GB:X13693) [Caenorhabditis elegans] >sp|O44438|O44438 B0546.2 PROTEIN. Length = 346	gi|2702370	2	988	58	81	HCHOL74	Lung, Breast/Ovarian
86	759878	nuclear pore complex protein NUP107 [Rattus norvegicus] >pir|A54142|A54142 nucleoporin NUP107 - rat >sp|P52590|N107_RAT NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105). Length = 926	gi|510717	526	1833	86	88	HNTAP78	Lung, Breast/Ovarian
87	760227	(AC003040) putative nicotinate phosphoribosyltransferase [Arabidopsis thaliana] >sp|O80459|O80459 PUTATIVE NICOTINATE PHOSPHORIBOSYLTRANSFERASE. Length = 574	gi|3242705	2	484	52	71	HCHMM71	Pancreas, Breast/Ovarian

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<tr><td>88</td><td>760312</td><td>chondroitin sulfate proteoglycan versican V0 splice-variant precursor peptide [Homo sapiens] >sp|P13611|PGCV_HUMAN VERSICAN CORE PROTEIN PRECURSOR (LARGE FIBROBLAST PROTEOGLYCAN) (CHONDROITIN SULFATE PROTEOGLYCAN CORE PROTEIN 2) (GLIAL HYALURONATE- BINDIN</td><td>gi|608515</td><td>993</td><td>3215</td><td>99</td><td>99</td><td>HMVDD07</td><td>Lung, Pancreas</td></tr>
<tr><td>89</td><td>766051</td><td></td><td></td><td>1</td><td>627</td><td></td><td></td><td>HMAFA79</td><td>Lung, Breast/Ovarian</td></tr>
<tr><td>90</td><td>767593</td><td></td><td></td><td>327</td><td>497</td><td></td><td></td><td>HCECT76</td><td>Pancreas, Colon</td></tr>
<tr><td>91</td><td>768053</td><td>(AF039688) antigen NY-CO-3 [Homo sapiens] >sp|O60525|O60525 ANTIGEN NY-CO-3 (FRAGMENT). Length = 192</td><td>gi|3170176</td><td>251</td><td>625</td><td>99</td><td>99</td><td>HTPEH71</td><td>Pancreas, Breast/Ovarian</td></tr>
<tr><td>92</td><td>768055</td><td>ATP synthase gamma-subunit [Homo sapiens] >gnl|PID|d1004512 ATP synthase gamma-subunit [Homo sapiens] >pir|A49108|A49108 H+-transporting ATP synthase (EC 3.6.1.34) gamma chain - human >sp|P36542|ATPG_HUMAN ATP SYNTHASE GAMMA CHAIN, MITOCHONDRIAL PRECURSOR</td><td>gnl|PID|d1004511</td><td>32</td><td>949</td><td>100</td><td>100</td><td>HAJAQ70</td><td>Lung, Pancreas</td></tr>
<tr><td>93</td><td>769685</td><td>src-like tyrosine kinase (put.); putative [Homo sapiens] Length = 537</td><td>gi|338228</td><td>1005</td><td>1409</td><td>100</td><td>100</td><td>HRADN48</td><td>Lung, Pancreas, Colon, Breast/Ovarian</td></tr>
<tr><td>94</td><td>771920</td><td>F36D4.2 gene product [Caenorhabditis elegans] >sp|Q20100|Q20100 COSMID F36D4. Length = 224</td><td>gi|1245686</td><td>711</td><td>1562</td><td>58</td><td>77</td><td>HAIDT44</td><td>Lung, Pancreas</td></tr>
<tr><td>95</td><td>772790</td><td>cell division inhibitor [Synechocystis sp.] >pir|S77404|S77404 cell division inhibitor - Synechocystis sp. (PCC 6803) >sp|P73467|P73467 CELL DIVISION INHIBITOR. Length = 339</td><td>gnl|PID|d1018240</td><td>145</td><td>1158</td><td>35</td><td>54</td><td>HCEOT95</td><td>Lung, Breast/Ovarian</td></tr>
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96	772916	similarto human ZFY protein. [Homo sapiens] >sp|Q92610|Q92610 MYELOBLAST KIAA0211. Length = 1267	gnl|PID|d1013891	3	965	99	99	HCEIT26	Lung, Pancreas
97	773225			52	504			HCLBI78	Lung, Pancreas
98	773632	Hrs [Homo sapiens] >gi|2731383 HGF receptor substrate Hrs [Homo sapiens] >sp|O14964|O14964 HRS, COMPLETE CDS. Length = 777	gnl|PID|d1024245	1	309	98	98	HCEVQ60	Pancreas, Prostate, Breast/Ovarian
99	774364	(AF080561) SYT interacting protein SIP [Homo sapiens] >sp|O75932|O75932 SYT INTERACTING PROTEIN SIP. Length = 669	gi|3746787	1	408	100	100	HCHAR77	Pancreas, Breast/Ovarian
100	775355			1599	1781			HDTBY31	Lung, Pancreas
101	775844	rfp transforming protein [Homo sapiens] >pir|A28101|TVHURF ret finger protein - human >gnl|PID|e308255 RFP [Homo sapiens] {SUB 250-513} Length = 513	gi|337372	138	1877	92	92	HISCU10	Lung, Pancreas
102	777760	(AF015040) NUMB protein [Homo sapiens] >sp|G4102705|G4102705 NUMB PROTEIN. >gi|4050088 (AF109907) S171 [Homo sapiens] {SUB 79-603} >gi|887362 ORF; putative [Homo sapiens] {SUB 469-603} Length = 603	gi|4102705	62	1372	88	88	HMSHK67	Pancreas, Breast/Ovarian
103	779837	tazarotene-induced gene 2 [Homo sapiens] >sp|Q99969|Q99969 TAZAROTENE-INDUCED GENE 2. Length = 163	gi|1848264	88	567	97	98	HSWBV38	Lung, Pancreas
104	780769	(AF084259) bromodomain-containing protein BP75 [Mus musculus] >sp|O88665|O88665 BROMODOMAIN-CONTAINING PROTEIN BP75. Length = 651	gi|3493162	100	762	35	58	HULBS08	Lung, Pancreas
105	781445			496	1443			HMVAP52	Pancreas, Breast/Ovarian

106	781531	lumican [Homo sapiens] Length = 338	gi|699577	1	486	100	100	HCHAF71	Pancreas. Breast/Ovarian
107	783018	ovary2 [Drosophila melanogaster] >sp|Q27924|Q27924 OVARY2. >gi|1208729 ovary2 [Drosophila melanogaster] {SUB 386-545} Length = 545	gi|1208732	120	674	58	76	HTPCZ45	Pancreas. Breast/Ovarian
108	783097	myogenic repressor I-mf [Homo sapiens] >sp|Q99750|Q99750 MYOGENIC REPRESSOR I-MF. Length = 246	gi|1763615	413	919	85	85	HMWGR19	Lung, Colon
109	784198	(AJ005893) JM26 [Homo sapiens] >sp|O60828|O60828 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)). Length = 265	gnl|PID|e1289747	80	943	81	81	HNTNB85	Lung, Pancreas, Breast/Ovarian
110	784868	WW-domain binding protein 1 [Mus musculus] >sp|P97764|P97764 WW-DOMAIN BINDING PROTEIN 1. Length = 305	gi|1777577	1	969	77	85	HNTNQ08	Lung, Pancreas, Breast/Ovarian
111	785428	translation initiation factor 5 [Homo sapiens] >sp|P55010|IF5_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5). Length = 431	gi|1229140	308	1606	87	87	HPMCI14	Lung, Pancreas, Breast/Ovarian
112	785845			67	1350			HCGBE06	Lung, Colon, Breast/Ovarian
113	785854			3	509			HUSXJ65	Lung, Pancreas
114	786705			64	180			HBJJB89	Lung, Pancreas, Breast/Ovarian
115	787186			319	975			HUKBB89	Lung, Pancreas
116	787279	proteasome subunit z [Homo sapiens] >sp|Q99436|Q99436 PROTEASOME SUBUNIT Z. Length = 277	gnl|PID|d1007816	80	856	94	94	HKAJZ91	Lung, Breast/Ovarian
117	789002			178	402			HATBM56	Lung, Pancreas, Breast/Ovarian

118	789008	1.8 kb mRNA (AA 1-84) [Homo sapiens] >pir|S03384|S03384 hypothetical protein (IGF-II 3' region) - human >sp|P09565|IG2R_HUMAN PUTATIVE INSULIN-LIKE GROWTH FACTOR II ASSOCIATED PROTEIN. Length = 84	gi|33000	1354	1737	100	100	HISCN20	Lung, Pancreas
119	789555	(AL035247) hypothetical trp-asp repeat protein [Schizosaccharomyces pombe] Length = 760	gnl|PID|e1371207	124	1815	42	66	HTTCB23	Pancreas, Breast/Ovarian
120	789631			192	320			HLICN93	Lung, Pancreas, Colon
121	789779			1	396			HCHMS40	Colon, Breast/Ovarian
122	790387			3	527			HLMNA32	Colon, Breast/Ovarian
123	790461	(AF008445) phospholipid scramblase [Homo sapiens] >gnl|PID|d1033532 (AB006746) hMmTRA1b [Homo sapiens] >gi|4092081 (AF098642) phospholipid scramblase; plasma membrane phospholipid scramblase [Homo sapiens] >sp|O15162|O15162 PHOSPHOLIPID SCRAMBLASE. >sp|G4	gi|2282601	105	1193	99	99	HTGAV10	Lung, Pancreas, Breast/Ovarian
124	790931			2	394			HBCAO30	Pancreas, Breast/Ovarian
125	791176	(AB002107) hPer [Homo sapiens] >gi|2435507 (AF022991) Rigui [Homo sapiens] >sp|O15534|O15534 RIGUI. Length = 1290	dbj||AB002107_1	3	1034	90	90	HNFCJ67	Lung, Pancreas
126	791983			637	837			HBJLE45	Lung, Pancreas, Colon, Breast/Ovarian

127	792539	(AF020833) eukaryotic translation initiation factor 3 subunit [Homo sapiens] >sp|O14801|O14801 EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT. Length = 320	gi|2460200	94	1068	94	94	HDPPX89	Lung, Pancreas, Breast/Ovarian
128	792749	protein arginine N-methyltransferase [Rattus norvegicus] >sp|Q63009|ANM1_RAT PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-). Length = 353	gi|1390025	34	1104	95	96	HDQEP64	Lung, Breast/Ovarian
129	792961	(AF036249) polymerase I-transcript release factor; PTRF [Mus musculus] >sp|O54724|O54724 POLYMERASE I AND TRANSCRIPT RELEASE FACTOR (POLYMERASE I-TRANSCRIPT RELEASE FACTOR). Length = 392	gi|2674195	778	1305	85	86	HMEKG25	Lung, Breast/Ovarian
130	793206	dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens] >sp|O76058|O76058 DJ14O9.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE). Length = 606	gnl|PID|e1311294	889	1365	99	99	HTWFN71	Lung, Pancreas
131	793249	proliferation associated gene (pag) gene product [Homo sapiens] >pir|A46711|A46711 proliferation associated gene (pag) protein - human Length = 199	gi|287641	3	701	100	100	HJAAE81	Lung, Pancreas, Breast/Ovarian
132	793626	alpha mannosidase II isozyme [Homo sapiens] >sp|P49641|MA2X_HUMAN ALPHA-MANNOSIDASE IIX (EC 3.2.1.114) (MANNOSYL-OLIGOSACCHARIDE 1,3-1,6-ALPHA-MANNOSIDASE) (MAN IIX). Length = 1139	gnl|PID|d1010153	119	640	99	99	HWABS13	Lung, Pancreas

133	794417	(AF047470) malate dehydrogenase precursor [Homo sapiens] >sp|O43682|O43682 MALATE DEHYDROGENASE (EC 1.1.1.37) PRECURSOR (EC 1.1.1.37). Length = 338	gi|2906146	3	1142	99	99	HFPBR03	Lung, Pancreas, Breast/Ovarian
134	795197			82	888			HDPFT26	Lung, Breast/Ovarian
135	795251	GAP SH3 binding protein [Homo sapiens] >sp|Q13283|Q13283 GAP SH3 BINDING PROTEIN. Length = 466	gi|1051170	101	1531	91	91	HE8FJ92	Pancreas, Breast/Ovarian
136	795752			2	1018			HWBDR92	Lung, Pancreas
137	796261	ubiquitin carrier protein E2 - human >gi|181916 ubiquitin carrier protein [Homo sapiens] {SUB 23-247} Length = 247	pir|B42856|B42856	3	851	87	87	HCHPQ06	Colon, Breast/Ovarian
138	796933	lumican [Homo sapiens] Length = 338	gi|699577	49	1107	94	94	HPMSD56	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
139	799424			525	1553			HEONK47	Lung, Pancreas, Breast/Ovarian
140	799698			1	426			HCHAM08	Colon, Breast/Ovarian
141	800351	DNAJ homolog [Homo sapiens] >gi|1127833 heat shock protein hsp40 homolog [Homo sapiens] >pir|G02272|G02272 heat shock protein hsp40 homolog - human >sp|Q13431|Q13431 HEAT SHOCK PROTEIN HSP40 HOMOLOG. Length = 178	gi|1518918	282	860	83	84	HEMFP05	Pancreas, Breast/Ovarian

142	800573	26S protease subunit [Sus scrofa] >gi|3193258 (AF069053) proteasome subunit SUG1 [Bos taurus] >gnl|PID|d1012606 proteasomal ATPase (rat SUG1) [Rattus norvegicus] >gnl|PID|d1023806 (AB000491) proteasome p45/SUG [Rattus norvegicus] >gnl|PID|e199326 mSUG1 pr	gnl|PID|e235521	178	1383	93	93	HCEVS28	Lung, Breast/Ovarian
143	805815			15	1055			HCHAP80	Lung, Colon, Breast/Ovarian
144	806445			711	1028			HTELC67	Lung, Pancreas
145	810309	(AF098482) transcriptional coactivator p52 [Homo sapiens] >sp|G4050034|G4050034 TRANSCRIPTIONAL COACTIVATOR P52. Length = 333	gi|4050034	226	741	61	75	HNTDX22	Lung, Pancreas
146	811022			168	881			HISEA13	Lung, Pancreas
147	811023			13	234			HLWAW17	Lung, Pancreas, Colon, Breast/Ovarian
148	811143	cytokine inducible SH2-containing protein [Mus musculus] >pir|S55551|S55551 cytokine-inducible protein CIS - mouse >sp|Q62225|Q62225 CYTOKINE INDUCIBLE SH2-CONTAINING PROTEIN (SH2 DOMAIN CONTAINING PROTEIN INDUCED BY MULTIPLE CYTOKINES, SIC). Length = 257	gnl|PID|d1007285	3	887	90	92	HDQPA25	Lung, Breast/Ovarian
149	811381	FIN14 gene product [Mus musculus] >sp|Q61077|FI14_MOUSE FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN14). Length = 61	gi|1353711	1338	1511	86	91	HLYEK93	Colon, Breast/Ovarian

150	811595	CIRP [Homo sapiens] >gi|2924760 (AC004258) CIRP [Homo sapiens] >gi|2541973 (AF021336) DNA damage-inducible RNA binding protein [Homo sapiens] >sp|Q14011|Q14011 GLYCINE-RICH RNA BINDING PROTEIN CIRP. Length = 172	gnl|PID|d1011874	1	609	100	100	HDTLA92	Pancreas, Breast/Ovarian
151	813000	Tera [Mus musculus] >sp|P70361|P70361 TERA. Length = 277	gi|1575505	95	850	84	86	HDPVZ64	Pancreas, Breast/Ovarian
152	813288	fau gene product [Homo sapiens] >gi|31305 fau 1 gene product [Homo sapiens] >pir|JC1278|JC1278 ubiquitin-like protein / ribosomal protein S30, cytosolic - human Length = 133	gi|31303	1	510	86	86	HCHMQ63	Lung, Breast/Ovarian
153	813431	DAP-1 [Homo sapiens] >pir|I37274|I37274 death-associated protein 1 - human >sp|P51397|DAP1_HUMAN DEATH-ASSOCIATED PROTEIN 1 (DAP-1). Length = 102	gi|434845	3	470	89	89	HWHQS70	Lung, Pancreas
154	813450	PISSLRE gene product [Homo sapiens] >pir|S49330|S49330 serine/threonine kinase (EC 2.7.1.-) pisslre - human >pir|I38116|I38116 gene PISSLRE protein - human >sp|Q15131|Q15131 PISSLRE MRNA. Length = 360	gi|556651	1	651	100	100	HCEEJ73	Lung, Pancreas
155	813478	retinoblastoma-binding protein mRbAp48 [Mus musculus] >pir|I49366|I49366 retinoblastoma-binding protein mRbAp48 - mouse Length = 461	gi|1016275	1	1398	99	100	HAJBI20	Lung, Pancreas, Breast/Ovarian
156	813505	ribosomal protein L23a [Homo sapiens] >gi|306549 homology to rat ribosomal protein L23 [Homo sapiens] {SUB 10-156} Length = 156	gi|404015	2	496	100	100	HDABR53	Lung, Pancreas

157	815552	(AJ011497) Claudin-9 [Homo sapiens] >sp|E1363658|E1363658 CLAUDIN-9. Length = 211	gnl|PID|e1363658	317	898	95	96	HUFEH29	Lung, Colon
158	815606	Ki-1/57 intracellular antigen [Homo sapiens] >sp|O75804|O75804 KI-1/57 INTRACELLULAR ANTIGEN (FRAGMENT). Length = 299	gi|3403154	218	1303	90	95	HDPRY63	Lung, Pancreas, Breast/Ovarian
159	816048	neutral protease alpha subunit [Homo sapiens] >gi|35328 protease small subunit (aa 1-268) [Homo sapiens] >gi|1905903 (AD001527) calcium-dependent protease, small (regulatory) subunit (calpain) (calcium-activated neutral proteinase) (CANP) [Homo sapiens] >	gi|179909	24	644	95	96	HTLCZ60	Lung, Breast/Ovarian
160	822978			94	156			HODEM46	Lung, Pancreas
161	823616			1449	1775			HCEME79	Pancreas, Colon
162	823981	(AF003130) similar to Achlya ambisexualis antheridiol steroid receptor (NID:g166306) [Caenorhabditis elegans] >sp|O01757|O01757 SIMILAR TO ACHLYA AMBISEXUALIS ANTHERIDIOL STEROID RECEPTOR. Length = 1043	gi|2088668	992	2617	60	78	HWHQH79	Lung, Breast/Ovarian
163	824364	drebrin E2 [Homo sapiens] >gnl|PID|d1005005 drebrin E [Homo sapiens] >pir|JN0809|JN0809 drebrin E (clone gDbh13) - human >sp|Q16643|DREB_HUMAN DREBRIN E. Length = 649	gi|392890	1	606	84	84	HCHPR34	Colon, Breast/Ovarian

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<tr><td>164</td><td>824423</td><td>UDP-GalNAc:polypeptide N-acetylgalactosaminyl transferase [Homo sapiens] >pir|JC4223|JC4223 polypeptide N-acetylgalactosaminyltransferase (EC 2.4.1.41) - human >sp|Q10472|PAGT_HUMAN POLYPEPTIDE N-ACETYLGALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UDP</td><td>gi|971459</td><td>61</td><td>1743</td><td>100</td><td>100</td><td>HPWDL83</td><td>Lung, Pancreas</td></tr>
<tr><td>165</td><td>825279</td><td></td><td></td><td>36</td><td>602</td><td></td><td></td><td>H6EDN61</td><td>Lung, Pancreas</td></tr>
<tr><td>166</td><td>825442</td><td></td><td></td><td>1</td><td>900</td><td></td><td></td><td>HTODA45</td><td>Colon, Breast/Ovarian</td></tr>
<tr><td>167</td><td>825548</td><td>ancient ubiquitous 46 kDa protein AUP46 precursor [Mus musculus] >sp|P70295|P70295 ANCIENT UBIQUITOUS PROTEIN PRECURSOR (AUP1). Length = 410</td><td>gi|1517822</td><td>473</td><td>1504</td><td>81</td><td>84</td><td>HLUDB77</td><td>Lung, Breast/Ovarian</td></tr>
<tr><td>168</td><td>825725</td><td>hNop56 [Homo sapiens] >sp|O00567|NO56_HUMAN NUCLEOLAR PROTEIN NOP56. Length = 602</td><td>gnl|PID|e1188703</td><td>25</td><td>723</td><td>99</td><td>99</td><td>HMWIV57</td><td>Lung, Pancreas</td></tr>
<tr><td>169</td><td>826639</td><td>H.sapiens mRNA for rat translocon-associated protein delta homolog [Homo sapiens] >gnl|PID|e212192 translocon-associated protein delta subunit precursor [Homo sapiens] >gnl|PID|e220312 translocon-associated protein delta subunit precursor [Homo sapiens] ></td><td>gi|1071681</td><td>1</td><td>561</td><td>100</td><td>100</td><td>HPTVX93</td><td>Lung, Colon, Breast/Ovarian</td></tr>
<tr><td>170</td><td>827079</td><td>(AL009171) 62D9.a [Drosophila melanogaster] >sp|E1198294|E1198294 62D9.A. Length = 1305</td><td>gnl|PID|e1198294</td><td>53</td><td>2176</td><td>71</td><td>85</td><td>HDAAD02</td><td>Lung, Breast/Ovarian</td></tr>
</table>

171	827153	pancreatitis-associated protein [Homo sapiens] >gi|312807 preprotein [Homo sapiens] >bbs|121222 PAP-H=pancreatitis-associated protein [human, pancreas, Peptide, 175 aa] [Homo sapiens] >gnl|PID|d1003233 PAP homologous protein [Homo sapiens] >pir|A49616|A49	gi|482909	54	602	90	90	HLQBS95	Pancreas, Colon, Breast/Ovarian
172	827351			1	639			HSKJE35	Colon, Breast/Ovarian
173	827503	(AC004003) serine/threonine kinase RICK; match to protein AF027706 (PID:g3123887) and mRNA AF027706 (NID:g3123886) [Homo sapiens] >gi|3290172 (AF064824) CARD-containing ICE associated kinase [Homo sapiens] >gi|3342910 (AF078530) receptor interacting prote	gi|3264574	255	1886	98	98	HLAAB36	Lung, Breast/Ovarian
174	827563	rhophilin [Mus musculus] >sp|Q61085|Q61085 GTP-RHO BINDING PROTEIN 1 (RHOPHILIN). Length = 643	gi|1176422	6	776	81	91	HBGDH11	Colon, Breast/Ovarian
175	827565	serine protease [Homo sapiens] Length = 492	gi|2507613	1	744	55	68	HCHAK72	Lung, Pancreas, Colon, Breast/Ovarian
176	827893	homology with GTP binding protein; putative [Caenorhabditis elegans] >pir|S44605|S44605 C02F5.3 protein - Caenorhabditis elegans Length = 573	gi|289610	165	836	62	75	HMSOT38	Lung, Pancreas
177	828072			1147	1305			HTECA53	Lung, Pancreas, Breast/Ovarian
178	828228			1105	1314			HWLAH78	Prostate, Colon

179	828241	cathepsin O [Homo sapiens] >pir|A55090|A55090 cathepsin O (EC 3.4.-.-) precursor - human >sp|P43234|CATO_HUMAN CATHEPSIN O PRECURSOR (EC 3.4.22.-). Length = 321	gi|574804	2	1012	93	93	HWBBP30	Lung, Pancreas, Prostate
180	828287	histone (H2A.Z) [Bos taurus] >gi|410 histone H2A.Z (AA 1-127) [Bos taurus] >gi|184060 histone (H2A.Z) [Homo sapiens] >gi|31975 histone H2A.Z (AA 1-127) [Homo sapiens] >gi|3649600 histone [Homo sapiens] >gi|204599 histone (H2A.Z) [Rattus norvegicus] >gi|57	gi|163150	171	572	100	100	HUSIS02	Lung, Pancreas, Prostate, Breast/Ovarian
181	828364			663	1340			HWHGT17	Pancreas, Breast/Ovarian
182	828371	complement component C1s [Homo sapiens] >gi|179648 complement subcomponent C1s precursor [Homo sapiens] >gi|763110 complement protein C1s precursor [Homo sapiens] >pir|A40496|C1HUS complement subcomponent C1s (EC 3.4.21.42) precursor - human >sp|P09871|C1	gi|179646	4	2283	97	97	HLQCQ12	Lung, Pancreas, Colon, Breast/Ovarian
183	828403	DNA-binding protein [Homo sapiens] >pir|A44478|A44478 probable cell growth or differentiation regulator (alternatively spliced type I transcript) - human >sp|Q02833|Q02833 PUTATIVE TRANSCRIPTIONAL REGULATORY PROTEIN HRC1. Length = 373	gi|184390	1	648	98	98	HDTHL82	Lung, Pancreas, Colon
184	828501	(AF056302) eIF-2alpha kinase [Drosophila melanogaster] >sp|O61651|O61651 EIF-2ALPHA KINASE. Length = 1589	gi|3046551	1	1812	36	58	HBMDG73	Lung, Colon, Breast/Ovarian

185	828520	(AJ010840) ATP-dependent RNA helicase [Homo sapiens] >sp|E1321519|E1321519 ATP-DEPENDENT RNA HELICASE (FRAGMENT). Length = 420	gnl|PID|e1321519	445	1821	91	91	HRGBN47	Prostate, Breast/Ovarian
186	828527			723	926			HSKGQ05	Lung, Pancreas, Prostate, Breast/Ovarian
187	828538			332	976			HPWDF55	Lung, Prostate, Breast/Ovarian
188	828541	pre-pump-1 proteinase (AA -17 to 250) [Homo sapiens] >gi|35803 PUMP [Homo sapiens] >pir|B28816|KCHUM matrilysin (EC 3.4.24.23) precursor - human >sp|P09237|COG7_HUMAN MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRI	gi|35799	43	933	100	100	HRACJ32	Pancreas, Prostate, Colon
189	828549	thrombospondin 2 [Homo sapiens] >pir|A47379|TSHUP2 thrombospondin 2 precursor - human Length = 1172	gi|307506	26	1738	94	94	HFIAL22	Pancreas, Colon
190	828562			1	342			HPWBR24	Pancreas, Prostate
191	828576			3	731			HPTVU91	Pancreas, Prostate, Colon
192	828602			1050	1568			HPRAT58	Lung, Prostate
193	828628	tumor-associated antigen [Homo sapiens] >pir|A36056|A36056 tumor-associated antigen CO-029 - human >sp|P19075|CO02_HUMAN TUMOR-ASSOCIATED ANTIGEN CO-029. Length = 237	gi|180926	307	1029	94	94	HPRCM33	Pancreas, Prostate, Colon

194	828667	cytochrome c-1 [Homo sapiens] >sp|P08574|CY1_HUMAN CYTOCHROME C1, HEME PROTEIN PRECURSOR. >gi|181238 cytochrome c1 [Homo sapiens] {SUB 99-325} Length = 325	gi|181240	2	1006	85	85	HKAOB02	Pancreas, Breast/Ovarian
195	828684	p55CDC [Homo sapiens] >pir|A56021|A56021 probable cell division control protein p55CDC - human >sp|Q12834|Q12834 P55CDC. Length = 499	gi|468032	41	1573	92	92	HPJAE35	Pancreas, Prostate
196	828727	(AF044954) NADH:ubiquinone oxidoreductase PDSW subunit [Homo sapiens] >gi|4165091 (AF088991) NADH-ubiquinone oxidoreductase PDSW subunit [Homo sapiens] Length = 172	gi|4164442	3	629	93	93	HMCBB12	Lung, Prostate, Breast/Ovarian
197	828734	homologue of Drosophila Fat protein [Homo sapiens] >sp|Q14517|Q14517 CADHERIN-RELATED TUMOR SUPPRESSOR HOMOLOG PRECURSOR (FAT PROTEIN HOMOLOG). >gnl|PID|d1022418 cadherin [Homo sapiens] {SUB 993-1132} Length = 4590	gi|1107687	1	657	99	99	HSRAB84	Pancreas, Colon, Breast/Ovarian
198	828750	(AF035940) similar to mago nashi [Homo sapiens] >gi|2330011 (AF007862) mm-Mago [Mus musculus] >gi|2909828 (AF035939) similar to mago nashi [Mus musculus] >sp|O35169|O35169 MM-MAGO. >sp|G2909830|G2909830 MAGOH. >sp|P50606|MGN_HUMAN MAGO NASHI PROTEIN HOMOL	gi|2909830	13	546	100	100	HPIAC11	Pancreas, Prostate, Breast/Ovarian

199	828842	(AB007191) AMY-1 [Homo sapiens] >gnl|PID|d1009980 c-myc binding protein [Homo sapiens] >sp|Q99417|Q99417 C-MYC BINDING PROTEIN. Length = 103	gnl|PID|d1023271	1	363	98	100	HOUGA12	Pancreas, Prostate, Breast/Ovarian
200	828843	p48 [Homo sapiens] >sp|P50502|HIP_HUMAN HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN). >gi|1857033 SCN6 gene product [Homo sapiens] {SUB 99-369} Length = 369	gi|904032	3	761	99	100	HOVBK85	Lung, Pancreas, Prostate
201	828851	(AF054284) spliceosomal protein SAP 155 [Homo sapiens] >sp|G4033735|G4033735 SPLICEOSOMAL PROTEIN SAP 155. >gi|3387899 (AF070540) putative nuclear protein [Homo sapiens] {SUB 1011-1304} Length = 1304	gi|4033735	1	1029	98	98	HOSGA73	Pancreas, Prostate
202	828856	thymidine kinase (EC 2.7.1.21) [Homo sapiens] >gi|339719 thymidine kinase [Homo sapiens] >pir|A27318|KIHUT thymidine kinase (EC 2.7.1.21), cytosolic - human >sp|P04183|KITH_HUMAN THYMIDINE KINASE, CYTOSOLIC (EC 2.7.1.21). >gi|339713 thymidine kinase [Homo	gi|339709	1	804	99	100	HOHEN75	Prostate, Breast/Ovarian
203	828862	tyrosine kinase receptor [Homo sapiens] >pir|B41527|B41527 transforming protein (axl(-)) - human Length = 885	gi|292870	1	417	98	98	HOHBI90	Prostate, Breast/Ovarian
204	828870	TRAM protein [Homo sapiens] >pir|S30034|S30034 translocating chain-associating membrane protein - human >sp|Q15629|Q15629 TRAM PROTEIN. Length = 374	gi|37265	32	1279	94	94	HOEKU65	Lung, Pancreas, Colon

205	828873	precursor polypeptide (AA -31 to 1139) [Homo sapiens] >gi|538354 thrombospondin [Homo sapiens] {SUB 1-397} >gi|339669 thrombospondin [Homo sapiens] {SUB 1028-1170} >gi|532689 thrombospondin-1p180 [Homo sapiens] {SUB 364-422} Length = 1170	gi|37465	1	1398	100	100	HOHCJ26	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
206	828892	keratin [Homo sapiens] >sp|Q14533|Q14533 KERATIN (HAIR TYPE II BASIC KERATIN) (KERATIN LIKE). >gnl|PID|e118093 hair type II basic keratin [Homo sapiens] {SUB 81-505} >gi|951272 keratin like [Homo sapiens] {SUB 249-505} >bbs|161491 type II hair keratin {cl	gnl|PID|c321549	3	653	90	91	HOGAA83	Lung, Prostate, Breast/Ovarian
207	828893	ESX [Homo sapiens] >gi|1841523 ESE-1b [Homo sapiens] >gi|2338756 (AF017307) Ets-related transcription factor [Homo sapiens] >gi|2384740 (AF016295) Ets transcription factor [Homo sapiens] >gi|2459797 epthelial-specific ets protein [Homo sapiens] >sp|P78545	gi|1754538	36	1253	86	86	HOGAS09	Pancreas, Prostate, Colon, Breast/Ovarian
208	828897	prostasin [Homo sapiens] >gi|862305 prostasin [Homo sapiens] >pir|A57014|A57014 prostasin (EC 3.4.21.-) precursor - human >sp|G565130|G565130 PROSTASIN=SERINE PROTEINASE (N-TERMINAL). {SUB 45-64} Length = 343	gi|1143194	59	811	92	92	HBCAY53	Pancreas, Colon, Breast/Ovarian

209	828910	light chain 3 subunit of microtubule-associated proteins 1A and 1B [Rattus norvegicus] >pir|A53624|A53624 microtubule-associated protein 1 light chain 3 - rat >sp|Q62625|MPL3_RAT MICROTUBULE-ASSOCIATED PROTEINS 1A/1B LIGHT CHAIN 3 (MAP1A/MAP1B LC3). {SUB	gi|455109	28	540	96	98	HOHDY41	Prostate, Colon
210	828927	cytochrome c oxidase subunit Va [Homo sapiens] >pir|JT0342|OTHU5A cytochrome-c oxidase (EC 1.9.3.1) chain Va precursor - human >sp|P20674|COXA_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE VA PRECURSOR (EC 1.9.3.1). >gi|3859864 (AF067635) cytochrome c oxidase su	gi|695360	1	567	99	99	HHFJM88	Lung, Breast/Ovarian
211	828932	80K-H protein [Homo sapiens] >gi|1293640 protein kinase C substrate 80K-H [Homo sapiens] >pir|A32469|A32469 80K protein H precursor - human >sp|P14314|G19P_HUMAN PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, HEAVY CHAIN (PKCSH) (80K-H PROTEIN). Length = 527	gi|182855	82	1026	83	83	HNTAC57	Lung, Pancreas, Prostate, Breast/Ovarian
212	828933	Csa-19 [Homo sapiens] Length = 217	gi|531171	439	852	97	98	HEMCA07	Lung, Pancreas, Breast/Ovarian
213	828941	ORF YJL115w [Saccharomyces cerevisiae] >gi|171091 ASF1 [Saccharomyces cerevisiae] >pir|S30766|S30766 ASF1 protein - yeast (Saccharomyces cerevisiae) >sp|P32447|ASF1_YEAST ANTI-SILENCING PROTEIN 1. Length = 279	gi|1008304	1	729	59	74	HMGBJ25	Lung, Pancreas, Colon, Breast/Ovarian

214	828957	F31C3.5 [Caenorhabditis elegans] >sp|O62193|O62193 F31C3.5 PROTEIN. Length = 180	gnl|PID|e1346411	3	635	37	68	HMWHG54	Prostate, Breast/Ovarian
215	828963	house-keeping protein [Mus musculus] >pir|S27870|S27870 house-keeping protein - mouse >sp|Q61669|Q61669 HOUSE-KEEPING PROTEIN 1. Length = 396	gi|193871	73	1293	55	77	HMWBH91	Lung, Prostate, Colon, Breast/Ovarian
216	828964			639	905			HMWFZ60	Pancreas, Prostate, Colon, Breast/Ovarian
217	828966	S-adenosylhomocysteine hydrolase [Homo sapiens] >pir|A43629|A43629 adenosylhomocysteinase (EC 3.3.1.1) - human Length = 432	gi|178279	2	1372	98	98	HMWFV54	Lung, Pancreas, Prostate, Breast/Ovarian
218	828967	putative tRNA synthetase-like protein [Homo sapiens] >gi|4104935 (AF042347) putative phenylalanyl-tRNA synthetase alpha-subunit; PheHA [Homo sapiens] >sp|E317305|E317305 PUTATIVE TRNA SYNTHETASE-LIKE PROTEIN. >sp|G2102679|G2102679 PUTATIVE TRNA SYNTHETASE	gi|2102679	3	1535	98	98	HMUBT12	Pancreas, Prostate, Breast/Ovarian
219	828977	insulin-like growth factor binding protein 2 [Homo sapiens] >bbs|106618 insulin-like growth factor binding protein-2, IGFBP-2 [human, placenta, Peptide, 328 aa] [Homo sapiens] >pir|A41927|A41927 insulin-like growth factor-binding protein 2 precursor - hum	gi|179477	2	685	100	100	HMVAW27	Lung, Pancreas, Prostate, Breast/Ovarian

220	828978	annexin IV (placental anticoagulant protein II) [Homo sapiens] >gnl|PID|d1011889 annexin IV (carbohydrtate-binding protein p33/41) [Homo sapiens] >pir|A42077|A42077 annexin IV - human >sp|P09525|ANX4_HUMAN ANNEXIN IV (LIPOCORTIN IV) (ENDONEXIN I) (CHROMOB	gi|178699	213	1184	100	100	HNTMH78	Lung, Pancreas, Prostate
221	828979			16	1080			HMUBO53	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
222	829001			1621	1959			HMSJR30	Lung, Pancreas, Prostate, Breast/Ovarian
223	829003	plasma gelsolin [Homo sapiens] >pir|A03011|FAHUP gelsolin precursor, plasma - human >sp|P06396|GELS_HUMAN GELSOLIN PRECURSOR, PLASMA (ACTIN-DEPOLYMERIZING FACTOR) (ADF) (BREVIN) (AGEL). >gnl|PID|e20565 plasma gelsolin (AA 49-117) [Homo sapiens] {SUB 49-11	gi|736249	635	2536	99	99	HMSKA53	Lung, Pancreas, Prostate
224	829016	(AB006625) The human homolog of a mouse imprinted gene, Peg3. [Homo sapiens] >sp|P78418|P78418 KIAA0287 (PEG3) (FRAGMENT). >gi|1899244 PEG3 [Homo sapiens] {SUB 518-1132} Length = 1132	dbj||AB006625_1	409	759	87	87	HMIAI73	Prostate, Breast/Ovarian
225	829027	ras-like protein [Homo sapiens] >pir|D34788|TVHUC4 transforming protein ras (teratocarcinoma clone TC10) - human Length = 213	gi|190881	2	577	100	100	HMIBE59	Prostate, Colon

226	829028	RnudC gene product [Rattus norvegicus] >pir|A55897|A55897 prolactin-induced T cell protein c15 - rat >sp|Q63525|Q63525 C15 MRNA. Length = 332	gi|619907	31	1110	95	98	HMGBQ56	Pancreas, Prostate, Breast/Ovarian
227	829031	protocadherin X [Mus musculus] >sp|G4099553|G4099553 PROTOCADHERIN X. Length = 928	gi|4099553	116	637	90	93	HMGBI69	Lung, Pancreas, Prostate, Breast/Ovarian
228	829034			28	1362			HMEIY69	Pancreas, Prostate
229	829036	Similar to B.subtilis Poly(A) polymerase (SW:PAPS_BACSU) [Caenorhabditis elegans] >sp|Q93795|Q93795 F55B12.4 PROTEIN. Length = 440	gnl|PID|e1347205	114	1151	67	81	HMELJ75	Pancreas, Prostate
230	829049	UDP-Gal:GlcNAc galactosyltransferase [Homo sapiens] >sp|O60910|O60910 UDP-GAL:GLCNAC GALACTOSYLTRANSFERASE. Length = 393	gnl|PID|e1283714	233	1444	94	94	HMEFQ33	Prostate, Colon
231	829073			193	843			HLYCD85	Pancreas, Prostate
232	829075			2	484			HMAAD66	Lung, Pancreas, Prostate, Breast/Ovarian
233	829076			3	665			HADDC41	Lung, Pancreas, Breast/Ovarian
234	829080			3	500			HMABG80	Prostate, Breast/Ovarian
235	829087	small GTP-binding protein [Oryctolagus cuniculus] >pir|A48500|A48500 small GTP-binding protein Rab25 - rabbit Length = 213	gi|436001	157	873	95	97	HLWBY67	Pancreas, Prostate, Breast/Ovarian

236	829092	UDP-galactose translocator [Homo sapiens] >pir|JC4903|JC4903 UDP-galactose transporter, splice form 1 - human Length = 393	gnl|PID|d1013353	1	513	85	85	HLWBC74	Pancreas, Prostate
237	829095			3	425			HLWBM89	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
238	829096	antiquitin=26g turgor protein homolog [human, kidney, Peptide, 511 aa] [Homo sapiens] >pir|A54676|A54676 antiquitin - human >sp|P49419|DHAX_HUMAN ANTIQUITIN (EC 1.2.1.-). Length = 511	bbs|158840	552	1628	97	97	HLWAO28	Prostate, Breast/Ovarian
239	829118	nuclear autoantigen fo 14 kDa [Homo sapiens] >sp|O43805|O43805 NUCLEAR AUTOANTIGEN FO 14 KDA. Length = 119	gnl|PID|e322419	2	415	99	99	HLSDA35	Lung, Prostate
240	829152	unknown protein precursor [Homo sapiens] >pir|JN0596|JN0596 fibrinogen-related protein HFREP-1 precursor - human >sp|Q08830|Q08830 FIBRINOGEN-LIKE PROTEIN 1 PRECURSOR. Length = 312	gnl|PID|d1003846	215	1231	95	95	HLICU82	Lung, Pancreas, Prostate
241	829160	ubiquitin-conjugating enzyme UbcH6 [Homo sapiens] Length = 193	gi|1064914	2	769	83	83	HLFBF56	Lung, Pancreas, Prostate, Colon
242	829163			403	930			HSPBG80	Lung, Pancreas, Breast/Ovarian
243	829176	C4b-binding protein alpha chain [Homo sapiens] >gi|190502 C4b-binding protein alpha chain [Homo sapiens] >pir|A33568|NBHUC4 C4b-binding protein alpha chain precursor - human >sp|P04003|C4BP_HUMAN C4B-BINDING PROTEIN ALPHA CHAIN PRECURSOR (PROLINE-RICH PRO	gi|190500	3	662	100	100	HLQBR92	Lung, Pancreas
244	829204			515	913			HLISB22	Prostate, Breast/Ovarian

245	829207			111	977			HL1SA66	Prostate, Breast/Ovarian
246	829228			1	2508			HKGBQ77	Lung, Prostate, Colon
247	829252			96	1322			HKAPI21	Pancreas, Prostate
248	829254			1	483			HKFBI96	Lung, Pancreas, Prostate, Breast/Ovarian
249	829269			121	474			HKAEE96	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
250	829277			3	596			HJPCG91	Lung, Prostate
251	829290			100	207			HJBDL52	Lung, Pancreas, Prostate, Breast/Ovarian
252	829294			3	1847			HISDU47	Pancreas, Prostate
253	829299			3	794			HISEC32	Lung, Pancreas, Prostate
254	829308	dJ14O9.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens] >sp|O76058|O76058 DJ14O9.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE). Length = 606	gnl|PID|e1311294	207	938	47	70	HIBCN93	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
255	829349	ribosomal protein S15a [Rattus norvegicus] >pir|JC2234|JC2234 ribosomal protein S15a - rat Length = 130	gi|495273	152	547	100	100	HICAF44	Lung, Pancreas, Prostate, Breast/Ovarian
256	829354	RAD4 gene product [Saccharomyces cerevisiae] Length = 730	gi|4271	1	1113	44	65	HAJBD51	Lung, Pancreas, Breast/Ovarian

257	829388	DNase protein [Homo sapiens] >gi|1620214 XIB [Homo sapiens] >pir|JC4633|JC4633 DNase I-like endonuclease (EC 3.1.-.-) - human >sp|P49184|DRNL_HUMAN MUSCLE-SPECIFIC DNASE I-LIKE PRECURSOR (EC 3.1.21.-) (DNASE X) (XIB). Length = 302	gi|929628	319	1281	94	94	HUVCJ22	Lung, Pancreas, Colon, Breast/Ovarian
258	829540			258	437			HAPOU28	Lung, Pancreas, Colon, Breast/Ovarian
259	829626	mannosyl-oligosaccharide 1,2-alpha-mannosidase (EC 3.2.1.113) - rabbit (fragment) >gi|474282 mannosyl-oligosaccharide alpha-1,2-mannosidase [Oryctolagus cuniculus] {SUB 12-480} Length = 480	pir|B54408|B54408	3	764	75	88	HCEES14	Lung, Pancreas, Colon, Breast/Ovarian
260	829730	underexpressed in thyroid tissue after TSH stimulation [Canis familiaris] >sp|Q28283|Q28283 C5FW PROTEIN. Length = 343	gnl|PID|e252512	455	1153	62	75	HAJBK53	Pancreas, Breast/Ovarian
261	829892	(AF053651) cellular apoptosis susceptibility protein [Homo sapiens] >sp|O75432|O75432 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN. Length = 971	gi|3598795	64	1053	85	85	HAMFJ43	Lung, Prostate
262	829933	(AF035606) calcium binding protein [Homo sapiens] >sp|O75340|O75340 CALCIUM BINDING PROTEIN. Length = 191	gi|3342794	1	540	86	86	HAICT76	Pancreas, Prostate
263	829938	(AF067855) geminin [Homo sapiens] >sp|O75496|O75496 GEMININ. Length = 209	gi|3249005	230	952	93	93	HAIBS55	Pancreas, Prostate
264	829969			551	814			HACCB64	Lung, Pancreas, Prostate, Breast/Ovarian

265	829982	(AF020352) NADH:ubiquinone oxidoreductase 15 kDa IP subunit [Homo sapiens] >gi|2911482 (AF047434) NADH-ubiquinone oxidoreductase 15kDa subunit; CI-15 protein [Homo sapiens] >sp|O43920|NIPM_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE 15 KD SUBUNIT (EC 1.6.5.3) (E	gi|2655055	28	399	100	100	HABGE25	Prostate, Breast/Ovarian
266	830007	catechol-O-methyltransferase [Homo sapiens] >gi|403304 catechol O-methyltransferase [Homo sapiens] >pir|S37406|A38459 catechol O-methyltransferase (EC 2.1.1.6) - human >sp|P21964|COMT_HUMAN CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (M	gi|180920	110	1006	99	99	H6EDW66	Lung, Prostate, Breast/Ovarian
267	830019	(AF030249) putative dienoyl-CoA isomerase [Homo sapiens] >gi|564065 peroxisomal enoyl-CoA hydratase-like protein [Homo sapiens] >pir|I38882|I38882 peroxisomal enoyl-CoA hydratase-like protein - human >sp|Q13011|ECH1_HUMAN PROBABLE PEROXISOMAL ENOYL-COA HY	gi|2623168	77	976	94	96	H2MAC92	Prostate, Breast/Ovarian
268	830073			1	690			HBWBK27	Lung, Pancreas, Breast/Ovarian
269	830130			1	177			H2LAD55	Lung, Prostate, Breast/Ovarian
270	830134			16	1290			H2CBP53	Lung, Pancreas, Prostate, Colon, Breast/Ovarian

271	830135	neutrophil gelatinase associated lipocalin [Homo sapiens] >sp|P80188|NGAL_HUMAN NEUTROPHIL GELATINASE-ASSOCIATED LIPOCALIN PRECURSOR (NGAL) (P25) (25 KD ALPHA-2-MICROGLOBULIN-RELATED SUBUNIT OF MMP-9) (LIPOCALIN-2) (ONCOGENE 24P3). Length = 198	gi|929657	2	763	100	100	H2MAC06	Pancreas, Prostate, Breast/Ovarian
272	830148	snRNP polypeptide B [Homo sapiens] >sp|Q15182|Q15182 SNRNP POLYPEPTIDE B. Length = 285	gi|190247	96	839	79	79	HAICK77	Lung, Prostate, Breast/Ovarian
273	830149	threonyl-tRNA synthetase [Homo sapiens] >pir|A38867|YSHUT threonine--tRNA ligase (EC 6.1.1.3) - human Length = 712	gi|1464742	3	2333	95	95	H2CBC04	Lung, Pancreas, Prostate
274	830154	spectrin SH3 domain binding protein 1 [Homo sapiens] >sp|O76049|O76049 SPECTRIN SH3 DOMAIN BINDING PROTEIN 1. Length = 508	gi|3165429	2	1081	100	100	HYAAC49	Lung, Pancreas
275	830183			92	358			HWLQF08	Pancreas, Breast/Ovarian
276	830194	heat shock protein 84 - mouse >pir|B34461|B34461 heat shock protein 90 beta - rabbit (fragment) {SUB 1-25} >sp|P30947|HS9B_RABIT HEAT SHOCK PROTEIN HSP 90-BETA (HSP 84) (FRAGMENT). {SUB 2-25} >pir|S13268|S13268 heat shock protein, 90K - bovine (fragment)	pir|A35569|HHMS84	3	1043	100	100	HLDCP20	Lung, Pancreas, Breast/Ovarian
277	830207	(AF016437) contains similarity to a C2H2-type zinc finger [Caenorhabditis elegans] >sp|O16350|O16350 F13H6.1 PROTEIN. Length = 631	gi|2315332	173	1051	45	63	HWLMF07	Pancreas, Colon
278	830242			85	654			HWLUF58	Lung, Pancreas

279	830328	putative cyclin G1 interacting protein [Homo sapiens] >sp|O43257|O43257 PUTATIVE CYCLIN G1 INTERACTING PROTEIN. Length = 154	gi|2668505	304	954	81	81	HWLEL26	Lung, Colon, Breast/Ovarian
280	830340	putative cell surface antigen [Rattus norvegicus] >sp|P97881|P97881 PUTATIVE CELL SURFACE ANTIGEN. Length = 547	gi|1890275	1	336	63	81	HWLEG68	Pancreas, Colon
281	830341	peroxisomal acyl-coenzyme A oxidase, AOX [human, liver, Peptide, 661 aa] [Homo sapiens] Length = 661	bbs|144907	1	648	100	100	HSIAH79	Lung, Pancreas
282	830351			3	656			HWHQT21	Colon, Breast/Ovarian
283	830358			456	716			HSUAE53	Lung, Colon, Breast/Ovarian
284	830390	platelet membrane glycoprotein IIIa beta subunit [Homo sapiens] >sp|O15495|O15495 PLATELET MEMBRANE GLYCOPROTEIN IIIA BETA SUBUNIT. Length = 784	gi|2443452	2	523	90	90	HWGQA69	Pancreas, Colon
285	830400	phosphate carrier protein [Homo sapiens] >pir|B53737|B53737 phosphate carrier protein, form B - human Length = 361	gi|38262	2	1078	99	100	HWHPY68	Lung, Pancreas, Breast/Ovarian
286	830437	IgG Fc receptor I [Homo sapiens] >gi|292169 Fc gamma receptor I [Homo sapiens] >pir|A39878|A39878 Fc gamma (IgG) receptor I-A (high affinity) precursor - human >sp|Q92663|Q92663 FC GAMMA RECEPTOR I. Length = 374	gi|180279	3	1199	91	91	HWABG32	Lung, Colon

287	830458	HBp15/L22 [Sus scrofa] >gnl|PID|d1005074 HBp15/L22 [Mus musculus] >pir|JC2121|JC2121 heparin-binding protein 15 - pig >pir|JC2119|JC2119 heparin-binding protein 15 - mouse Length = 128	gnl|PID|d1005075	1	441	70	70	HDQMF96	Lung, Pancreas
288	830466			988	1260			HOEEZ61	Lung, Colon
289	830497	tenascin X [Homo sapiens] >sp|P78530|P78530 TENASCIN X (TENASCIN-X). >gi|2347137 (AF019413) tenascin X [Homo sapiens] {SUB 2593-4289} >pir|A42175|A42175 tenascin homolog 3.9kF3-3 - human (fragment) {SUB 2793-2880} >pir|B42175|B42175 tenascin homolog 3.9kF	gi|1841546	2	1531	99	99	HUFBX52	Lung, Breast/Ovarian
290	830511	carcinoembryonic antigen [Homo sapiens] >gi|178677 carcinoembryonic antigen precursor [Homo sapiens] >pir|A36319|A36319 carcinoembryonic antigen precursor - human >sp|P06731|CCEM_HUMAN CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E	gi|180223	3	1292	99	99	HWLGV67	Pancreas, Colon
291	830512	carcinoembryonic antigen [Homo sapiens] >gi|178677 carcinoembryonic antigen precursor [Homo sapiens] >pir|A36319|A36319 carcinoembryonic antigen precursor - human >sp|P06731|CCEM_HUMAN CARCINOEMBRYONIC ANTIGEN PRECURSOR (CEA) (MECONIUM ANTIGEN 100) (CD66E	gi|180223	3	2213	87	89	HUFCI29	Lung, Pancreas

292	830513			3	215			HPRTG72	Lung, Colon, Breast/Ovarian
293	830540	protein kinase MUK2 [Rattus norvegicus] >gi|2772514 serine/threonine protein kinase [Rattus norvegicus] >sp|P35465|PAK1_RAT SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21-ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MUK2). Length	gi|1399508	2	733	100	100	HTLHR67	Lung, Pancreas, Colon
294	830550	guanine nucleotide-binding regulatory protein-beta-2 subunit [Homo sapiens] >gi|339935 transducin beta-2 subunit [Homo sapiens] >gi|3135310 (AF053356) GNB2 [Homo sapiens] >pir|B26617|RGHUB2 GTP-binding regulatory protein beta-2 chain - human >sp|P11016|GB	gi|386751	3	500	100	100	HTWJC08	Lung, Breast/Ovarian
295	830567			141	377			HTTBH33	Lung, Pancreas
296	830586	(2'-5')oligoadenylate synthetase [Homo sapiens] Length = 364	gnl|PID|d1000487	2	1192	98	98	HKACP86	Pancreas, Prostate, Breast/Ovarian
297	830632	P2 gene for c subunit of mitochondrial ATP synthase gene product [Homo sapiens] >gnl|PID|d1002921 ATP synthase subunit c precursor [Homo sapiens] >pir|S34067|S34067 H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein P2 precursor, mitochondri	gi|38432	264	803	85	85	HTPCV95	Lung, Breast/Ovarian

298	830645	propionyl CoA carboxylase beta subunit, beta PCC {EC 6.4.1.3} [human, liver, placenta, HL 1008, Peptide, 539 aa] [Homo sapiens] >pir|A53020|A53020 propionyl-CoA carboxylase (EC 6.4.1.3) beta chain precursor - human >gi|3036995 propionyl-CoA carboxylase B	bbs|140816	54	1505	99	99	HTEDS58	Lung, Pancreas, Colon
299	830652	strong homology to human RING3 sequence [Homo sapiens] >sp|O60885|O60885 HUNKI MRNA. Length = 722	gnl|PID|e1290115	1	177	64	64	HUKFL74	Lung, Colon
300	830659	CDC42 GTP-binding protein [Canis familiaris] >gi|183490 GTP-binding protein G25K [Homo sapiens] >gi|293321 CDC42Mm [Mus musculus] >gi|1049309 CDC42 protein [Mus musculus] >pir|A39265|A39265 GTP-binding protein G25K, placental - human >pir|S57563|S57563 CD	gi|887408	118	714	100	100	HKAOE74	Lung, Pancreas, Breast/Ovarian
301	830696			2	514			HSTBJ95	Lung, Breast/Ovarian
302	830706			2457	2909			HELFG05	Pancreas, Breast/Ovarian
303	830743	ATP SYNTHASE EPSILON CHAIN, MITOCHONDRIAL (EC 3.6.1.34). Length = 50	sp|P56381|ATPE_HUMAN	53	262	100	100	HCBBA51	Lung, Colon
304	830770	p21-activated protein kinase [Homo sapiens] >pir|S58682|S58682 protein kinase, p21-activated (EC 2.7.1.-) - human Length = 525	gi|780808	1	498	99	99	HEMCG27	Lung, Colon, Breast/Ovarian
305	830830	(AF002822) cyclin B2 [Homo sapiens] >sp|G4101270|G4101270 CYCLIN B2. Length = 398	gi|4101270	99	1358	99	99	HROCE57	Lung, Pancreas, Colon

306	830838			1	747			HS2AF59	Lung, Pancreas, Colon, Breast/Ovarian
307	830851			2	718			HTXLJ25	Pancreas, Colon
308	830853			2	1183			HRDDS42	Pancreas, Colon
309	830856			542	874			HSAAX81	Colon, Breast/Ovarian
310	830862	ribosomal protein [Homo sapiens] >gi|453281 ribosomal protein S23 [Rattus norvegicus] >pir|S41955|S41955 ribosomal protein S23, cytosolic - rat >pir|S42105|S42105 ribosomal protein S23, cytosolic - human >pir|I52292|I52292 ribosomal protein S23 - rat >gnl	gnl|PID|d1003910	3	518	100	100	HLLCC05	Lung, Prostate, Breast/Ovarian
311	830879	(AJ002120) Zfx [Monodelphis domestica] >sp|O19019|O19019 ZFX TYPE GENE (FRAGMENT). Length = 180	gnl|PID|e354749	2	592	39	58	HVAAB82	Pancreas, Colon
312	830919			69	536			HOUHK65	Pancreas, Breast/Ovarian
313	830969	(AF005046) serine/threonine kinase [Homo sapiens] >gnl|PID|e1371371 (AJ011855) PAK4 protein [Homo sapiens] >sp|G4101587|G4101587 SERINE/THREONINE KINASE. Length = 591	gi|4101587	140	514	96	96	HOGAU20	Pancreas, Breast/Ovarian
314	830991	insulin-like growth factor-binding protein [Homo sapiens] >gi|386791 growth factor-binding protein-3 [Homo sapiens] >gi|398164 insulin-like growth factor binding protein 3 [Homo sapiens] >pir|A36578|IOHU3 insulin-like growth factor-binding protein 3 precu	gi|183116	2	607	86	86	HDLAE73	Pancreas, Breast/Ovarian

315	831002	cyclin [Homo sapiens] >gi|387005 proliferating cell nuclear antigen (PCNA) [Homo sapiens] >pir|A27445|WMHUET proliferating cell nuclear antigen - human >sp|P12004|PCNA_HUMAN PROLIFERATING CELL NUCLEAR ANTIGEN (PCNA) (CYCLIN). Length = 261	gi|181272	168	974	100	100	HOEMJ36	Colon, Breast/Ovarian
316	831003	T-plastin - human >sp|P13797|PLST_HUMAN T-PLASTIN. {SUB 4-630} >gi|190028 T-plastin polypeptide [Homo sapiens] {SUB 61-630} >gi|339848 T-plastin [Homo sapiens] {SUB 1-143} >gi|292832 T-plastin [Homo sapiens] {SUB 588-630} Length = 630	pir|A34789|A34789	91	2007	94	95	HAIBD64	Lung, Pancreas
317	831021			474	662			HE8BN45	Pancreas, Colon, Breast/Ovarian
318	831036	(AJ006068) dTDP-D-glucose 4,6-dehydratase [Homo sapiens] >sp|E1363774|E1363774 DTDP-D-GLUCOSE 4,6-DEHYDRATASE (EC 4.2.1.46). Length = 350	gnl|PID|e1363774	1	621	100	100	HNTSQ61	Pancreas, Colon
319	831071	lrp gene product [Homo sapiens] >pir|S57723|S57723 lrp protein - human >sp|Q14764|MVP_HUMAN MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN). Length = 896	gi|895840	67	2610	94	94	HWLEG93	Lung, Pancreas
320	831094			755	928			HNFEO67	Colon, Breast/Ovarian

321	831099	fibronectin receptor beta subunit precursor (AA -20 to 778) [Homo sapiens] >pir|B27079|B27079 fibronectin receptor beta chain precursor - human >sp|P05556|ITB1_HUMAN FIBRONECTIN RECEPTOR BETA SUBUNIT PRECURSOR (INTEGRIN BETA-1) (CD29) (INTEGRIN VLA-4 BETA	gi|31442	3	1697	99	100	HA5AB03	Lung, Pancreas, Colon, Breast/Ovarian
322	831113	4E-binding protein 1 [Homo sapiens] >pir|S50866|S50866 4E-BP1 protein - human >pir|JC5899|JC5899 initiation factor 4E-binding protein 1 - human >sp|Q13541|Q13541 4E-BINDING PROTEIN 1. Length = 118	gi|561630	1	414	100	100	HMWHP74	Lung, Pancreas, Colon, Breast/Ovarian
323	831120			1	1221			HWLHY12	Pancreas, Colon
324	831172	Similarity to Human hnRNP F protein (PIR Acc. No. S43484);	gnl|PID|e1349655	2	721	52	66	HLWBE22	Pancreas, Breast/Ovarian
325	831178	(AF042501) cytochrome b [Homo sapiens] >sp|O78829|O78829 CYTOCHROME B (FRAGMENT). Length = 380	gi|3372365	512	829	69	70	HDLAG61	Lung, Colon
326	831184			770	1399			HWLGP91	Lung, Pancreas, Colon
327	831203			3	545			HMICQ42	Pancreas, Colon, Breast/Ovarian
328	831210	TGF-beta masking protein large subunit [Rattus norvegicus] >pir|A38261|A38261 masking protein precursor - rat Length = 1712	gi|207286	1	498	86	91	HMEU62	Pancreas, Colon
329	831228			104	214			HMEAM30	Lung, Pancreas, Breast/Ovarian

330	831256	MLN 64 [Homo sapiens] >dbj||D38255_1 CAB1 [Homo sapiens] >pir|I38027|I38027 MLN 64 protein - human >sp|Q14849|Q14849 MLN64 MRNA. Length = 445	gi|951279	658	1164	94	94	HMTBL29	Lung, Pancreas
331	831257	MLN 64 [Homo sapiens] >dbj||D38255_1 CAB1 [Homo sapiens] >pir|I38027|I38027 MLN 64 protein - human >sp|Q14849|Q14849 MLN64 MRNA. Length = 445	gi|951279	323	862	91	91	HLWDQ05	Pancreas, Colon
332	831277			3	1310			HUTHD56	Lung, Pancreas, Colon
333	831317	inter-alpha-trypsin inhibitor light chain [Homo sapiens] >gi|32047 HC polypeptide [Homo sapiens] >gi|24479 precursor polypeptide [Homo sapiens] >gi|825614 alpha1-microglobulin [Homo sapiens] >pir|S13433|HCHU alpha-1-microglobulin/inter-alpha-trypsin inhib	gi|186600	193	1290	100	100	HLQAC21	Pancreas, Breast/Ovarian
334	831339	(AB012276) ATFx [Mus musculus] >sp|O70191|O70191 ATFX (FRAGMENT). >sp|G246896|G246896 ATFX=ATF4 RELATED PROTEIN. {SUB 1-37} >sp|G246899|G246899 ATFX=ATF-4-RELATED PROTEIN. {SUB 38-76} Length = 84	gnl|PID|d1026241	631	1029	90	93	HLICC93	Lung, Colon, Breast/Ovarian
335	831363	acyl coenzyme A:cholesterol acyltransferase, carboxylesterase, ACAT {EC 2.3.1.26} [human, liver, Peptide, 568 aa] [Homo sapiens] >sp|G415564|G415564 CARBOXYLESTERASE {EC 3.1.1.1}. {SUB 20-568} >gi|179930 carboxylesterase [Homo sapiens] {SUB 62-568} Length	bbs|156481	123	1871	98	98	HLDNR55	Lung, Colon

336	831367	D-dopachrome tautomerase [Homo sapiens] >gi|1864028 D-dopachrome tautomerase [Homo sapiens] >gi|3047378 (AF058293) D-dopachrome tautomerase [Homo sapiens] >gnl|PID|e311354 phenylpyruvate tautomerase II [Homo sapiens] >gi|2352915 (AF012434) D-dopachrome ta	gi|1805303	325	618	100	100	HLDDR74	Lung, Colon
337	831379	cDNA from hypercalcemic tumour [Rattus norvegicus] >pir|S28223|S28223 parathyroid hormone-like protein - rat >sp|Q05310|L10K_RAT LEYDIG CELL TUMOR 10 KD PROTEIN. Length = 93	gi|57064	3	383	90	95	HKQAC03	Lung, Pancreas, Colon, Breast/Ovarian
338	831385			96	377			HKIMC75	Lung, Pancreas, Colon, Breast/Ovarian
339	831390	aldehyde reductase (EC 1.1.1.2) [Homo sapiens] >gi|2707824 (AF036683) aldehyde reductase [Homo sapiens] >pir|A33851|A33851 alcohol dehydrogenase (NADP+) (EC 1.1.1.2) - human >sp|G2707824|G2707824 ALDEHYDE REDUCTASE. >sp|P14550|ALDX_HUMAN ALCOHOL DEHYDROGE	gi|178481	254	1312	94	94	HKGDF04	Lung, Pancreas

<table>
<tr><td>340</td><td>831391</td><td>islet regenerating protein [Homo sapiens] >pir|A35197|RGHU1A regenerating islet lectin 1-alpha precursor - human >sp|P05451|LITA_HUMAN LITHOSTATHINE 1 ALPHA PRECURSOR (PANCREATIC STONE PROTEIN) (PSP) (PANCREATIC THREAD PROTEIN) (PTP) (ISLET OF LANGERHANS</td><td>gi|190979</td><td>71</td><td>592</td><td>100</td><td>100</td><td>HLDBE06</td><td>Pancreas, Colon</td></tr>
<tr><td>341</td><td>831405</td><td>factor H homologue [Homo sapiens] >pir|I56100|I56100 factor H homologue - human >sp|Q03591|CFH1_HUMAN COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36). Length = 330</td><td>gi|183763</td><td>53</td><td>1078</td><td>94</td><td>94</td><td>HLDOB31</td><td>Lung, Pancreas, Colon, Breast/Ovarian</td></tr>
<tr><td>342</td><td>831442</td><td>PDGF associated protein [Homo sapiens] >sp|Q13442|HP28_HUMAN 28 KD HEAT- AND ACID-STABLE PHOSPHOPROTEIN (HASPP28) (PDGF ASSOCIATED PROTEIN). Length = 181</td><td>gi|1136584</td><td>2</td><td>595</td><td>60</td><td>60</td><td>HKAEB15</td><td>Lung, Pancreas, Colon, Breast/Ovarian</td></tr>
<tr><td>343</td><td>831476</td><td>dermatopontin [Homo sapiens] >pir|A47220|A47220 dermatopontin precursor - human >sp|Q07507|DERM_HUMAN DERMATOPONTIN PRECURSOR. >pir|S34838|S34838 tyrosine-rich acidic matrix protein - pig {SUB 101-144} Length = 201</td><td>gi|311614</td><td>1</td><td>630</td><td>91</td><td>91</td><td>HJMBK21</td><td>Lung, Pancreas, Colon</td></tr>
<tr><td>344</td><td>831488</td><td>similar to Saccharomyces cerevisiae Spt4; protein has potential N-terminal zinc-finger [Homo sapiens] >gi|1401053 SUPT4H [Homo sapiens] >gi|1401055 SUPT4H [Homo sapiens] >gi|1401066 Supt4h [Mus musculus] >gi|3779194 chromatin structural protein homolog [M</td><td>gi|1209779</td><td>158</td><td>580</td><td>100</td><td>100</td><td>HJBCG39</td><td>Colon, Breast/Ovarian</td></tr>
</table>

345	831518			240	467			HATCV09	Pancreas, Colon, Breast/Ovarian
346	831519	(AF062536) cullin 1 [Homo sapiens] >sp|O60719|O60719 CULLIN 1. >gi|4153866 (AC005229) cullin 1 [Homo sapiens] {SUB 1-263} Length = 776	gi|3139077	165	1712	100	100	HOECI49	Pancreas, Breast/Ovarian
347	831521			3	863			HIBCE91	Colon, Breast/Ovarian
348	831550	mel-13a protein - mouse Length = 132	pir|S65785|S65785	158	457	70	75	HCHNH46	Lung, Pancreas, Breast/Ovarian
349	831560			1474	1818			HCROA68	Pancreas, Breast/Ovarian
350	831562	fibromodulin [Homo sapiens] >sp|Q06828|FMOD_HUMAN FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN). Length = 376	gi|297091	28	1272	90	91	HEGAD80	Pancreas, Breast/Ovarian
351	831570	(AF042822) epithin [Mus musculus] >sp|G4104970|G4104970 EPITHIN. Length = 902	gi|4104970	2	1861	77	85	HLWCC68	Lung, Pancreas, Colon
352	831593			726	878			HHBFW28	Lung, Pancreas
353	831596	32 kd accessory protein [Bos taurus] >gi|190376 proton ATPase accessory subunit [Homo sapiens] {SUB 264-351} Length = 351	gi|736727	2	808	100	100	HHEDJ61	Colon, Breast/Ovarian
354	831627			1	903			HBJHI46	Lung, Pancreas
355	831649			1	738			HFTDD09	Lung, Colon
356	831664	transformation upregulated nuclear protein - human Length = 464	pir|S43363|S43363	180	1574	94	94	HFPCU40	Lung, Colon

357	831674	complement protein C8 beta subunit precursor [Homo sapiens] >pir|A43071|C8HUB complement C8 beta chain precursor - human >sp|P07358|CO8B_HUMAN COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR. Length = 591	gi|179720	1	1338	96	96	HLDOX36	Pancreas, Colon
358	831684	(AF053630) monocyte/neutrophil elastase inhibitor [Homo sapiens] >pir|S27383|S27383 elastase inhibitor - human >sp|P30740|ILEU_HUMAN LEUKOCYTE ELASTASE INHIBITOR (LEI) (MONOCYTE/NEUTROPHIL ELASTASE INHIBITOR) (EI). >sp|G2997692|G2997692 MONOCYTE/NEUTROPHI	gi|2997692	1	1311	96	96	HFOXE22	Pancreas, Colon
359	831687	Mpv17 [Mus musculus] >pir|S29031|S29031 mpv17 protein - mouse >sp|P19258|MPV1_MOUSE MPV17 PROTEIN. >gi|3252875 (AF038632) Mpv17 protein [Mus musculus] {SUB 155-176} Length = 176	gi|199790	60	305	89	93	HFKHD75	Pancreas, Colon
360	831726	rat ribosomal protein L36 [Rattus norvegicus] >pir|JN0483|JN0483 ribosomal protein L36 - rat Length = 105	gi|312345	77	454	98	98	HAGDQ96	Lung, Breast/Ovarian
361	831736			95	484			HLWEQ18	Colon, Breast/Ovarian
362	831762			37	720			HEQB179	Pancreas, Colon
363	831801	ear-2 gene product [Homo sapiens] >pir|S02709|S02709 ear-2 protein - human >sp|P10588|EAR2_HUMAN V-ERBA RELATED PROTEIN EAR-2. Length = 403	gi|31065	3	812	76	77	HKAHB85	Lung, Pancreas, Breast/Ovarian

364	831848			2018	2284			HE8AF82	Lung, Colon, Breast/Ovarian
365	831861	(AF076786) serum amyloid A-activating factor SAF-8 [Oryctolagus cuniculus] >sp|G3986442|G3986442 SERUM AMYLOID A-ACTIVATING FACTOR SAF-8 (FRAGMENT). Length = 214	gi|3986442	341	775	77	77	HJPCX51	Lung, Pancreas, Breast/Ovarian
366	831866	(AF054174) histone macroH2A1.2 [Homo sapiens] >sp|G3341992|G3341992 HISTONE MACROH2A1.2. Length = 371	gi|3341992	53	1186	100	100	HE6FG90	Lung, Colon
367	831878			2	661			HDTLN67	Colon, Breast/Ovarian
368	831899			1	693			HDTBQ51	Colon, Breast/Ovarian
369	831913	nuclear antigen H731 [Homo sapiens] >pir|JC5193|JC5193 nuclear protein H731 - human >sp|Q99834|Q99834 NUCLEAR ANTIGEN H731. Length = 458	gi|1825562	95	1132	96	97	HLYGA31	Lung, Colon
370	831972	p619 [Homo sapiens] >pir|S71752|S71752 giant protein p619 - human >sp|Q15751|Q15751 P619. Length = 4861	gi|1477565	331	855	33	58	HDPKK57	Lung, Pancreas, Breast/Ovarian
371	831985			425	805			HDPFP36	Lung, Pancreas, Colon, Breast/Ovarian
372	831986			30	467			HCHCH68	Pancreas, Colon, Breast/Ovarian
373	832010	(AL021918) b3418.1 (Kruppel related Zinc Finger protein 184) [Homo sapiens] >sp|O60792|O60792 B3418.1 (KRUPPEL RELATED ZINC FINGER PROTEIN 184). Length = 751	gnl|PID|e1293199	1	348	57	69	HDFUB44	Lung, Pancreas, Colon

374	832016	C protein (AA 1-159) [Homo sapiens] >pir|S01387|S01387 U1 snRNP protein C - human Length = 159	gi|37543	2	604	100	100	HTTDG34	Lung, Breast/Ovarian
375	832041	metalloelastase HME (EC 3.4.24.-) - human >sp|P39900|COGM_HUMAN MACROPHAGE METALLOELASTASE PRECURSOR (EC 3.4.24.65) (HME) (MATRIX METALLOPROTEINASE-12) (MMP-12). Length = 470	pir|A49499|A49499	54	1472	100	100	HDPGC33	Lung, Pancreas, Colon
376	832044	5-aminoimidazole-4-carboxamide-1-beta-D-ribonucl eotide transformylase/inosinicase [Homo sapiens] >gnl|PID|d1022617 5-aminoimidazole-4-carboxamide ribonucleotide transformylase [Homo sapiens] >pir|JC4642|JC4642 purH bifunctional enzyme - human >sp|Q13856|	gnl|PID|d1012226	1	1794	99	99	HGCOL40	Lung, Pancreas, Colon, Breast/Ovarian
377	832049	proteasome subunit HsC10-II [Homo sapiens] >pir|S55041|S55041 multicatalytic endopeptidase complex (EC 3.4.99.46) beta chain C10-II - human >sp|P49720|PRCT_HUMAN PROTEASOME THETA CHAIN (EC 3.4.99.46) (MACROPAIN THETA CHAIN) (MULTICATALYTIC ENDOPEPTIDASE C	gnl|PID|d1006190	84	710	99	100	HCFAU68	Lung, Pancreas, Breast/Ovarian
378	832122			427	846			HCUDT18	Lung, Pancreas, Colon, Breast/Ovarian
379	832148			246	380			HFIHN81	Colon, Breast/Ovarian
380	832197			433	642			HCQAH51	Pancreas, Breast/Ovarian
381	832237			290	553			HOCTE23	Lung, Colon
382	832246			66	959			HCMSD61	Lung, Pancreas

383	832256	ligand for eph-related receptor tyrosine kinases [Homo sapiens] >gi|1809292 putative EPH-related PTK receptor ligand LERK-8 [Homo sapiens] >sp|Q15768|EFB3_HUMAN EPHRIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LERK-8) (EPH-RELATED RECE	gi|1469782	1	81	100	100	HBXAC19	Pancreas, Colon, Breast/Ovarian
384	832280	(AF071747) topoisomerase II alpha [Homo sapiens] >sp|G3869316|G3869316 TOPOISOMERASE II ALPHA. Length = 1531	gi|3869316	2	1141	79	79	HNTSQ37	Lung, Colon, Breast/Ovarian
385	832285			1550	1783			HLTBQ50	Lung, Prostate
386	832294			1	666			HBMCR80	Lung, Colon
387	832326			472	1131			HJPAT43	Lung, Colon, Breast/Ovarian
388	832333	CENP-B protein [Ovis aries] >sp|P49451|CENB_SHEEP MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP-B) (FRAGMENT). Length = 239	gi|1016292	3	551	96	96	HCHMS55	Pancreas, Breast/Ovarian
389	832346			295	471			HBAGU45	Colon, Breast/Ovarian
390	832370	HER2 receptor [Homo sapiens] >gi|553282 c-erb-2 protein [Homo sapiens] {SUB 737-1031} >gi|553332 HER-2/neu [Homo sapiens] {SUB 1-191} >gi|183989 HER2 receptor (AA at 3) [Homo sapiens] {SUB 740-910} >gi|182169 c-erb B2/neu protein [Homo sapiens] {SUB 1081-	gi|306840	2	406	83	83	HFIEC83	Lung, Breast/Ovarian
391	832381			138	539			HATAA19	Pancreas, Breast/Ovarian

392	832394	platelet-endothelial tetraspan antigen 3 [Homo sapiens] >sp|P48509|C151_HUMAN PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN). Length = 253	gi|541613	2	847	85	85	HFTD21	Lung, Pancreas
393	832454	precursor polypeptide [Homo sapiens] >pir|A25971|C2HU complement C2 precursor - human >gi|187765 MHC complement component C2 [Homo sapiens] {SUB 21-46} Length = 752	gi|34628	160	357	100	100	HLQBT44	Prostate, Breast/Ovarian
394	832465			1	324			HAJBC51	Lung, Pancreas
395	832475	X box binding protein-1 [Homo sapiens] >pir|A36299|A36299 transcription factor hXBP-1 - human Length = 260	gi|306893	470	817	100	100	HTJMJ52	Pancreas, Breast/Ovarian
396	832495	EB1 [Homo sapiens] >pir|I52726|I52726 EB1 - human >sp|Q15691|Q15691 EB1. Length = 268	gi|998357	1	933	100	100	HAIDB85	Lung, Pancreas
397	832498	pyrroline-5-carboxylate synthase [Homo sapiens] >sp|G4097816|G4097816 PYRROLINE-5-CARBOXYLATE SYNTHASE. Length = 793	gi|4097816	2	1036	95	95	HLTGQ24	Lung, Pancreas
398	832501			736	996			HAGFI57	Lung, Pancreas, Colon
399	832505	protein synthesis factor [Homo sapiens] >sp|P47813|IF1A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 1A (EIF-1A) (EIF-4C). {SUB 2-144} Length = 144	gi|306725	61	648	100	100	HRABV57	Lung, Pancreas, Prostate
400	832539	protein synthesis initiation factor 4A [Mus musculus] Length = 408	gi|673433	472	1125	93	93	HRABO69	Lung, Breast/Ovarian
401	832554	HsGCN1 [Homo sapiens] >sp|Q99736|Q99736 HSGCN1 (FRAGMENT). Length = 1928	gi|2282576	409	927	99	99	HCHOX71	Pancreas, Breast/Ovarian

402	832569			2	667			HFCAE43	Lung, Colon
403	832578	(AL023777) rna binding protein [Schizosaccharomyces pombe] >sp|O74978|O74978 RNA BINDING PROTEIN. Length = 276	gnl|PID|e1295805	123	956	40	64	HBBBD67	Pancreas, Colon, Breast/Ovarian
404	832615			630	992			H2CBK94	Lung, Colon
405	832620			190	297			H2CBG53	Colon, Breast/Ovarian
406	832632	(AC002388) 60S ribosomal protein L30 isolog [Arabidopsis thaliana] >sp|O22165|O22165 60S RIBOSOMAL PROTEIN L30 ISOLOG. Length = 159	gi|2344898	41	592	52	69	H2CBD94	Lung, Colon, Breast/Ovarian
407	832633	putative phospho-beta-glucosidase [Bacillus stearothermophilus] >pir|D49898|D49898 cellobiose phosphotransferase system celC - Bacillus stearothermophilus >sp|Q45401|Q45401 PUTATIVE PHOSPHO-BETA-GLUCOSIDASE. Length = 245	gi|466475	3	566	52	64	HWACF51	Pancreas, Breast/Ovarian
408	833483			2	604			HCFCK33	Lung, Breast/Ovarian
409	834574	similar to S. cerevisiae longevity-assurance protein 1 (SP:P38703) [Caenorhabditis elegans] >sp|Q17870|Q17870 SIMILAR TO S. CEREVISIAE LONGEVITY-ASSURANCE PROTEIN 1. Length = 362	gi|1123105	634	1431	44	59	HHBEI26	Lung, Pancreas, Colon, Breast/Ovarian
410	834859	acidic calponin [human, kidney, Peptide, 329 aa] [Homo sapiens] >pir|JC4501|JC4501 acidic calponin - human >sp|Q15417|Q15417 ACIDIC CALPONIN. Length = 329	hbs|174416	53	541	99	100	HSTAT70	Lung, Pancreas, Colon, Breast/Ovarian

411	834861	factor activating exoenzyme S [Bos taurus] >gi|189953 phospholipase A2 [Homo sapiens] >gi|899459 14-3-3 protein [Homo sapiens] >pir|A38246|PSHUAM 14-3-3 protein zeta - human >pir|A47389|A47389 14-3-3 protein zeta - bovine >sp|P29312|143Z_HUMAN 14-3-3 PROT	gi|163042	74	967	99	99	HBXFL41	Lung, Pancreas, Prostate, Breast/Ovarian
412	834890	TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3). Length = 204	sp|Q64152|BTF3_MOUSE	70	588	90	91	H2CBT12	Lung, Pancreas, Prostate, Breast/Ovarian
413	835079			151	348			HOELH62	Lung, Pancreas, Breast/Ovarian
414	835554	homologue to sec61 [Rattus rattus] Length = 476	gi|206886	121	1287	98	98	HOHBH04	Lung, Pancreas
415	835560			2	574			HE9NK60	Lung, Pancreas
416	835723	immunoglobulin M heavy chain [Homo sapiens] >gi|38408 immunoglobulin M heavy chain [Homo sapiens] >pir|S37768|S37768 Ig mu chain C region - human Length = 453	gi|38406	48	1421	100	100	HLYFY90	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
417	835791	(AJ005890) JM1 [Homo sapiens] >sp|O60826|O60826 JM1 PROTEIN, COMPLETE CDS (CLONE LLNLC110M0111Q7 (RZPD BERLIN)AND LLNLC110K2140Q7 (RZPD BERLIN)). Length = 627	gnl|PID|e1289743	437	1177	87	87	HTXJH25	Pancreas, Breast/Ovarian
418	835817			1369	1554			HAJAZ17	Lung, Breast/Ovarian
419	835840			2	730			HHEOJ47	Lung, Pancreas
420	836048			2052	2276			HDQDV21	Lung, Prostate

421	836898	human P5 [Homo sapiens] >pir|JC4369|JC4369 P5 protein - human >sp|Q15084|ERP5_HUMAN PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1). Length = 440	gnl|PID|d1009061	3	1427	90	90	HWHPA75	Lung, Pancreas, Colon, Breast/Ovarian
422	836927	(AF027299) protein 4.1-G [Homo sapiens] >sp|O43491|O43491 PROTEIN 4.1-G. Length = 1005	gi|2739096	3	1196	84	84	HDTKY58	Lung, Pancreas
423	837344	S1R [Cowpox virus] >sp|O72763|O72763 S1R PROTEIN. Length = 210	gnl|PID|e1289272	38	658	48	58	HLDAG32	Lung, Prostate
424	837789	bikunin [Homo sapiens] >sp|O00271|O00271 BIKUNIN. Length = 252	gi|2065529	365	1231	91	91	HDABR73	Colon, Breast/Ovarian
425	838549	(AL023828) Y17G7B.14 [Caenorhabditis elegans] >sp|E1323274|E1323274 Y17G7B.14 PROTEIN. Length = 364	gnl|PID|e1323274	2	853	42	55	HDQDW56	Lung, Breast/Ovarian
426	838754			437	1198			HTEQK83	Lung, Pancreas, Breast/Ovarian
427	838768			570	770			HWBCW80	Lung, Pancreas, Breast/Ovarian
428	839486	fibronectin precursor [Homo sapiens] >gi|4096846 fibronectin [Homo sapiens] {SUB 76-454} >gi|4096848 fibronectin [Homo sapiens] {SUB 1892-2103} >gi|182706 fibronectin [Homo sapiens] {SUB 1921-2040} >gi|182684 fibronectin [Homo sapiens] {SUB 2233-2328} Len	gi|31397	2	493	98	98	HSLGC71	Lung, Breast/Ovarian
429	839561	p34 protein [Rattus sp.] >pir|S36779|S36779 ribosome-binding protein p34 - rat >sp|Q63742|Q63742 P34 PROTEIN. Length = 307	gnl|PID|d1003291	45	1133	86	88	HUVFB27	Lung, Pancreas, Prostate

430	839816	similar to plasmodium merozite surface antigen precursor (SP:P04933) [Caenorhabditis elegans] >sp|Q22585|Q22585 SIMILAR TO PLASMODIUM MEROZITE SURFACE ANTIGEN PRECURSOR. Length = 634	gi|1293808	1	432	46	61	HWADY11	Lung, Breast/Ovarian
431	840068	UMP-CMP kinase [Sus scrofa] >pir|JC4181|JC4181 cytidylate kinase (EC 2.7.4.14) - pig >sp|Q29561|KCY_PIG UMP-CMP KINASE (EC 2.7.4.14) (CYTIDYLATE KINASE) (DEOXYCYTIDYLATE KINASE). Length = 196	gnl|PID|d1006692	2	757	97	99	HE8EH64	Lung, Pancreas, Breast/Ovarian
432	840279	(AF062328) p120 catenin isoform 1AB [Homo sapiens] >sp|O60715|O60715 P120 CATENIN ISOFORMS 1AB, 2AB, 3AB AND 4AB. >gi|3152823 (AF062322) p120 catenin isoform 2AB [Homo sapiens] {SUB 55-962} >gi|3152855 (AF062338) p120 catenin isoform 3AB [Homo sapiens] {S	gi|3152835	219	1493	93	93	HSRBI81	Lung, Pancreas
433	840489	connective tissue growth factor [Homo sapiens] >gi|474934 connective tissue growth factor [Homo sapiens] >pir|A40551|A40551 connective tissue growth factor - human >sp|P29279|CTGF_HUMAN CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR. >gi|984956 connective tiss	gi|180924	1038	1370	100	100	HOEMS29	Lung, Pancreas

434	840538	glycyl tRNA synthetase [Homo sapiens] >pir|A55314|A55314 glycine--tRNA ligase (EC 6.1.1.14) precursor - human >gi|600727 glycyl-tRNA synthetase [Homo sapiens] {SUB 55-739} >gi|3845409 (AC004976) glycyl tRNA synthetase [Homo sapiens] {SUB 348-739} Length =	gnl|PID|d1006904	1	2298	100	100	HYAAN81	Lung, Pancreas, Prostate, Breast/Ovarian
435	840545			145	1302			HMCFK75	Lung, Pancreas, Colon, Breast/Ovarian
436	840549			1	492			HWHGB33	Lung, Prostate
437	840551	IgG Fc binding protein [Homo sapiens] Length = 5405	gnl|PID|d1020288	3	1409	93	93	HWLKM77	Lung, Prostate, Colon
438	840557			346	1014			H6EDS19	Prostate, Colon
439	840561	putative [Mus musculus] >pir|S15785|S15785 heat-stable antigen-related hypothetical protein HSA-C - mouse >sp|Q61692|Q61692 HSA-C GENE CODING FOR HEAT STABLE ANTIGEN. Length = 141	gi|51442	385	495	48	72	HLIBZ07	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
440	840562	(AB008549) type 1 procollagen C-proteinase enhancer protein [Homo sapiens] >gi|3135316 (AF053356) PCOLCE [Homo sapiens] >sp|O14550|O14550 TYPE 1 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN. Length = 449	gi|2589011	103	1476	96	96	HSSDI65	Lung, Pancreas, Prostate, Colon
441	840564	PQ-rich protein [Homo sapiens] >pir|S58222|S58222 PQ-rich protein - human >sp|Q15184|Q15184 PQ-RICH PROTEIN. Length = 400	gi|929660	2	688	67	68	HPJDB01	Lung, Pancreas

442	840572	putative [Homo sapiens] >pir|I54339|I54339 proto-oncogene - human >sp|P35226|BMI1_HUMAN DNA-BINDING PROTEIN BMI-1. Length = 326	gi|291873	3	1172	95	95	HTGAZ34	Prostate, Colon
443	840600			3	119			HYABI30	Prostate, Breast/Ovarian
444	840604	Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE);	gnl|PID|e1344589	1	1359	82	87	HWLHN58	Lung, Pancreas, Prostate, Breast/Ovarian
445	840608	olfactomedin [Rana catesbeiana] >pir|A47442|A47442 olfactomedin precursor - bullfrog >sp|Q07081|OLFM_RANCA OLFACTOMEDIN PRECURSOR (OLFACTORY MUCUS PROTEIN). Length = 464	gi|294502	200	1549	55	75	HWLFY46	Pancreas, Colon
446	840620			776	1267			HTXGB37	Lung, Prostate
447	840625			138	257			HTXDT74	Lung, Prostate
448	840626	nicotinamide N-methyltransferase [Homo sapiens] >gi|1063610 nicotinamide N-methyltransferase [Homo sapiens] >pir|A54060|A54060 nicotinamide N-methyltransferase (EC 2.1.1.1) - human >sp|P40261|NNMT_HUMAN NICOTINAMIDE N-METHYLTRANSFERASE (EC 2.1.1.1). Lengt	gi|494989	485	1282	100	100	HULAS90	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
449	840638			16	351			HTTDV02	Prostate, Breast/Ovarian
450	840649	BL34=B cell activation gene [human, Peptide, 196 aa] [Homo sapiens] >pir|I56165|I56165 B cell activation protein BL34 - human Length = 196	bbs|129951	1	651	100	100	HTWCY84	Lung, Prostate
451	840651			2	706			HTTAD76	Pancreas, Prostate

452	840666			2	826			HTOAF86	Lung, Prostate
453	840681			157	2187			HTAER63	Lung, Prostate
454	840682	siah binding protein 1 [Homo sapiens] >sp|Q99628|Q99628 SIAH BINDING PROTEIN 1 (FRAGMENT). Length = 541	gi|1809248	1	1734	99	99	HE9PW64	Lung, Breast/Ovarian
455	840684			3	539			HTGBT14	Pancreas, Prostate, Breast/Ovarian
456	840697			96	560			HTECA52	Lung, Prostate
457	840698	t-complex-type molecular chaperone TCP1 - human >gi|339211 t-complex 1 protein [Homo sapiens] {SUB 308-365} Length = 556	pir|S10486|S10486	507	1853	96	97	HDABW50	Pancreas, Prostate
458	840708			1200	1487			HTEAF73	Lung, Prostate
459	840714	(AF053304) mitotic checkpoint component Bub3 [Homo sapiens] >gi|2921873 (AF047472) spleen mitotic checkpoint BUB3 [Homo sapiens] >gi|3639060 (AF081496) kinetochore protein BUB3 [Homo sapiens] >sp|O43684|O43684 SPLEEN MITOTIC CHECKPOINT BUB3. Length = 328	gi|2981231	175	1170	100	100	HTEGU90	Lung, Pancreas, Prostate, Breast/Ovarian
460	840716	(AC005326) asparagine synthetase [Homo sapiens] >sp|G3341715|G3341715 ASPARAGINE SYNTHETASE. >gi|703119 asparagine synthetase [Homo sapiens] {SUB 1-83} Length = 561	gi|3341715	166	1860	94	94	HSYAJ64	Lung, Prostate, Colon, Breast/Ovarian
461	840721			2	1324			HSUSE92	Lung, Pancreas, Prostate, Colon

462	840735	(AC002425) Gene product with similarity to Rat P8 [Homo sapiens] >gi|3202004 (AF069073) P8 protein [Homo sapiens] >gi|3202006 (AF069074) P8 protein [Homo sapiens] >sp|O60356|O60356 GENE PRODUCT WITH SIMILARITY TO RAT P8. Length = 82	gi|2947054	111	392	64	64	HSRDN44	Lung, Pancreas, Prostate, Breast/Ovarian
463	840738			985	1230			HTOJK11	Prostate, Colon
464	840745	52-kD SS-A/Ro autoantigen [Homo sapiens] Length = 475	gi|338490	2	694	46	63	HSSGC06	Lung, Prostate, Colon
465	840747	(AC004522) Zn-alpha2-glycoprotein [Homo sapiens] >sp|O60386|O60386 ZN-ALPHA2-GLYCOPROTEIN. Length = 334	gi|3006228	368	877	95	95	HLDOL02	Lung, Pancreas, Breast/Ovarian
466	840756	(AB005624) rig-analog DNA-binding protein [Sus scrofa] >gi|306898 rig-analog protein (putative); putative [Homo sapiens] >gi|337416 human homologue of rat insulinoma gene (rig); putative [Homo sapiens] >gi|305361 Rig DNA-binding protein (putative); putati	gnl|PID|d1022359	148	480	97	97	HCHBQ33	Lung, Pancreas, Colon, Breast/Ovarian
467	840776	Notch3 [Homo sapiens] >sp|G2668592|G2668592 NOTCH3. Length = 2321	gi|2668592	2	364	82	82	HSKJZ22	Lung, Breast/Ovarian
468	840784	aldehyde dehydrogenase 6 [Homo sapiens] >pir|A55684|A55684 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 6 precursor, salivary - human >sp|P47895|DHA6_HUMAN ALDEHYDE DEHYDROGENASE 6 (EC 1.2.1.5). Length = 512	gi|544482	1	618	94	95	HSKAC75	Lung, Prostate, Colon, Breast/Ovarian

469	840788	P1 gene for c subunit of human mitochondrial ATP synthase gene product [Homo sapiens] >gnl|PID|d1002920 ATP synthase subunit c precursor [Homo sapiens] >pir|S34066|S34066 H+-transporting ATP synthase (EC 3.6.1.34) lipid-binding protein P1 precursor, mitoc	gi|38430	59	484	85	85	HHFUM32	Lung, Prostate, Colon, Breast/Ovarian
470	840794			162	1646			HOHBT28	Lung, Pancreas, Prostate, Colon
471	840797	OSF-2p1 [Homo sapiens] >pir|S36111|S36111 osteoblast-specific factor 2 - human >sp|Q15064|Q15064 OSF-2P1. Length = 779	gnl|PID|d1003341	2	2371	93	93	HDTIM52	Pancreas, Breast/Ovarian
472	840799			292	510			HWBCI48	Lung, Pancreas, Colon, Breast/Ovarian
473	840818	translational initiation factor eIF-2, alpha subunit [Homo sapiens] >sp|P05198|IF2A_HUMAN EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2- ALPHA). {SUB 2-315} Length = 315	gi|181995	3	806	100	100	HHBHM68	Lung, Prostate
474	840822	fatty acid synthase [Homo sapiens] >pir|G01880|G01880 fatty-acid synthase (EC 2.3.1.85) - human >sp|Q16702|Q16702 FATTY ACID SYNTHASE (EC 2.3.1.85) (FATTY-ACID SYNTHASE). Length = 2509	gi|915392	1423	2367	93	93	HGBHX28	Lung, Prostate, Colon, Breast/Ovarian
475	840830	diubiquitin [Homo sapiens] >sp|O15205|O15205 DIUBIQUITIN. Length = 165	gnl|PID|e321293	1	573	99	99	HFXHP85	Pancreas, Prostate

476	840846	glutathione S-transferase Ha subunit 1 (EC 2.5.1.18) [Homo sapiens] >gi|306815 glutathione S-transferase (GST, EC 2.5.1.18) [Homo sapiens] >gi|306809 glutathione S-transferase [Homo sapiens] >bbs|76373 glutathione S-transferase Ha1 subunit {EC 2.5.1.18} |	gi|306810	144	833	95	95	HFVHP57	Prostate, Breast/Ovarian
477	840848	prohibitin [human, Peptide, 272 aa] [Homo sapiens] >pir|I52690|I52690 prohibitin - human >sp|P35232|PHB_HUMAN PROHIBITIN. Length = 272	bbs|85658	81	917	93	93	HHBHM75	Lung, Pancreas, Prostate, Breast/Ovarian
478	840860	NAP [Homo sapiens] >pir|S40510|S40510 nucleosome assembly protein 1-like 1 - human >sp|P55209|NPL1_HUMAN NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 1 (NAP-1 RELATED PROTEIN). Length = 391	gi|189067	92	1309	80	80	HDTLJ39	Lung, Pancreas, Colon, Breast/Ovarian
479	840861	(AL021546) Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1) [Homo sapiens] >sp|O43714|O43714 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) (CYTOCHROME-C OXIDASE) (CYTOCHROME OXIDASE) (CYTOCHROME A(3)) (CYTOCHROME AA(3)	gnl|PID|e1248288	2	520	100	100	HFPBO29	Lung, Prostate, Breast/Ovarian
480	840871	DNA polymerase delta small subunit [Homo sapiens] >pir|I38950|I38950 DNA-directed DNA polymerase (EC 2.7.7.7) delta regulatory chain - human >sp|P49005|DPD2_HUMAN DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7). Length = 469	gi|1008458	2	628	99	99	HSDJX61	Pancreas, Colon, Breast/Ovarian

481	840874	secreted cyclophilin-like protein [Homo sapiens] >gi|181335 cyclophilin B [Homo sapiens] {SUB 9-216} >gi|181250 cyclophilin [Homo sapiens] {SUB 10-216} Length = 216	gi|337999	1	873	94	94	HFTDK64	Lung, Prostate
482	840878	unknown [Homo sapiens] >sp|P41271|DAN_HUMAN ZINC FINGER PROTEIN DAN (N03). Length = 180	gnl|PID|d1006216	227	676	99	100	H2MBT19	Lung, Pancreas, Colon, Breast/Ovarian
483	840880			153	320			HFIXK16	Prostate, Colon, Breast/Ovarian
484	840884	mutY homolog [Homo sapiens] >sp|Q15830|Q15830 MUTY HOMOLOG. Length = 535	gi|1458228	108	1565	99	99	HBCH18	Lung, Prostate
485	840907			103	366			HETAD58	Pancreas, Prostate
486	840926			76	1347			HEOMT66	Lung, Pancreas, Prostate
487	840932	ATP synthase beta subunit precursor [Homo sapiens] >pir|A33370|A33370 H+-transporting ATP synthase (EC 3.6.1.34) beta chain precursor, mitochondrial - human >sp|P06576|ATPB_HUMAN ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL PRECURSOR (EC 3.6.1.34). >gi|28931 be	gi|179281	2	1675	93	93	HFBB89	Lung, Prostate
488	840940	carbonyl reductase [Sus scrofa] >pir|JN0703|JN0703 carbonyl reductase (NADPH) (EC 1.1.1.184) - pig >sp|Q29529|CBR2_PIG LUNG CARBONYL REDUCTASE [NADPH] (EC 1.1.1.184) (NADPH-DEPENDENT CARBONYL REDUCTASE) (LCR). Length = 244	gnl|PID|d1004479	277	678	61	76	HCHNJ32	Pancreas, Breast/Ovarian

489	840947			2	565			HEGAN45	Lung, Pancreas, Prostate, Breast/Ovarian
490	840959	signal peptidase complex 25 kDa subunit [Canis familiaris] >pir|A55012|A55012 signal peptidase 25k chain - dog Length = 226	gi|533111	2	712	99	99	HEDAD53	Lung, Pancreas, Prostate, Breast/Ovarian
491	840964			177	344			HE8UK92	Prostate, Colon
492	840979	transcription factor-like protein 4 - human Length = 298	pir|JC5333|JC5333	11	631	99	100	HE9HD45	Lung, Pancreas, Prostate, Colon
493	840984	p167 [Homo sapiens] >gnl|PID|d1010130 The KIAA0139 gene product is related to mouse centrosomin B. [Homo sapiens] >gi|2501783 translation initiation factor 3 large subunit [Homo sapiens] >sp|Q14152|Q14152 KIAA0139 PROTEIN. >gi|1399801 p167 [Homo sapiens]	gi|1808985	3	3017	91	91	HE8OC40	Lung, Pancreas, Prostate, Breast/Ovarian
494	840986			1	693			HE8TB60	Pancreas, Prostate, Colon
495	840988			1	465			HE8QQ04	Pancreas, Prostate, Breast/Ovarian
496	840990	(AB010415) dTDP-4-keto-L-rhamnose reductase [Actinobacillus actinomycetemcomitans] >sp|O66251|O66251 DTDP-4-KETO-L-RHAMNOSE REDUCTASE. Length = 294	gnl|PID|d1029073	157	1140	32	59	HE8AM92	Pancreas, Prostate
497	840992	nidogen gene product [Homo sapiens] Length = 1246	gnl|PID|e218221	3	194	96	98	HE8BX38	Lung, Prostate, Colon, Breast/Ovarian
498	841009	sin3 associated polypeptide p18 [Homo sapiens] >sp|O00422|O00422 SIN3 ASSOCIATED POLYPEPTIDE P18. Length = 153	gi|2108210	59	523	92	92	HDTGP88	Lung, Pancreas, Prostate, Colon, Breast/Ovarian

499	841012	ribosomal protein L39 [Homo sapiens] >gnl|PID|d1012131 ribosomal protein L39 [Homo sapiens] >gi|575382 ribosomal protein L39 [Rattus norvegicus] >pir|JC4229|R6RT39 ribosomal protein L39 - rat >pir|G02654|G02654 ribosomal protein L39 - human Length = 51	gi|1373419	2	217	100	100	HSKXP01	Lung, Pancreas, Breast/Ovarian
500	841016	connexin 43 [Homo sapiens] >gi|29917 gap junction protein (AA 1-382) [Homo sapiens] >pir|A35853|A35853 gap junction protein Cx43, cardiac - human >sp|P17302|CXA1_HUMAN GAP JUNCTION ALPHA-1 PROTEIN (CONNEXIN 43) (CX43) (GAP JUNCTION 43 KD HEART PROTEIN). {	gi|181209	1	810	94	94	HDTDH13	Lung, Pancreas, Prostate, Colon
501	841017			402	683			HE2AY01	Lung, Prostate
502	841021			983	1357			HNAAE75	Lung, Pancreas, Colon, Breast/Ovarian
503	841032	(AB000910) ribosomal protein [Sus scrofa] >gi|1684917 L44-like ribosomal protein [Homo sapiens] >gi|1666702 ribosomal protein [Mus musculus] >gi|206732 ribosomal protein L36a [Rattus norvegicus] >pir|A29820|R6RT36 ribosomal protein L36a - rat Length = 106	gnl|PID|d1019960	3	395	100	100	HDQAD36	Lung, Colon
504	841051			656	880			HDPDC65	Lung, Pancreas
505	841064	small subunit ribonucleotide reductase [Homo sapiens] >pir|S25854|S25854 ribonucleoside-diphosphate reductase (EC 1.17.4.1) small chain - human Length = 389	gi|36155	6	1244	96	96	HDPMF32	Prostate, Colon, Breast/Ovarian

506	841069			81	809			HDPMJ48	Prostate, Breast/Ovarian
507	841072	regulatory protein [Mus musculus] >gi|452276 npdcf-1 [Mus musculus] >pir|I48691|I48691 regulatory protein - mouse >sp|Q64322|NPD1_MOUSE NPDC-1 PROTEIN PRECURSOR. Length = 332	gi|456107	162	1139	91	95	HDPGF81	Lung, Prostate, Colon, Breast/Ovarian
508	841078			521	706			HDPKD92	Pancreas, Prostate
509	841080	HCNGP gene product [Mus musculus] >pir|S26660|S26660 HCNGP protein - mouse >sp|Q02614|HCGP_MOUSE TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP. Length = 308	gi|57912	1	936	88	88	HDPJR07	Prostate, Breast/Ovarian
510	841088	quinone oxidoreductase [Homo sapiens] >gi|516534 quinone oxidoreductase2 [Homo sapiens] >pir|A32667|A32667 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) 2 - human Length = 231	gi|190818	320	1096	100	100	HDPFX64	Lung, Pancreas, Prostate, Breast/Ovarian
511	841092			1187	1402			HJMBH15	Lung, Colon
512	841095	L protein (AA 1-558) [Homo sapiens] >pir|A33616|A33616 heterogeneous ribonuclear particle protein L - human Length = 558	gi|32356	2	904	84	84	H2LAT51	Lung, Pancreas, Colon, Breast/Ovarian
513	841096	(AB013357) 49 kDa zinc finger protein [Mus musculus] Length = 460	gnl|PID|d1038083	510	1907	80	80	HCFLJ15	Lung, Pancreas, Breast/Ovarian
514	841102			2	256			HDLAV12	Lung, Pancreas, Prostate, Breast/Ovarian
515	841104	zinc finger protein [Homo sapiens] >pir|S35305|S35305 finger protein ZNF91 - human Length = 1191	gi|186774	712	2451	54	70	HDLAB16	Pancreas, Prostate, Breast/Ovarian
516	841108	factor XIII a subunit [Homo sapiens] Length = 732	gi|182309	3	1838	99	99	HDPFE82	Lung, Pancreas, Colon

517	841118			320	487			HDLAE34	Lung, Pancreas, Prostate
518	841119	C11 protein [Homo sapiens] >gi|1890300 eukaryotic release factor 1 [Homo sapiens] >gnl|PID|e118068 C11 protein [Mesocricetus auratus] >pir|S50853|S50853 translation releasing factor eRF-1 - human >sp|P46055|ERF1_HUMAN EUKARYOTIC PEPTIDE CHAIN RELEASE FACT	gnl|PID|e118910	123	1367	100	100	HDPAE95	Lung, Pancreas, Prostate
519	841124	similar to deoxyribose-phosphate aldolase [Caenorhabditis elegans] >sp|Q19264|DEOC_CAEEL PUTATIVE DEOXYRIBOSE-PHOSPHATE ALDOLASE (EC 4.1.2.4) (PHOSPHODEOXYRIBOALDOLASE) (DEOXYRIBOALDOLASE). Length = 303	gi|1019952	2	358	62	80	HDAAB17	Prostate, Colon
520	841137	(AF096285) serine-threonine kinase receptor-associated protein [Mus musculus] >sp|G4063383|G4063383 SERINE-THREONINE KINASE RECEPTOR-ASSOCIATED PROTEIN. Length = 351	gi|4063383	3	848	98	99	HDAAP84	Lung, Pancreas, Prostate, Breast/Ovarian
521	841143	fibrillarin [Homo sapiens] >pir|A38712|A38712 fibrillarin - human >gi|3399667 (AC005393) FBRL_HUMAN; 34 KD NUCLEOLAR SCLERODERMA ANTIGEN [Homo sapiens] {SUB 4-321} Length = 321	gi|31395	39	1040	100	100	HCRMJ87	Pancreas, Prostate, Breast/Ovarian
522	841148			2	1807			HCRNF38	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
523	841149			324	797			HCRBS04	Prostate, Breast/Ovarian

524	841151	keratin [Carassius auratus] Length = 455	gi|212995	2	1399	45	64	HCRNY54	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
525	841155			103	561			HCHOF85	Prostate, Breast/Ovarian
526	841161	(AB014458) ubiquitin specific protease [Homo sapiens] >sp|D1035685|D1035685 UBIQUITIN SPECIFIC PROTEASE. Length = 785	gnl|PID|d1035685	3	1199	95	95	HCLCA56	Lung, Prostate
527	841162	set [Homo sapiens] >pir|A57984|A45018 template activating factor-I, splice form beta - human Length = 277	gi|338039	284	1063	99	100	HCWFR92	Prostate, Colon
528	841163	histone H2A [Mus musculus domesticus] >pir|S45110|S45110 histone H2A - mouse >sp|Q64426|Q64426 HISTONE H2A (FRAGMENT). Length = 137	gi|817939	201	665	100	100	HBMBF44	Pancreas, Breast/Ovarian
529	841169			21	440			HCFOF83	Lung, Prostate, Colon, Breast/Ovarian
530	841172	CLN3 protein [Homo sapiens] >gnl|PID|e283670 CLN3 protein [Homo sapiens] >gi|2947055 (AC002425) CLN3 [Homo sapiens] >gi|3337387 (AC002544) CLN [Homo sapiens] >gi|4102729 (AF015593) CLN3 protein [Homo sapiens] >pir|A57219|A57219 Batten disease-related prot	gi|1039423	291	740	100	100	HCHAG93	Prostate, Breast/Ovarian
531	841174	zinc finger protein 7 (ZFP7) [Homo sapiens] >pir|A34612|A34612 zinc finger protein ZNF7 - human Length = 686	gi|340446	3	386	98	98	HCHAW34	Prostate, Breast/Ovarian

532	841179	(AF069517) RNA binding protein DEF-3 [Homo sapiens] >sp|O75524|O75524 RNA BINDING PROTEIN DEF-3. Length = 1123	gi|3212101	549	1742	85	85	HCHBU86	Lung, Pancreas, Prostate
533	841183	keratin 18 [Homo sapiens] >gi|307081 keratin 18 precursor [Homo sapiens] >gi|34037 cytokeratin 18 [Homo sapiens] >pir|S05481|S05481 keratin 18, type I, cytoskeletal - human >sp|P05783|K1CR_HUMAN KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 1	gi|386844	1	501	80	92	HCHCE20	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
534	841186	(AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus] >sp|O88719|O88719 CMP-N-ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLYLTRANSFERASE) (CMP-SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE). Length = 432	gnl|PID|e1314953	78	1421	95	97	HCFCG26	Lung, Prostate
535	841204	similar to beta-mannosyltransferase [Caenorhabditis elegans] >sp|Q22797|Q22797 SIMILAR TO BETA-MANNOSYLTRANSFERASE. Length = 487	gi|470340	1	1407	51	72	HCEFZ02	Lung, Pancreas, Prostate, Colon
536	841206			251	1192			HCEEM52	Lung, Prostate
537	841207	(AF062484) SDP8 [Mus musculus] >sp|O70493|O70493 SDP8. Length = 165	gi|3126981	193	585	41	63	HMTAR23	Prostate, Colon
538	841211	(AC004908) zinc finger protein from gene of uncertain exon structure; similar to Q99676 (PID:g3025333) [Homo sapiens] Length = 430	gi|4159888	110	766	47	62	HCEDM42	Prostate, Breast/Ovarian

539	841225	membrane protein [Homo sapiens] >gi|1048989 CD9 antigen [Homo sapiens] >gi|34769 MRP-1 (motility related protein) [Homo sapiens] >bbs|131345 CD9 antigen [human, leukocytes, Peptide, 228 aa] [Homo sapiens] >pir|A46123|A40402 CD9 antigen - human >sp|P21926|	gi|508496	41	865	88	88	HCRBB01	Lung, Pancreas, Prostate, Colon
540	841229	P1cdc47 [Homo sapiens] >pir|S70583|S70583 CDC47 homolog - human >sp|P33993|MCM7_HUMAN DNA REPLICATION LICENSING FACTOR MCM7 (CDC47 HOMOLOG) (P1.1-MCM3). >gnl|PID|d1006386 hMCM2 [Homo sapiens] {SUB 177-719} Length = 719	gnl|PID|d1010177	1	2298	98	98	HCE1D58	Lung, Pancreas, Prostate, Breast/Ovarian
541	841237	NAD(P)H:menadione oxidoreductase [Homo sapiens] >gi|189292 NAD(P)H:quinone oxireductase [Homo sapiens] >pir|A41135|A30879 NAD(P)H dehydrogenase (quinone) (EC 1.6.99.2) 1 - human >sp|P15559|DHQU_HUMAN NAD(P)H DEHYDROGENASE (QUINONE) 1 (EC 1.6.99.2) (QUINON	gi|189246	141	1028	95	95	HBMTA19	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
542	841241	Thy-1 [Homo sapiens] >pir|A02106|TDHU Thy-1 membrane glycoprotein precursor - human Length = 161	gi|339683	128	622	86	87	HBXFG67	Lung, Pancreas, Prostate, Breast/Ovarian
543	841259	(AD001528) spermidine aminopropyltransferase [Homo sapiens] >sp|O00544|O00544 SPERMIDINE AMINOPROPYLTRANSFERASE. Length = 366	gi|2198557	3	1199	93	93	HCEIC53	Lung, Pancreas, Prostate, Breast/Ovarian

544	841260	FKBP51 [Homo sapiens] >pir|JC5422|JC5422 FK506-binding protein, FKBP51 - human >sp|Q13451|FKB5_HUMAN 51 KD FK506-BINDING PROTEIN (FKBP51) (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (EC 5.2.1.8) (PPIASE) (ROTAMASE) (54 KD PROGESTERONE RECEPTOR-ASSOCIATED IMMUNO	gi|1916641	3	863	88	91	HBODM14	Lung, Prostate
545	841264			1	618			HBJHU33	Lung, Pancreas, Prostate
546	841275	Lutheran blood group glycoprotein [Homo sapiens] >pir|I38000|I38000 Lutheran blood group glycoprotein precursor - human >sp|P50895|LU_HUMAN LUTHERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B-CAM CELL SURFACE GLYCOPROTEIN) (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN	gi|603560	2	1183	89	89	HBGMO35	Prostate, Breast/Ovarian
547	841311	(AF019661) zeta proteasome chain; PSMA5 [Mus musculus] >sp|G3805976|G3805976 ZETA PROTEASOME CHAIN. Length = 241	gi|3805976	45	836	100	100	HCFMY64	Lung, Pancreas, Prostate, Breast/Ovarian
548	841313	neuronal protein 15.6 [unidentified] >sp|O09111|O09111 NEURONAL PROTEIN 15.6. Length = 133	gnl|PID|e274746	11	544	75	82	HBGNM82	Lung, Prostate, Colon, Breast/Ovarian
549	841317			1155	1553			HAPSG63	Lung, Prostate
550	841322	unnamed protein product [unidentified] >gi|496609 basic transcripion factor 2, 44 kD subunit [Homo sapiens] >sp|Q13888|Q13888 BASIC TRANSCRIPION FACTOR 2, 44 KD SUBUNIT (BASIC TRANSCRIPTION FACTOR 2 P44) (FRAGMENT). >gi|1737212 basic transcription factor	gnl|PID|e306259	200	1402	95	95	HAMGE23	Pancreas, Prostate

551	841331			2	955			HHFJL19	Lung, Breast/Ovarian
552	841332	alpha-2-macroglobulin precursor [Homo sapiens] >pir|A94033|MAHU alpha-2-macroglobulin precursor - human >sp|P01023|A2MG_HUMAN ALPHA-2-MACROGLOBULIN PRECURSOR (ALPHA-2-M). >gi|825615 alpha2-macroglobulin [Homo sapiens] {SUB 672-746} Length = 1474	gi|177870	2	3856	98	98	HAPQO79	Lung, Prostate
553	841338			1139	1363			HAJBU58	Pancreas, Prostate
554	841345	yeast methionyl-tRNA synthetase homolog [Homo sapiens] >pir|JC5224|JC5224 methionine--tRNA ligase (EC 6.1.1.10) - human >gi|804996 mitoxantrone-resistance associated gene [Homo sapiens] {SUB 423-900} Length = 900	gnl|PID|e218477	2	2761	94	94	HAJAQ46	Lung, Pancreas, Prostate, Breast/Ovarian
555	841349			151	1578			HMWFM73	Lung, Pancreas, Prostate, Breast/Ovarian
556	841355	glucose regulated protein 94 (400 AA) [Mesocricetus auratus] >pir|A26258|A26258 endoplasmin - hamster (fragment) >sp|P08712|ENPL_MESAU ENDOPLASMIN (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (FRAGMENT). Length = 400	gi|49628	2	562	96	99	HAJAA78	Prostate, Breast/Ovarian
557	841417	arginine-rich nuclear protein [Homo sapiens] >pir|A40988|A40988 54K arginine-rich nuclear protein - human >sp|Q05519|Q05519 ARGININE-RICH 54 KD NUCLEAR PROTEIN. Length = 484	gi|178997	708	1835	73	73	HNTCL10	Lung, Pancreas, Colon, Breast/Ovarian

558	841548			278	613			HBXDN79	Lung, Breast/Ovarian
559	841632	(AF073298) 4F5rel [Homo sapiens] >gi|3641536 (AF073297) 4F5rel [Mus musculus] >sp|O75918|O75918 4F5REL. >sp|O88891|O88891 4F5REL. Length = 59	gi|3641538	49	255	100	100	HTLGV25	Lung, Breast/Ovarian
560	841662	HYA22 protein - human Length = 338	pir|JC5707|JC5707	2	532	78	81	HLQCP61	Prostate, Colon
561	841771			901	1146			HSYDN46	Lung, Pancreas
562	841827	RTP [Homo sapiens] >gi|3046386 (AF004162) nickel-specific induction protein [Homo sapiens] >sp|Q92597|Q92597 RTP, COMPLETE CDS. Length = 394	gnl|PID|d1014198	358	1110	97	97	HHFDI26	Pancreas, Prostate
563	841835			1232	1612			HWLJT54	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
564	842259			2	691			HHFGF52	Lung, Pancreas, Prostate, Colon
565	842463			600	836			HETJY08	Lung, Pancreas
566	842595	ERp28 [Homo sapiens] >sp|P30040|ER29_HUMAN ENDOPLASMIC RETICULUM PROTEIN ERP29 PRECURSOR (ERP31) (ERP28). >sp|E1314951|E1314951 ERP28 PRECURSOR. Length = 261	gnl|PID|e1314951	50	916	92	92	HUFAB73	Lung, Breast/Ovarian
567	842722			2	1465			HYABB24	Lung, Pancreas, Prostate, Breast/Ovarian
568	842815			780	971			HPMSG47	Pancreas, Colon
569	842818	(AF038954) vacuolar H(+)-ATPase subunit [Homo sapiens] >sp|O75348|O75348 VACUOLAR H(+)-ATPASE SUBUNIT. Length = 118	gi|3329378	91	477	79	79	HSKJF03	Lung, Pancreas, Prostate, Breast/Ovarian

570	843251	(AF057297) ornithine decarboxylase antizyme 2 [Homo sapiens] >gi|3766170 (AF057297) ornithine decarboxylase antizyme 2 [Homo sapiens] >sp|G3766170|G3766170 ORNITHINE DECARBOXYLASE ANTIZYME 2. >gnl|PID|d1020346 product is unknown; seizure-related gene [Mus	gi|3766170	215	745	92	92	HTLIF83	Lung, Breast/Ovarian
571	843422			563	898			HISCW60	Lung, Pancreas, Colon, Breast/Ovarian
572	843784			1307	1864			HCECS78	Lung, Pancreas
573	844017			243	566			HKABG31	Lung, Colon
574	844138	Epithelin 1 & 2 [Homo sapiens] >gi|3005730 (AF055008) epithelin 1 and 2 [Homo sapiens] >pir|JC1284|GYHU granulin precursor - human >sp|G3005730|G3005730 EPITHELIN 1 AND 2. Length = 593	gi|31193	104	1966	100	100	HDPWW59	Lung, Breast/Ovarian
575	844166	(AF039689) antigen NY-CO-7 [Homo sapiens] >sp|O60526|O60526 ANTIGEN NY-CO-7. Length = 303	gi|3170178	1	1020	94	94	HABAE22	Lung, Pancreas, Prostate, Breast/Ovarian
576	844194			3	707			HE8PB56	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
577	844394			378	635			HHEUP26	Lung, Pancreas, Breast/Ovarian
578	844450	weak similarity to rat TEGT protein (GI:456207) [Caenorhabditis elegans] >sp|P91373|P91373 SIMILARITY TO RAT TEGT PROTEIN. Length = 342	gi|1825601	113	1165	61	78	HTXOX92	Lung, Pancreas
579	844534			2	244			HCE3I65	Lung, Pancreas, Breast/Ovarian

580	844535	isocitrate dehydrogenase (NADP+) [Homo sapiens] >pir|S57499|S57499 isocitrate dehydrogenase (NADP+) (EC 1.1.1.42) precursor, mitochondrial - human >sp|P48735|IDHP_HUMAN ISOCITRATE DEHYDROGENASE [NADP], MITOCHONDRIAL PRECURSOR (EC 1.1.1.42) (OXALOSUCCINATE	gi|872121	3	1454	96	96	HCWGE38	Lung, Breast/Ovarian
581	844644	(AJ002308) synaptogyrin 2 [Homo sapiens] >sp|O43760|O43760 SYNAPTOGYRIN 2. Length = 224	gnl|PID|e1254905	1	720	91	91	HDPBQ51	Lung, Breast/Ovarian
582	844653	immunoglobulin lambda light chain gene product [Homo sapiens] >pir|S25745|S25745 Ig lambda chain - human (fragment) Length = 226	gi|33718	1	732	89	91	HCRQC91	Lung, Pancreas, Colon
583	844659	cathepsin D [Homo sapiens] >gi|29678 precursor polypeptide (AA -20 to 392) [Homo sapiens] >gi|181180 preprocathepsin D [Homo sapiens] >pir|A25771|KHHUD cathepsin D (EC 3.4.23.5) precursor - human >sp|P07339|CATD_HUMAN CATHEPSIN D PRECURSOR (EC 3.4.23.5).	gi|179948	21	539	94	94	HLDDQ71	Lung, Breast/Ovarian
584	844796			2	1054			HE6BS09	Colon, Breast/Ovarian
585	844812	(AF040642) contains similarity to transacylases [Caenorhabditis elegans] >sp|O44793|O44793 C50D2.7 PROTEIN. Length = 895	gi|2746788	13	1542	33	59	HDPFV13	Lung, Pancreas
586	844894	E25B protein [Mus musculus] >sp|O89051|O89051 E25B PROTEIN. Length = 266	gi|3746127	66	1013	96	99	HCLBO47	Lung, Pancreas, Colon

<table>
<tr><td>587</td><td>845361</td><td>phosphoglycerate kinase (EC 2.7.2.3) [Homo sapiens] >gi|387021 phosphoglycerate kinase [Homo sapiens] >gi|35435 coding sequence [Homo sapiens] >pir|I59050|KIHUG phosphoglycerate kinase (EC 2.7.2.3) - human Length = 417</td><td>gi|387020</td><td>39</td><td>1232</td><td>100</td><td>100</td><td>HHEUJ91</td><td>Pancreas, Colon</td></tr>
<tr><td>588</td><td>845620</td><td></td><td></td><td>508</td><td>1254</td><td></td><td></td><td>HWHGQ46</td><td>Lung, Pancreas, Prostate, Breast/Ovarian</td></tr>
<tr><td>589</td><td>845639</td><td>leukocyte antigen F [Homo sapiens] >gi|3273731 (AF055066) MHC class I HLA-F [Homo sapiens] >pir|A60384|A60384 MHC class I histocompatibility antigen HLA-F alpha chain Dew3 precursor - human >sp|P30511|HLAF_HUMAN HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, F A</td><td>gi|312407</td><td>2</td><td>814</td><td>90</td><td>90</td><td>HCFNA68</td><td>Lung, Pancreas, Colon, Breast/Ovarian</td></tr>
<tr><td>590</td><td>845660</td><td>Cyr61 [Homo sapiens] >gnl|PID|e311857 Gig1 protein [Homo sapiens] >gi|2196782 (AF003594) growth-factor inducible immediate early gene product CYR61 [Homo sapiens] >gnl|PID|e1249319 hCYR61 protein [Homo sapiens] >sp|O00622|CYR6_HUMAN CYR61 PROTEIN PRECURSO</td><td>gi|2130527</td><td>1</td><td>1365</td><td>91</td><td>91</td><td>HKAJW79</td><td>Lung, Pancreas, Prostate, Breast/Ovarian</td></tr>
<tr><td>591</td><td>845720</td><td></td><td></td><td>1</td><td>261</td><td></td><td></td><td>HKDAF83</td><td>Lung, Breast/Ovarian</td></tr>
<tr><td>592</td><td>845785</td><td></td><td></td><td>180</td><td>509</td><td></td><td></td><td>HSODT09</td><td>Pancreas, Colon, Breast/Ovarian</td></tr>
<tr><td>593</td><td>845897</td><td></td><td></td><td>1369</td><td>1677</td><td></td><td></td><td>HADAB09</td><td>Pancreas, Breast/Ovarian</td></tr>
</table>

594	845922	beta actin [Ovis aries] >gi|2661136 (AF035774) beta actin [Equus caballus] >gi|3320892 (AF076190) beta-actin [Trichosurus vulpecula] >gi|177968 cytoplasmic beta actin [Homo sapiens] >gnl|PID|d1021082 (AB004047) beta-actin [Homo sapiens] >gi|28252 beta-act	gi|2182269	1	1239	100	100	HWLQQ65	Lung, Pancreas, Colon
595	846016	(AB005894) ecalectin [Homo sapiens] >sp|O75028|O75028 ECALECTIN. Length = 323	gnl|PID|d1032501	47	337	97	97	HDPIT90	Lung, Pancreas
596	846040	0-44 protein [Rattus sp.] >pir|I57612|I57612 Rat brain 0-44 mRNA, segment 2 - rat >sp|P38718|P044_RAT 0-44 PROTEIN. Length = 127	gi|203072	127	585	84	88	HLICQ57	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
597	846073	protein p68 (AA 1-614) [Homo sapiens] >gi|35220 p68 protein (AA 1-614) [Homo sapiens] >gi|2599360 (AF015812) RNA helicase p68 [Homo sapiens] >pir|JC1087|JC1087 RNA helicase, ATP-dependent - human >sp|P17844|DDX5_HUMAN PROBABLE RNA-DEPENDENT HELICASE P68 (	gi|38318	23	1051	91	92	HCWDW01	Lung, Pancreas
598	846257			286	651			HPWDE09	Lung, Prostate
599	HTXPN06R			65	286			HTXPN06	Lung, Breast/Ovarian
600	H2LAQ12R			3	311	71	79	H2LAQ12	Pancreas, Colon
601	HWAFU16R	(AB000911) ribosomal protein [Sus scrofa] >gnl|PID|e1339008 (AL031228) dJ1033B10.4 (40S ribosomal protein S18 (RPS18, KE-3)) [Homo sapiens] >gi|198580 ribosomal protein [Mus musculus] >gi|433447 ribosomal protein S18 [Rattus rattus] >gi|3811382 (AF100956)	gnl|PID|d1019961	3	320	86	86	HWAFU16	Lung, Pancreas, Colon, Breast/Ovarian

602	HAEAM91R	(AB005218) L subunit of photosynthetic reaction center complex [Acidiphilium rubrum] >gnl|PID|d1026488 (AB005219) L subunit of photosynthetic reaction center complex [Acidiphilium angustum] >sp|O70105|O70105 L SUBUNIT OF PHOTOSYNTHETIC REACTION CENTER COM	gnl|PID|d1026481	174	215	66	66	HAEAM91	Pancreas, Colon, Breast/Ovarian
603	HOEMT44R	(AB010959) natural killer cell enhancing factor [Cyprinus carpio] Length = 199	gnl|PID|d1033048	54	431	84	93	HOEMT44	Lung, Colon, Breast/Ovarian
604	HE2OW04R	(AF001631) glucose-regulated protein GRP94 [Oryctolagus cuniculus] >sp|O18750|ENPL_RABIT ENDOPLASMIN (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (FRAGMENT). Length = 716	gi|2581793	7	297	87	89	HE2OW04	Lung, Colon
605	HFCFG25R	(AF012422) ribosomal protein 46 [Drosophila melanogaster] Length = 51	gi|2307014	3	143	65	87	HFCFG25	Lung, Colon, Breast/Ovarian
606	HAPQP94R	(AF018432) dUTPase [Homo sapiens] >gi|1144332 deoxyuridine nucleotidohydrolase [Homo sapiens] >gi|1421818 deoxyuridine triphosphatase [Homo sapiens] >pir|G02777|G02777 dUTP pyrophosphatase (EC 3.6.1.23) - human >gi|292877 dUTP nucleotidohydrolase [Homo sa	gi|2443581	3	320	97	97	HAPQP94	Lung, Pancreas, Colon
607	H2CBI37R	(AF042107) ribosomal protein S3a [Eimeria tenella] >gi|2792508 (AF042107) ribosomal protein S3a [Eimeria tenella] Length = 264	gi|2792508	3	182	64	64	H2CBI37	Colon, Breast/Ovarian
608	HEOPQ13R	(AF042505) cytochrome b [Homo sapiens] >sp|G3372377|G3372377 CYTOCHROME B (FRAGMENT). Length = 380	gi|3372377	82	216	80	82	HEOPQ13	Lung, Colon

609	HCRNC25R	(AF051894) 15 kDa selenoprotein [Homo sapiens] Length = 161	gi|3095111	61	162	100	100	HCRNC25	Lung, Pancreas, Colon
610	HFITF28R	(AF056218) superficial zone protein [Bos taurus] >sp|O77765|O77765 SUPERFICIAL ZONE PROTEIN (FRAGMENT). Length = 401	gi|3676501	3	185	73	80	HFITF28	Pancreas, Colon
611	H2LAY26R			24	155			H2LAY26	Pancreas, Colon
612	HAPQA06R	40-kDa keratin protein [Homo sapiens] >pir|A31370|KRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gi|386803	2	355	62	62	HAPQA06	Lung, Pancreas, Colon, Breast/Ovarian
613	HAQBM72R	40-kDa keratin protein [Homo sapiens] >pir|A31370|KRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gi|386803	2	145	81	81	HAQBM72	Pancreas, Colon
614	HBGOK18R	40-kDa keratin protein [Homo sapiens] >pir|A31370|KRHU9 keratin 19, type I, cytoskeletal - human Length = 400	gi|386803	1	429	91	92	HBGOK18	Lung, Pancreas, Colon, Breast/Ovarian
615	H2MAC07R	acidic ribosomal phosphoprotein (P1) [Homo sapiens] >pir|B27125|R6HUP1 acidic ribosomal protein P1 - human Length = 114	gi|190234	111	458	100	100	H2MAC07	Lung, Colon, Breast/Ovarian
616	HTWKF26R	acidic ribosomal phosphoprotein (P2) [Homo sapiens] >pir|C27125|R6HUP2 acidic ribosomal protein P2 - human Length = 115	gi|190236	1	345	95	96	HTWKF26	Lung, Pancreas, Breast/Ovarian
617	HTAHR89R	ADP,ATP carrier protein T2 - human >sp|P12236|ADT3_HUMAN ADP,ATP CARRIER PROTEIN, LIVER ISOFORM T2 (ADP/ATP TRANSLOCASE 3) (ADENINE NUCLEOTIDE TRANSLOCATOR 3) (ANT 3). Length = 298	pir|S03894|S03894	13	408	96	96	HTAHR89	Lung, Pancreas

<table>
<tr><td>618</td><td>HOACE24R</td><td>alcohol dehydrogenase [Homo sapiens] >pir|A33371|DEHUE1 aldehyde dehydrogenase (NAD+) (EC 1.2.1.3) 1, cytosolic - human >sp|P00352|DHAC_HUMAN ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS I) (ALHDII) (ALDH-E1). {SUB 2-501} Length = 501</td><td>gi|178372</td><td>3</td><td>374</td><td>91</td><td>92</td><td>HOACE24</td><td>Pancreas, Colon</td></tr>
<tr><td>619</td><td>HOELC27R</td><td>aldolase A (EC 4.1.3.13) [Homo sapiens] >gi|28597 aldolase A (AA 1-364) [Homo sapiens] >pir|S14084|ADHUA fructose-bisphosphate aldolase (EC 4.1.2.13) A - human >sp|P04075|ALFA_HUMAN FRUCTOSE-BISPHOSPHATE ALDOLASE A (EC 4.1.2.13) (MUSCLE-TYPE ALDOLASE). {S</td><td>gi|178351</td><td>68</td><td>604</td><td>100</td><td>100</td><td>HOELC27</td><td>Lung, Pancreas, Breast/Ovarian</td></tr>
<tr><td>620</td><td>HWLBS25R</td><td>aldolase A [Gallus gallus] >gi|409193 aldolase A [Gallus gallus] >bbs|167536 aldolase C=fructose-1,6-biphosphate aldolase {EC 4.1.2.13} {chickens, brain, Peptide Partial, 42 aa] [Gallus gallus] >pir|I51291|I51291 aldolase C - chicken (fragment) Length = 4</td><td>gi|409191</td><td>3</td><td>95</td><td>90</td><td>93</td><td>HWLBS25</td><td>Lung, Pancreas, Colon, Breast/Ovarian</td></tr>
<tr><td>621</td><td>HWLVW62R</td><td>alpha-1 type III collagen [Homo sapiens] Length = 345</td><td>gi|180414</td><td>1</td><td>213</td><td>97</td><td>97</td><td>HWLVW62</td><td>Lung, Colon, Breast/Ovarian</td></tr>
<tr><td>622</td><td>HALSE08R</td><td>ALPHA-1-ANTICHYMOTRYPSIN PRECURSOR (ACT). >gi|4165890 (AF089747) alpha-1-antichymotrypsin precursor [Homo sapiens] {SUB 17-423} >gi|177933 alpha-1-antichymotrypsin precursor [Homo sapiens] {SUB 22-423} >gi|28332 alpha 1 antichymotrypsin [Homo sapiens] {SU</td><td>sp|P01011|AACT_HUMAN</td><td>3</td><td>233</td><td>95</td><td>97</td><td>HALSE08</td><td>Lung, Pancreas</td></tr>
</table>

623	HFKHD94R	alpha-2 chain precursor (AA -25 to 1018) (3416 is 2nd base in codon) [Homo sapiens] Length = 1043	gi|30076	2	316	97	97	HFKHD94	Pancreas, Breast/Ovarian
624	HCE2M86R	alpha-adaptin (A) (AA 1-977) [Mus musculus] >pir|A30111|A30111 alpha-adaptin A - mouse >sp|P17426|ADAA_MOUSE ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPT	gi|49878	58	165	75	80	HCE2M86	Lung, Colon, Breast/Ovarian
625	HOFOA89R	annexin IV (placental anticoagulant protein II) [Homo sapiens] >gnl|PID|d1011889 annexin IV (carbohydrtate-binding protein p33/41) [Homo sapiens] >pir|A42077|A42077 annexin IV - human >sp|P09525|ANX4_HUMAN ANNEXIN IV (LIPOCORTIN IV) (ENDONEXIN I) (CHROMOB	gi|178699	154	399	94	94	HOFOA89	Pancreas, Colon, Breast/Ovarian
626	HBWCN69R	beta-1,2-N-acetylglucosaminyltransferase II [Homo sapiens] >pir|S66256|S66256 alpha-1,6-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase (EC 2.4.1.143) - human >sp|Q10469|GNT2_HUMAN ALPHA-1,6-MANNOSYL-GLYCOPROTEIN BETA-1,2-N-ACETYLGLUCOSAM	gi|902745	60	308	88	90	HBWCN69	Pancreas, Colon
627	HLQGB43R	beta-2-microglobulin [Homo sapiens] Length = 119	gi|179318	1	78	100	100	HLQGB43	Lung, Pancreas, Colon
628	HCROL58R			3	506			HCROL58	Pancreas, Colon
629	HS2IF12R			83	475			HS2IF12	Pancreas, Colon
630	HWLWA01R			2	538			HWLWA01	Pancreas, Colon

631	HCHMV24R			12	185			HCHMV24	Pancreas, Colon, Breast/Ovarian
632	HCHPT49R			94	303			HCHPT49	Colon, Breast/Ovarian
633	HCRMG12R			2	187			HCRMG12	Pancreas, Colon
634	HWLWE68R			2	241			HWLWE68	Pancreas, Colon
635	HCHPF59R			24	179			HCHPF59	Pancreas, Breast/Ovarian
636	HS2IA81R			90	551			HS2IA81	Pancreas, Colon
637	HCRNC17R			11	400			HCRNC17	Pancreas, Colon
638	HISDJ39R			14	406			HISDJ39	Pancreas, Colon
639	HWLEL43R			2	337			HWLEL43	Pancreas, Colon
640	HASCG71R			91	249			HASCG71	Lung, Colon, Breast/Ovarian
641	HOEMO43R			2	184			HOEMO43	Lung, Pancreas, Colon, Breast/Ovarian
642	HRDFT95R	c-erb-B-2 precursor [Homo sapiens] >pir|A24571|A24571 protein-tyrosine kinase (EC 2.7.1.112) crbB2 precursor - human >sp|P04626|ERB2_HUMAN ERBB-2 RECEPTOR PROTEIN-TYROSINE KINASE PRECURSOR (EC 2.7.1.112) (P185ERBB2) (NEU PROTO-ONCOGENE) (C-ERBB-2). Length	gi|31198	151	231	76	82	HRDFT95	Pancreas, Colon
643	HAGEP27R	C10 protein [Bos taurus] >pir|A38464|A38464 33K laminin receptor homolog - bovine Length = 295	gi|163303	3	137	86	86	HAGEP27	Lung, Pancreas, Colon, Breast/Ovarian

644	HSYDG18R	calmodulin [Homo sapiens] >sp|Q13942|Q13942 CALMODULIN. >pir|A56785|A56785 calmodulin - pig (fragment) {SUB 80-130} >gi|3243222 (AF069912) calmodulin [Xiphias gladius] {SUB 80-114} >pir|E44101|E44101 calmodulin, vasoactive intestinal peptide-binding prote	gi|825635	3	422	100	100	HSYDG18	Lung, Pancreas, Colon
645	HLJDZ15R	cathepsin C [Homo sapiens] >gi|1947071 prepro dipeptidyl peptidase I [Homo sapiens] >pir|S66504|S66504 dipeptidyl-peptidase I (EC 3.4.14.1) precursor - human >sp|P53634|CATC_HUMAN DIPEPTIDYL-PEPTIDASE I PRECURSOR (EC 3.4.14.1) (DPP-I) (CATHEPSIN C) (CATHE	gi|1006657	3	110	71	77	HLJDZ15	Lung, Colon
646	HAHDQ54R	cathepsin D [Homo sapiens] >gi|29678 precursor polypeptide (AA -20 to 392) [Homo sapiens] >gi|181180 preprocathepsin D [Homo sapiens] >pir|A25771|KHHUD cathepsin D (EC 3.4.23.5) precursor - human >sp|P07339|CATD_HUMAN CATHEPSIN D PRECURSOR (EC 3.4.23.5).	gi|179948	2	103	100	100	HAHDQ54	Lung, Pancreas
647	HTLHI18R	collagen alpha 2(VI) chain precursor, long splice form - human >gi|179711 alpha-2 collagen type VI-a' [Homo sapiens] {SUB 590-1018} >gi|291918 alpha-2 type VI collagen [Homo sapiens] {SUB 315-358} Length = 1018	pir|S05378|CGHU2A	2	481	89	89	HTLHI18	Lung, Pancreas

648	HACAC47R	complement component C3 [Homo sapiens] >pir|A94065|C3HU complement C3 precursor - human >sp|P01024|CO3_HUMAN COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN]. >gi|181130 complement component C3 [Homo sapiens] {SUB 1-24} Length = 1663	gi|179665	1	315	79	80	HACAC47	Lung, Pancreas, Breast/Ovarian
649	HLQFY41R	complement component C3 [Homo sapiens] >pir|A94065|C3HU complement C3 precursor - human >sp|P01024|CO3_HUMAN COMPLEMENT C3 PRECURSOR [CONTAINS: C3A ANAPHYLATOXIN]. >gi|181130 complement component C3 [Homo sapiens] {SUB 1-24} Length = 1663	gi|179665	3	377	96	98	HLQFY41	Lung, Pancreas, Colon, Breast/Ovarian
650	HOFMO83R	cyclin G [Homo sapiens] >gi|1236233 cyclin G1 [Homo sapiens] >gi|1236913 cyclin G1 [Homo sapiens] >pir|G02401|G02401 cyclin G1 - human >sp|P51959|CG2G_HUMAN G2/MITOTIC-SPECIFIC CYCLIN G1. >gnl|PID|d1013694 cyclin G [Homo sapiens] {SUB 1-279} >gi|1486361 c	gnl|PID|d1012016	2	205	87	93	HOFMO83	Pancreas, Breast/Ovarian
651	HFTDR22R	cytochrome b5, hepatic - brown howler monkey (fragment) Length = 87	pir|S07959|S07959	136	357	100	100	HFTDR22	Pancreas, Colon, Breast/Ovarian
652	HPJCZ01R	cytochrome c oxidase II [Macaca fascicularis] >pir|A27420|A27420 cytochrome-c oxidase (EC 1.9.3.1) chain II - crab-eating macaque mitochondrion (SGC1) >sp|P11948|COX2_MACFA CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1). Length = 227	gi|342255	2	163	44	50	HPJCZ01	Lung, Pancreas, Colon

653	HOEKC39R	cytochrome oxidase I [Homo sapiens] >gi|506829 cytochrome oxidase subunit 1 [Homo sapiens] >pir|A00463|ODHU1 cytochrome-c oxidase (EC 1.9.3.1) chain I - human mitochondrion (SGC1) >sp|P00395|COX1_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE I (EC 1.9.3.1). Leng	gi|13006	54	167	91	95	HOEKC39	Lung, Pancreas, Colon
654	HOELI24R	cytochrome oxidase subunit 3 [Homo sapiens] Length = 260	gi|2052365	29	166	97	97	HOELI24	Lung, Pancreas, Colon
655	HODEI18R	cytochrome oxidase subunit II [Homo sapiens] >gi|530071 cytochrome oxidase subunit II [Homo sapiens] >gi|530073 cytochrome oxidase subunit II [Homo sapiens] >gi|530077 cytochrome oxidase subunit II [Homo sapiens] >gi|337187 cytochrome oxidase subunit II [	gi|530069	1	180	69	72	HODEI18	Lung, Pancreas, Colon
656	HOSNR06R	cytochrome oxidase subunit II [Homo sapiens] >gi|530071 cytochrome oxidase subunit II [Homo sapiens] >gi|530073 cytochrome oxidase subunit II [Homo sapiens] >gi|530077 cytochrome oxidase subunit II [Homo sapiens] >gi|337187 cytochrome oxidase subunit II [	gi|530069	269	403	93	95	HOSNR06	Lung, Pancreas
657	HCQDL20R	cytochrome P450 PCN3 [Homo sapiens] >pir|A34101|A34101 cytochrome P450 3A5 - human >sp|P20815|CP35_HUMAN CYTOCHROME P450 3A5 (EC 1.14.14.1) (CYPIIIA5) (P450-PCN3). >gi|950342 cytochrome P450 [Homo sapiens] {SUB 1-24} Length = 502	gi|181346	39	245	98	98	HCQDL20	Pancreas, Colon

658	HTOHI64R	cytokeratin 15 (AA 1 - 456) [Homo sapiens] >pir|S01069|KRHU5 keratin 15, type I, cytoskeletal - human >sp|P19012|K1CO_HUMAN KERATIN, TYPE I CYTOSKELETAL 15 (CYTOKERATIN 15) (K15) (CK 15). Length = 456	gi|34071	149	253	89	89	HTOHI64	Prostate, Breast/Ovarian
659	HCHBR11R	cytokeratin 8 [Homo sapiens] Length = 483	gi|181400	3	380	55	57	HCHBR11	Lung, Pancreas, Colon, Breast/Ovarian
660	HADBE77R	cytoplasmic chaperonin hTRiC5 [Homo sapiens] Length = 201	gi|609308	43	294	80	84	HADBE77	Lung, Pancreas, Colon, Breast/Ovarian
661	HFKHD49R	D-beta-hydroxybutyrate dehydogenase [Rattus norvegicus] Length = 93	gi|930260	1	210	100	100	HFKHD49	Lung, Colon, Breast/Ovarian
662	HOEMJ59R	decorin [Homo sapiens] >gi|609452 decorin [Homo sapiens] {SUB 1-70} Length = 347	gi|181519	3	128	72	75	HOEMJ59	Lung, Colon
663	HTYNC43R	elongation factor 1-alpha 1 [Homo sapiens] >gi|927067 longation factor 1-alpha 1 [Homo sapiens] >pir|I59399|I59399 oncogene PTI-1 - human >sp|Q16577|Q16577 ONCOGENE. Length = 398	gi|927065	2	217	92	94	HTYNC43	Lung, Pancreas, Colon
664	H6EAQ15R	elongation factor 2 [Homo sapiens] >gi|31108 human elongation factor 2 [Homo sapiens] >pir|S18294|EFHU2 translation elongation factor eEF-2 - human >sp|P13639|EF2_HUMAN ELONGATION FACTOR 2 (EF-2). >gi|181969 elongation factor 2 [Homo sapiens] {SUB 501-858	gi|31106	2	70	100	100	H6EAQ15	Lung, Pancreas, Breast/Ovarian

665	HCFLM34R	elongation factor Tu [Mus musculus] >sp|Q61511|Q61511 EUKARYOTIC TRANSLATION ELONGATION FACTOR 1 ALPHA 1 (EEF-TU GENE ENCODING ELONGATION FACTOR TU, 5' END) (FRAGMENT). Length = 108	gi|553907	48	308	94	95	HCFLM34	Lung, Breast/Ovarian
666	HTTID16R	ENA-78 prepeptide [Homo sapiens] >gi|607031 neutrophil-activating peptide 78 [Homo sapiens] >gi|471243 ENA-78 gene product [Homo sapiens] >pir|JC2433|A55010 neutrophil-activating peptide ENA-78 - human >sp|P42830|EN78_HUMAN NEUTROPHIL ACTIVATING PROTEIN E	gi|684922	2	331	85	85	HTTID16	Pancreas, Colon
667	HDPAI45R	endoglin [Homo sapiens] >pir|S37628|S37628 endoglin - human Length = 625	gi|402207	2	181	65	65	HDPAI45	Pancreas, Colon
668	HKIXL19R	epoxide hydrolase [Homo sapiens] >gi|340390 epoxide hydrolase [Homo sapiens] >gi|34543 epoxide hydrolase (AA 1-455) [Homo sapiens] >gi|458701 epoxide hydrolase [Homo sapiens] >pir|A29939|A29939 epoxide hydrolase (EC 3.3.2.3) 1, microsomal - human >sp|P070	gi|450271	1	348	100	100	HKIXL19	Lung, Pancreas, Colon
669	H2LAY52R	EWS gene product [Mus musculus] >pir|A55726|A55726 RNA-binding protein Ews - mouse >sp|Q61545|EWS_MOUSE RNA-BINDING PROTEIN EWS. Length = 655	gi|488513	27	494	100	100	H2LAY52	Lung, Pancreas, Colon, Breast/Ovarian
670	HAJRB09R	FAST kinase [Homo sapiens] >pir|I37386|I37386 FAST kinase - human >sp|Q14296|Q14296 FAST KINASE. Length = 549	gi|1006659	19	324	77	77	HAJRB09	Pancreas, Colon

671	HAPNI86R	G9a [Homo sapiens] >pir|S30385|S30385 G9a protein - human >sp|Q14349|Q14349 G9A PROTEIN CONTAINING ANKYRIN-LIKE REPEATS. Length = 1001	gi|287865	3	419	97	97	HAPNI86	Lung, Colon
672	HCEVB92R	glutamate dehydrogenase [Homo sapiens] >sp|Q14400|Q14400 GLUTAMATE DEHYDROGENASE (FRAGMENT). Length = 258	gi|183056	2	217	78	81	HCEVB92	Pancreas, Colon
673	HAPRJ22R	glutamate--ammonia ligase [Homo sapiens] >pir|S18455|AJHUQ glutamate--ammonia ligase (EC 6.3.1.2) - human Length = 373	gi|31831	168	431	100	100	HAPRJ22	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
674	HCRMZ32R	glutamine:fructose-6-phosphate amidotransferase [Homo sapiens] >pir|A45055|A45055 glutamine--fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - human >sp|Q06210|GFAT_HUMAN GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2	gi|183082	2	316	91	91	HCRMZ32	Pancreas, Colon, Breast/Ovarian
675	HBMVM42R	guanine nucleotide regulatory protein [Homo sapiens] >gi|3041860 (AC004534) guanine nucleotide regulatory protein [Homo sapiens] >pir|I38402|I38402 guanine nucleotide regulatory protein - human >sp|Q12774|Q12774 GUANINE NUCLEOTIDE REGULATORY PROTEIN. Leng	gi|484102	1	363	84	87	HBMVM42	Colon, Breast/Ovarian

676	HADGE45R	guanine nucleotide-binding protein G-s-alpha-4 [Homo sapiens] >gi|31913 alpha-S1 (AA 1-380) [Homo sapiens] >pir|C31927|RGHUA1 GTP-binding regulatory protein Gs alpha chain (adenylate cyclase-stimulating), splice form 4 - human Length = 380	gi|386746	2	439	96	96	HADGE45	Lung, Pancreas, Colon
677	HTXPN11R	heat shock-induced protein [Homo sapiens] >pir|B45871|B45871 dnaK-type molecular chaperone HSP70-Hom - human >sp|P34931|HS7H_HUMAN HEAT SHOCK 70 KD PROTEIN 1-HOM (HSP70-HOM). Length = 641	gi|188492	3	413	94	98	HTXPN11	Lung, Pancreas, Colon
678	HCDBN37R	heterogeneous nuclear ribonucleoprotein C-like protein - human Length = 328	pir|A44192|A44192	1	300	96	96	HCDBN37	Colon, Breast/Ovarian
679	HABGC02R	HLA-DR-beta-B [Homo sapiens] Length = 266	gi|490048	3	389	89	94	HABGC02	Lung, Colon
680	HNTSA70R	HsMcm6 [Homo sapiens] >sp|Q14566|MCM6_HUMAN DNA REPLICATION LICENSING FACTOR MCM6 (P105MCM). Length = 821	gnl|PID|d1013380	3	341	69	72	HNTSA70	Lung, Colon
681	HDTKP24R	hypothetical 18K protein (rRNA) - goldfish mitochondrion (SGC1) Length = 166	pir|JC1348|JC1348	397	492	64	67	HDTKP24	Lung, Pancreas, Colon
682	HODEI14R	hypothetical 18K protein (rRNA) - goldfish mitochondrion (SGC1) Length = 166	pir|JC1348|JC1348	164	247	62	68	HODEI14	Lung, Pancreas, Colon
683	HOELC42R	IGF-BP 4 [Homo sapiens] >gnl|PID|e1227579 insulin-like growth factor binding protein 4 [Homo sapiens] >pir|B37252|B37252 insulin-like growth factor-binding protein 4 precursor - human >sp|P22692|IBP4_HUMAN INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 4 PREC	gi|184816	13	288	83	83	HOELC42	Pancreas, Colon

684	HWAFL44R	immunoglobulin heavy chain [Homo sapiens] >pir|D36005|D36005 Ig heavy chain V region (M43) - human {SUB 38-156} Length = 156	gi|567121	2	463	83	90	HWAFL44	Lung, Colon
685	HABGF46R	immunoglobulin light chain variable region [Homo sapiens] >gi|2970534 (AF049692) immunoglobulin kappa light chain [Homo sapiens] {SUB 3-106} Length = 143	gi|1136555	42	446	71	85	HABGF46	Lung, Pancreas, Colon, Breast/Ovarian
686	HOELC15R	insulin-like growth factor-binding protein [Homo sapiens] >gi|386791 growth factor-binding protein-3 [Homo sapiens] >gi|398164 insulin-like growth factor binding protein 3 [Homo sapiens] >pir|A36578|IOHU3 insulin-like growth factor-binding protein 3 precu	gi|183116	8	424	96	96	HOELC15	Pancreas, Colon, Breast/Ovarian
687	H2LAR26R	keratin 18 [Homo sapiens] >gi|307081 keratin 18 precursor [Homo sapiens] >gi|34037 cytokeratin 18 [Homo sapiens] >pir|S05481|S05481 keratin 18, type I, cytoskeletal - human >sp|P05783|K1CR_HUMAN KERATIN, TYPE I CYTOSKELETAL 18 (CYTOKERATIN 18) (K18) (CK 1	gi|386844	72	476	97	98	H2LAR26	Colon, Breast/Ovarian
688	H2LAV85R	Ku (p70/p80) subunit [Homo sapiens] >gi|307093 Ku antigen [Homo sapiens] >pir|A35051|A32626 Ku antigen 80K chain - human >sp|P13010|KU86_HUMAN ATP-DEPENDENT DNA HELICASE II, 86 KD SUBUNIT (LUPUS KU AUTOANTIGEN PROTEIN P86) (86 KD SUBUNIT OF KU ANTIGEN) (T	gi|307094	67	462	97	98	H2LAV85	Lung, Pancreas
689	HBSDC92R	l-caldesmon II [Homo sapiens] Length = 532	gnl|PID|d1015132	56	337	64	76	HBSDC92	Lung, Breast/Ovarian

690	HUTHN01R	L6 [Homo sapiens] >pir|A42926|A42926 L6 surface protein - human Length = 202	gi|186804	87	545	91	91	HUTHN01	Lung, Pancreas, Colon, Breast/Ovarian
691	H2LAW03R	lactate dehydrogenase B [Homo sapiens] >gi|34329 lactate dehydrogenase B (AA 1 - 334) [Homo sapiens] >pir|S02795|DEHULH L-lactate dehydrogenase (EC 1.1.1.27) chain H - human >sp|P07195|LDHH_HUMAN L-LACTATE DEHYDROGENASE H CHAIN (EC 1.1.1.27) (LDH-B). {SUB	gnl|PID|e223241	111	536	99	100	H2LAW03	Lung, Pancreas
692	HOEMO60R	lactate dehydrogenase-A [Homo sapiens] >gi|34313 lactate dehydrogenase-A [Homo sapiens] >pir|A00347|DEHULM L-lactate dehydrogenase (EC 1.1.1.27) chain M - human >sp|P00338|LDHM_HUMAN L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A). {SUB 2-332} Lengt	gi|780261	1	201	59	59	HOEMO60	Pancreas, Breast/Ovarian
693	HKAHJ14R			1	216			HKAHJ14	Pancreas, Colon
694	HOHEA39R	latent transforming growth factor-beta-binding protein - human Length = 1820	pir|A55494|A55494	1	240	85	86	HOHEA39	Pancreas, Breast/Ovarian
695	HOELF72R	lumican [Homo sapiens] Length = 338	gi|699577	58	468	97	97	HOELF72	Pancreas, Colon
696	HAPNX59R	M130 antigen [Homo sapiens] >pir|I38003|S36077 M130 antigen - human >sp|Q07898|Q07898 M130 ANTIGEN PRECURSOR. Length = 1116	gi|312142	1	432	85	88	HAPNX59	Lung, Colon
697	HBJJS17R	methionine aminopeptidase [Homo sapiens] >gi|687243 eIF-2-associated p67 homolog [Homo sapiens] >pir|S52112|DPHUM2 methionyl aminopeptidase (EC 3.4.11.18) 2 - human >sp|P50579|AMP2_HUMAN METHIONINE AMINOPEPTIDASE 2 (EC 3.4.11.18) (METAP 2) (PEPTIDASE M 2)	gi|903982	1	255	100	100	HBJJS17	Lung, Pancreas

698	HATDU61R	midkine [Homo sapiens] >gi|188571 retinoic acid inducible factor [Homo sapiens] >gi|35087 neurite outgrowth-promoting protein [Homo sapiens] >gnl|PID|d1001932 midkine [Homo sapiens] >pir|JH0385|JH0385 midkine precursor - human >sp|P21741|MK_HUMAN MIDKINE	gi|182651	1	108	67	67	HATDU61	Pancreas, Colon
699	HCWHT65R	mitochondrial intermediate peptidase precursor [Homo sapiens] >sp|Q99797|Q99797 MITOCHONDRIAL INTERMEDIATE PEPTIDASE PRECURSOR (EC 3.4.24.59). Length = 713	gi|1763642	1	432	74	77	HCWHT65	Prostate, Colon
700	H2CBN02R	mitochondrial matrix protein [Homo sapiens] >pir|A32800|A32800 chaperonin GroEL precursor - human >sp|P10809|P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (	gi|190127	1	435	99	99	H2CBN02	Pancreas, Colon
701	H2CBV68R	mitochondrial matrix protein [Homo sapiens] >pir|A32800|A32800 chaperonin GroEL precursor - human >sp|P10809|P60_HUMAN MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (	gi|190127	2	406	100	100	H2CBV68	Colon, Breast/Ovarian

702	H6EDK07R	Mr 110,000 antigen [Homo sapiens] >pir|I52703|I52703 42K membrane glycoprotein - human >sp|Q16186|G100_HUMAN 110 KD CELL MEMBRANE GLYCOPROTEIN. Length = 407	gnl|PID|d1011683	1	252	90	90	H6EDK07	Lung, Breast/Ovarian
703	HACAH10R	NADH dehydrogenase subunit 2, ND2 [human, brain, Peptide Mitochondrial Partial Mutant, 67 aa] [Homo sapiens] >sp|Q36734|Q36734 NADH DEHYDROGENASE SUBUNIT 2 (FRAGMENT). Length = 67	bbs|75898	1	66	89	96	HACAH10	Lung, Pancreas, Colon
704	HCCMC56R	NADH-UBIQUINONE OXIDOREDUCTASE B18 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B18) (CI-B18) (CELL ADHESION PROTEIN SQM1). Length = 134	sp|P17568|NB8M_HUMAN	16	351	83	83	HCCMC56	Lung, Colon, Breast/Ovarian
705	H2CBN54R	NADH-ubiquinone oxidoreductase B22 subunit {C-terminal} [human, placenta, Peptide Mitochondrial Partial, 179 aa] [Homo sapiens] Length = 179	bbs|178894	2	427	99	99	H2CBN54	Pancreas, Colon
706	HMCGL12R	NMB gene product [Homo sapiens] >pir|I38065|I38065 gene NMB protein - human >sp|Q14956|NMB_HUMAN PUTATIVE TRANSMEMBRANE PROTEIN NMB PRECURSOR. Length = 560	gi|666043	96	389	76	80	HMCGL12	Lung, Pancreas
707	HWHPX50R	nucleolar protein [Mus musculus] >pir|I52858|I52858 nucleolar protein - mouse >sp|Q61937|NPM_MOUSE NUCLEOPHOSMIN (NPM) (NUCLEOLAR PHOSPHOPROTEIN B23) (NUMATRIN) (NUCLEOLAR PROTEIN NO38). Length = 292	gi|200011	1	414	87	87	HWHPX50	Lung, Pancreas, Colon, Breast/Ovarian

708	HAPQD84R			115	267			HAPQD84	Lung, Pancreas, Colon, Breast/Ovarian
709	HLIBN66R			1	219			HLIBN66	Lung, Pancreas
710	HE2BD84R	OSF-2p1 [Homo sapiens] >pir|S36111|S36111 osteoblast-specific factor 2 - human >sp|Q15064|Q15064 OSF-2P1. Length = 779	gnl|PID|d1003341	2	394	77	81	HE2BD84	Pancreas, Colon, Breast/Ovarian
711	HLQFY45R	pancreatitis-associated protein [Homo sapiens] >gi|312807 preprotein [Homo sapiens] >bbs|121222 PAP-H=pancreatitis-associated protein [human, pancreas, Peptide, 175 aa] [Homo sapiens] >gnl|PID|d1003233 PAP homologous protein [Homo sapiens] >pir|A49616|A49	gi|482909	57	374	60	66	HLQFY45	Pancreas, Colon
712	HAMGQ78R	phosphate carrier isoform A (alternatively spliced, exon IIIA) - human >sp|Q00325|MPCP_HUMAN MITOCHONDRIAL PHOSPHATE CARRIER PROTEIN PRECURSOR. Length = 362	pir|A53737|A53737	2	352	82	82	HAMGQ78	Lung, Colon
713	HODEV64R	poly(A)-binding protein [Homo sapiens] >gi|1562511 poly(A)-binding protein [Homo sapiens] >sp|P11940|PAB1_HUMAN POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1). Length = 636	gi|1562511	1	492	97	98	HODEV64	Lung, Pancreas

714	H2CBD48R	precursor polypeptide (AA -21 to 782) [Homo sapiens] >pir|A35954|A35954 endoplasmin precursor - human >sp|P14625|ENPL_HUMAN ENDOPLASMIN PRECURSOR (94 KD GLUCOSE-REGULATED PROTEIN) (GRP94) (GP96 HOMOLOG) (TUMOR REJECTION ANTIGEN 1). Length = 803	gi|37261	2	499	95	97	H2CBD48	Pancreas, Colon
715	HCCMA82R	procarboxypeptidase B [Homo sapiens] >pir|A42332|A42332 carboxypeptidase B (EC 3.4.17.2) precursor, pancreatic - human Length = 416	gi|189625	3	383	94	94	HCCMA82	Pancreas, Colon
716	HOEMK78R	prostacyclin-stimulating factor, PGI2-stimulating factor, PSF [human, cultured diploid fibroblast cells, Peptide, 282 aa] [Homo sapiens] >pir|S50031|S50031 prostacyclin-stimulating factor - human >sp|Q16270|Q16270 PROSTACYCLIN-STIMULATING FACTOR. Length =	bbs|161346	3	329	95	95	HOEMK78	Lung, Pancreas
717	H2CBD13R	proteasome subunit C9 [Homo sapiens] >pir|S15972|SNHUC9 multicatalytic endopeptidase complex (EC 3.4.99.46) chain C9 - human >sp|P25789|PRC9_HUMAN PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT	gnl|PID|d1001118	156	461	100	100	H2CBD13	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
718	HCFMU61R	protein-tyrosine kinase (EC 2.7.1.112) ZAP-70 - human Length = 619	pir|A44266|A44266	1	477	98	98	HCFMU61	Pancreas, Colon

719	HOSNE94R	proteoglycan core protein [Homo sapiens] >pir|A45016|NBHUC8 decorin precursor - human >sp|P07585|PGS2_HUMAN BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN) (PG40). >gi|1161226 decorin [Rattus norvegicus] {SUB 204-299} Length = 359	gi|181170	2	466	85	85	HOSNE94	Lung, Pancreas
720	HCROZ08R	putative precursor (AA 1-304) [Homo sapiens] >gnl|PID|e224276 uracil-DNA-glycosylase, UNG1 [Homo sapiens] >pir|S05964|A60472 uracil-DNA glycosylase (EC 3.-.-.-) precursor - human >gnl|PID|e1296296 MITOCHONDRIAL LOCALIZATION PEPTIDE [unidentified] {SUB 1-3	gi|37599	3	218	100	100	HCROZ08	Lung, Pancreas, Colon
721	HHBEF47R	pyruvate dehydrogenase E1-alpha precursor [Homo sapiens] >pir|A60225|A60225 pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain - bovine (fragment) {SUB 54-74} Length = 414	gi|387011	1	330	88	88	HHBEF47	Colon, Breast/Ovarian
722	HTXPI31R	pyruvate kinase M2 [Sus scrofa] >sp|Q29582|Q29582 PYRUVATE KINASE M2 (EC 2.7.1.40) (PHOSPHOENOLPYRUVATE KINASE) (PHOSPHOENOL TRANSPHOSPHORYLASE) (FRAGMENT). Length = 108	gi|972104	2	286	84	85	HTXPI31	Pancreas, Breast/Ovarian
723	HOEKC30R	rhoC coding region (AA 1-193) [Homo sapiens] >gi|407699 GTPase [Homo sapiens] >pir|S01029|TVHURC GTP-binding protein rhoC - human Length = 193	gi|36034	2	151	94	94	HOEKC30	Lung, Pancreas, Breast/Ovarian
724	HOSNR67R	ribosmal protein small subunit [Homo sapiens] Length = 264	gi|306553	1	483	97	98	HOSNR67	Lung, Pancreas

725	H2LAV92R	ribosomal protein [Homo sapiens] >gi|57078 ribosomal protein L38 [Rattus rattus] >pir|S15658|R5RT38 ribosomal protein L38 - rat >pir|S38385|S38385 ribosomal protein L38 - human >gnl|PID|d1026783 (AB007185) ribosomal protein L38 [Homo sapiens] {SUB 34-70}	gi|407423	13	351	72	72	H2LAV92	Lung, Pancreas, Prostate, Colon, Breast/Ovarian
726	H2LAO74R	ribosomal protein L10 [Homo sapiens] >sp|D1026771|D1026771 RIBOSOMAL PROTEIN L15 (FRAGMENT). {SUB 16-57} Length = 205	gi|414587	359	502	83	83	H2LAO74	Lung, Pancreas, Colon, Breast/Ovarian
727	HKMMF85R	ribosomal protein L18a [Homo sapiens] >gi|3702270 (AC005796) ribosomal protein L18a [Homo sapiens] >gnl|PID|d1029536 (AB007175) ribosomal protein L18a [Homo sapiens] {SUB 111-176} Length = 176	gi|401845	1	360	96	96	HKMMF85	Lung, Breast/Ovarian
728	HCLBZ27R	ribosomal protein L19 [Homo sapiens] >bbs|127872 ribosomal protein L19 [human, breast cancer cell line, MCF-7, Peptide, 196 aa] [Homo sapiens] >gi|206726 ribosomal protein L19 [Rattus norvegicus] >gnl|PID|e218038 ribosomal protein L19 [Rattus norvegicus]	gi|36128	19	273	93	98	HCLBZ27	Lung, Pancreas, Colon
729	H2LAV11R	ribosomal protein L21 [Homo sapiens] >gi|984143 ribosomal protein L21 [Homo sapiens] >pir|S55913|S55913 ribosomal protein L21, cytosolic - human >sp|D1026774|D1026774 RIBOSOMAL PROTEIN L21 (FRAGMENT). {SUB 124-154} Length = 160	gi|550015	126	530	99	99	H2LAV11	Lung, Pancreas, Colon

730	HBAGP60R	ribosomal protein L27 [Homo sapiens] >gi|3115335 ribosomal protein L27 [Homo sapiens] >gi|57694 ribosomal protein L27 (AA 1 - 136) [Rattus norvegicus] >gi|62981 ribosomal protein L27 [Gallus gallus] >pir|S00401|R5RT27 ribosomal protein L27, cytosolic - ra	gi|388769	161	373	66	70	HBAGP60	Pancreas, Colon
731	HOEMJ56R	ribosomal protein L28 [Homo sapiens] >pir|S55915|S55915 ribosomal protein L28 - human Length = 137	gi|550019	3	206	94	94	HOEMJ56	Lung, Colon, Breast/Ovarian
732	HA5AF77R	ribosomal protein L31 [Sus scrofa] >gi|36130 ribosomal protein L31 (AA 1-125) [Homo sapiens] >gi|57115 ribosomal protein L31 (AA 1-125) [Rattus norvegicus] >pir|S05576|R5HU31 ribosomal protein L31 - human >pir|A26417|R5RT31 ribosomal protein L31 - rat >gn	gnl|PID|e276436	1	381	82	82	HA5AF77	Lung, Prostate, Colon, Breast/Ovarian
733	H2MAC95R	ribosomal protein L37 [Homo sapiens] >bbs|172744 ribosomal protein L37 {C2-C2 zinc-finger-like} [human, HeLa cells, Peptide, 97 aa] [Homo sapiens] >gnl|PID|d1005426 ribosomal protein L37 [Homo sapiens] >gi|57121 ribosomal protein L37 [Rattus norvegicus] >	gi|292441	67	411	79	79	H2MAC95	Lung, Colon, Breast/Ovarian
734	HDPLP40R	ribosomal protein L37 [Homo sapiens] >bbs|172744 ribosomal protein L37 {C2-C2 zinc-finger-like} [human, HeLa cells, Peptide, 97 aa] [Homo sapiens] >gnl|PID|d1005426 ribosomal protein L37 [Homo sapiens] >gi|57121 ribosomal protein L37 [Rattus norvegicus] >	gi|292441	1	363	100	100	HDPLP40	Lung, Pancreas, Breast/Ovarian

735	HOEMK92R	ribosomal protein L37a [Homo sapiens] >gi|36134 ribosomal protein L37a [Homo sapiens] >gi|57123 ribosomal protein L37a (AA 1 - 92) [Rattus rattus] >gi|312414 ribosomal protein L37a [Mus musculus] >pir|S05014|R5RT37 ribosomal protein L37a - rat >pir|S42109	gi|292439	3	185	96	96	HOEMK92	Lung, Pancreas, Breast/Ovarian
736	HABAD57R	ribosomal protein L4 [Homo sapiens] >pir|S39803|S39803 ribosomal protein L4 - human Length = 425	gi|307385	210	431	80	90	HABAD57	Lung, Pancreas
737	HLXNA52R	ribosomal protein L4 [Rattus norvegicus] Length = 421	gnl|PID|e121603	3	296	86	86	HLXNA52	Lung, Pancreas
738	HWAFK82R	ribosomal protein L9 [Homo sapiens] >gnl|PID|d1003911 'human homologue of rat ribosomal protein L9' [Homo sapiens] Length = 192	gi|710366	139	354	77	78	HWAFK82	Lung, Colon, Breast/Ovarian
739	H2CBL68R	ribosomal protein S13 [Homo sapiens] >gi|488417 ribosomal protein S13 [Homo sapiens] >gnl|PID|d1014222 ribosomal protein S13 [Homo sapiens] >gi|57730 ribosomal protein S13 [Rattus rattus] >pir|S34109|S34109 ribosomal protein S13, cytosolic - human >pir|A3	gi|307391	3	461	100	100	H2CBL68	Lung, Pancreas
740	HNTNE17R	ribosomal protein S17 [Homo sapiens] >gi|337503 S17 ribosomal protein [Homo sapiens] >pir|JT0405|R4HU17 ribosomal protein S17, cytosolic - human Length = 135	gi|337501	1	387	100	100	HNTNE17	Lung, Pancreas, Breast/Ovarian
741	HBJLR37R	ribosomal protein S26 [Homo sapiens] Length = 115	gi|296452	2	328	98	100	HBJLR37	Pancreas, Colon, Breast/Ovarian

742	HOSNG20R	ribosomal protein S4X isoform [Homo sapiens] >gi|2791861 (AF041428) ribosomal protein s4 X isoform [Homo sapiens] >gi|200864 ribosomal protein S4 [Mus musculus] >gi|57135 ribosomal protein S4 (AA 1 - 263) [Rattus rattus] >gnl|PID|d1002335 ribosomal protei	gi|337510	1	357	97	98	HOSNG20	Lung, Pancreas, Colon, Breast/Ovarian
743	HCLBZ30R	ribosomal protein S5 [Mus musculus] Length = 204	gi|1685071	2	244	89	89	HCLBZ30	Lung, Pancreas, Colon, Breast/Ovarian
744	HBGNY11R	ribosomal protein S8 [Homo sapiens] >gi|57139 ribosomal protein S8 (AA 1-208) [Rattus norvegicus] >gi|313298 ribosomal protein S8 [Mus musculus] >pir|S01609|R3RT8 ribosomal protein S8 - rat >pir|S42110|S42110 ribosomal protein S8 - mouse >pir|S25022|S2502	gi|36150	2	334	100	100	HBGNY11	Lung, Pancreas, Breast/Ovarian
745	HOEKC80R	S19 ribosomal protein [Homo sapiens] >pir|I52692|I52692 ribosomal protein S19, cytosolic - human Length = 145	gi|337733	2	376	98	98	HOEKC80	Lung, Pancreas, Colon, Breast/Ovarian
746	HCHBM70R	secretory protein [Homo sapiens] >gi|940946 intestinal trefoil factor [Homo sapiens] >pir|A48284|A48284 intestinal trefoil factor 3 precursor - human >sp|Q07654|ITF_HUMAN INTESTINAL TREFOIL FACTOR PRECURSOR (HP1.B). Length = 80	gi|402483	1	114	57	57	HCHBM70	Colon, Breast/Ovarian
747	HFCES53R	semaphorin C [Mus musculus] >pir|I48746|I48746 semaphorin C - mouse (fragment) >sp|Q62179|Q62179 SEMAPHORIN C (SEM C) (FRAGMENT). Length = 782	gi|854328	1	165	80	86	HFCES53	Colon, Breast/Ovarian

748	HCRQC92R	spermidine/spermine N1-acetyltransferase [Homo sapiens] >gi|338336 spermidine/spermine N1-acetyltransferase [Homo sapiens] >sp|P21673|ATDA_HUMAN DIAMINE ACETYLTRANSFERASE (EC 2.3.1.57) (SPERMIDINE/SPERMINE N1-ACETYLTRANSFERASE) (SSAT) (PUTRESCINE ACETYLT	gi|338392	3	278	98	98	HCRQC92	Lung. Colon. Breast/Ovarian
749	HAOAG75R	TARBP-b gene product [Homo sapiens] Length = 277	gi|347964	2	418	100	100	HAOAG75	Lung. Colon
750	HWAFE36R	TEGT gene product [Homo sapiens] >pir|I38334|I38334 TEGT (testis enhanced gene transcript) - human Length = 237	gi|458545	2	127	100	100	HWAFE36	Pancreas. Colon
751	HBGOU57R	TIMP gene product [Homo sapiens] >gi|182483 prefibroblast collagenase inhibitor [Homo sapiens] >gi|189382 collagenase inhibitor [Homo sapiens] >gi|37183 precursor [Homo sapiens] >pir|A93372|ZYHUEP metalloproteinase tissue inhibitor 1 precursor - human >gi	gi|490094	60	314	75	75	HBGOU57	Lung. Pancreas. Breast/Ovarian
752	HTXPF20R	TIMP gene product [Homo sapiens] >gi|182483 prefibroblast collagenase inhibitor [Homo sapiens] >gi|189382 collagenase inhibitor [Homo sapiens] >gi|37183 precursor [Homo sapiens] >pir|A93372|ZYHUEP metalloproteinase tissue inhibitor 1 precursor - human >gi	gi|490094	1	549	84	84	HTXPF20	Lung. Pancreas. Colon. Breast/Ovarian
753	HCRMD09R	transforming growth factor-beta 1 binding protein precursor [Homo sapiens] >pir|A35626|A35626 transforming growth factor beta-1-binding protein - human Length = 1394	gi|339548	2	460	86	87	HCRMD09	Lung. Pancreas. Colon

754	HAJRB47R	triose-phosphate isomerase [Pan troglodytes] >gi|37247 triosephosphate isomerase [Homo sapiens] >gi|1200507 triosephosphate isomerase [Homo sapiens] >gi|339841 triosephosphate isomerase (EC 5.3.1.1) [Homo sapiens] >pir|S29743|ISHUT triose-phosphate isomer	gi|176960	2	334	100	100	HAJRB47	Lung, Pancreas, Breast/Ovarian
755	HABGB36R			6	251			HABGB36	Lung, Breast/Ovarian
756	HADBF86R			3	158			HADBF86	Lung, Colon
757	HADDP09R			2	97			HADDP09	Lung, Pancreas, Colon, Breast/Ovarian
758	HAGCY06R			2	58			HAGCY06	Pancreas, Breast/Ovarian
759	HAGDI75R			1	66			HAGDI75	Colon, Breast/Ovarian
760	HAHBD47R			118	429			HAHBD47	Lung, Pancreas
761	HAHCR61R			165	422			HAHCR61	Pancreas, Colon
762	HAJAU22R			101	202			HAJAU22	Pancreas, Colon
763	HAMGB62R			212	370			HAMGB62	Lung, Pancreas, Colon, Breast/Ovarian
764	HANGC52R			3	98			HANGC52	Lung, Pancreas, Colon
765	HAPCF30R			2	94			HAPCF30	Lung, Colon
766	HAPPV45R			216	536			HAPPV45	Lung, Pancreas
767	HAPQK19R			200	415			HAPQK19	Lung, Pancreas
768	HAPRL82R			3	233			HAPRL82	Lung, Pancreas
769	HAQBT45R			40	255			HAQBT45	Lung, Colon
770	HAUAL56R			127	315			HAUAL56	Pancreas, Breast/Ovarian

771	HAUBR22R	2	67	HAUBR22	Pancreas, Colon, Breast/Ovarian
772	HBAFN19R	3	257	HBAFN19	Lung, Colon, Breast/Ovarian
773	HBGOK25R	274	528	HBGOK25	Pancreas, Colon
774	HBGRA76R	2	88	HBGRA76	Pancreas, Colon
775	HBGRB47R	1	111	HBGRB47	Lung, Pancreas, Colon, Breast/Ovarian
776	HBJAS24R	1	66	HBJAS24	Colon, Breast/Ovarian
777	HBJKI05R	207	362	HBJKI05	Pancreas, Colon
778	HBKEC86R	254	409	HBKEC86	Pancreas, Colon
779	HBLGD42R	3	341	HBLGD42	Lung, Pancreas, Colon, Breast/Ovarian
780	HBPAF10R	3	65	HBPAF10	Lung, Pancreas
781	HCDBU02R	65	184	HCDBU02	Pancreas, Colon
782	HCDBU04R	64	348	HCDBU04	Lung, Pancreas, Colon
783	HCDDT61R	2	121	HCDDT61	Pancreas, Colon
784	HCEGY65R	2	79	HCEGY65	Pancreas, Colon
785	HCHAK80R	1	513	HCHAK80	Colon, Breast/Ovarian
786	HCHMW79R	73	432	HCHMW79	Pancreas, Breast/Ovarian
787	HCHOB92R	93	350	HCHOB92	Colon, Breast/Ovarian
788	HCLBO01R	45	149	HCLBO01	Lung, Colon
789	HCQAN60R	3	122	HCQAN60	Pancreas, Colon
790	HCRAK70R	3	293	HCRAK70	Colon, Breast/Ovarian
791	HCRPC63R	1	129	HCRPC63	Pancreas, Colon
792	HCUDC51R	2	265	HCUDC51	Lung, Colon

793	HDPFI40R	139	453	HDPFI40	Lung, Pancreas, Breast/Ovarian
794	HDPLP23R	1	141	HDPLP23	Pancreas, Colon, Breast/Ovarian
795	HDPRZ54R	1	165	HDPRZ54	Colon, Breast/Ovarian
796	HE9DP46R	2	166	HE9DP46	Lung, Pancreas, Colon
797	HEGAR19R	361	534	HEGAR19	Lung, Colon
798	HFAUO64R	27	137	HFAUO64	Colon, Breast/Ovarian
799	HFIAL90R	186	308	HFIAL90	Lung, Colon
800	HHBEQ12R	218	514	HHBEQ12	Lung, Pancreas
801	HHEUL94R	2	127	HHEUL94	Lung, Pancreas, Colon
802	HISCF76R	16	153	HISCF76	Pancreas, Colon
803	HJMAU64R	1	207	HJMAU64	Lung, Colon
804	HJPCI25R	275	508	HJPCI25	Lung, Pancreas, Colon
805	HKBAC48R	369	542	HKBAC48	Lung, Pancreas, Colon, Breast/Ovarian
806	HKBAD57R	165	341	HKBAD57	Lung, Pancreas
807	HKDBA91R	3	332	HKDBA91	Pancreas, Colon
808	HKGDB80R	3	224	HKGDB80	Lung, Colon
809	HLDNC95R	289	537	HLDNC95	Lung, Pancreas, Prostate, Colon
810	HMSNI52R	2	271	HMSNI52	Lung, Pancreas
811	HODAY16R	134	298	HODAY16	Colon, Breast/Ovarian
812	HODEA57R	289	471	HODEA57	Lung, Pancreas
813	HOEMO27R	1	60	HOEMO27	Colon, Breast/Ovarian

814	HOEMO62R	2	73	HOEMO62	Pancreas, Breast/Ovarian
815	HOEMS18R	1	102	HOEMS18	Lung, Pancreas, Colon, Breast/Ovarian
816	HOENU53R	115	267	HOENU53	Lung, Colon
817	HOGAP33R	1	498	HOGAP33	Pancreas, Prostate, Breast/Ovarian
818	HOSMV34R	124	327	HOSMV34	Lung, Pancreas, Breast/Ovarian
819	HOSNF25R	405	587	HOSNF25	Pancreas, Colon
820	HOUHO32R	230	391	HOUHO32	Lung, Colon
821	HPIAC23R	2	286	HPIAC23	Lung, Breast/Ovarian
822	HRAAD31R	115	414	HRAAD31	Lung, Colon
823	HRACR12R	2	100	HRACR12	Pancreas, Colon
824	HRADJ57R	2	142	HRADJ57	Lung, Colon
825	HROAX48R	184	285	HROAX48	Pancreas, Colon
826	HTAHR87R	369	491	HTAHR87	Lung, Pancreas
827	HTTIO45R	1	288	HTTIO45	Colon, Breast/Ovarian
828	HTWDH05R	1	420	HTWDH05	Lung, Pancreas, Colon, Breast/Ovarian
829	HUFDS13R	51	152	HUFDS13	Pancreas, Colon
830	HUSZE86R	2	340	HUSZE86	Pancreas, Colon
831	HUTHF75R	161	418	HUTHF75	Lung, Pancreas, Breast/Ovarian
832	HWAFW07R	3	170	HWAFW07	Lung, Pancreas, Colon
833	HWLIB82R	209	403	HWLIB82	Pancreas, Colon
834	HWLLX91R	147	302	HWLLX91	Lung, Colon
835	HWLMZ54R	1	120	HWLMZ54	Pancreas, Colon

836	HMIAI78R			173	319			HMIAI78	Pancreas, Colon, Breast/Ovarian
837	HBGFJ39R	unknown product specific to adipose tissue [Homo sapiens] >sp|Q15847|Q15847 HYPOTHETICAL 7.9 KD PROTEIN. Length = 76	gnl|PID|d1008821	1	153	100	100	HBGFJ39	Pancreas, Colon
838	HAMHH32R			1	123			HAMHH32	Lung, Colon
839	HAQBQ95R			104	205			HAQBQ95	Colon, Breast/Ovarian
840	HAGHY58R	URF 1 (NADH dehydrogenase subunit) [Homo sapiens] >gi|337189 protein 1 [Homo sapiens] >pir|A00407|DNHUN1 NADH dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - human mitochondrion (SGC1) >sp|P03886|NU1M_HUMAN NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6	gi|13004	157	411	95	95	HAGHY58	Lung, Colon
841	HOSNE37R	URF 2 (NADH dehydrogenase subunit) [Homo sapiens] >gi|2052363 protein 2 [Homo sapiens] >gi|2582057 (AF014882) NADH dehydrogenase subunit 2 [Homo sapiens] >gi|2582061 (AF014884) NADH dehydrogenase subunit 2 [Homo sapiens] >gi|2582063 (AF014885) NADH dehydr	gi|578710	73	231	59	62	HOSNE37	Lung, Pancreas, Colon
842	HWAFE41R	VDUP1=1,25-dihydroxyvitamin D-3 up-regulated [human, HL-60 promyelocytic leukemia cells, Peptide, 391 aa] [Homo sapiens] Length = 391	bbs|155932	2	508	84	84	HWAFE41	Pancreas, Colon

The first column of Table 1 shows the "SEQ ID NO:" for each of the 842 cancer antigen polynucleotide sequences of the invention.

The second column in Table 1, provides a unique "Sequence/Contig ID" identification for each cancer associated sequence. The third column in Table 1, "Gene Name," provides a putative identification of the gene based on the sequence similarity of its translation product to an amino acid sequence found in a publicly accessible gene database, such as GenBank (NCBI). The great majority of the cDNA sequences reported in Table 1 are unrelated to any sequences previously described in the literature. The fourth column, in Table 1, "Overlap," provides the database accession no. for the database sequence having similarity. The fifth and sixth columns in Table 1 provide the location (nucleotide position nos. within the contig), "Start" and "End", in the polynucleotide sequence "SEQ ID NO:X" that delineate the preferred ORF shown in the sequence listing as SEQ ID NO:Y. In one embodiment, the invention provides a protein comprising, or alternatively consisting of, a polypeptide encoded by the portion of SEQ ID NO:X delineated by the nucleotide position nos. "Start" and "End". Also provided are polynucleotides encoding such proteins and the complementary strand thereto. The seventh and eighth columns provide the "% Identity" (percent identity) and "% Similarity" (percent similarity) observed between the aligned sequence segments of the translation product of SEQ ID NO:X and the database sequence.

The ninth column of Table 1 provides a unique "Clone ID" for a clone related to each contig sequence. This clone ID references the cDNA clone which contains at least the 5' most sequence of the assembled contig and at least a portion of SEQ ID NO:X was determined by directly sequencing the referenced clone. The reference clone may have more sequence than described in the sequence listing or the clone may have less. In the vast majority of cases, however, the clone is believed to encode a full-length polypeptide. In the case where a clone is not full-length, a full-length cDNA can be obtained by methods described elsewhere herein.

The tenth column of Table 1, "Tissue," provides the tissue source where each unique SEQ ID NO:X was found to be predominantly expressed.

Table 3 indicates public ESTs, of which at least one, two, three, four, five, ten, or more of any one or more of these public ESTs are optionally excluded from the invention.

SEQ ID NO:X (where X may be any of the polynucleotide sequences disclosed in the sequence listing as SEQ ID NO:1 through SEQ ID NO:842) and the translated SEQ ID NO:Y

(where Y may be any of the polypeptide sequences disclosed in the sequence listing as SEQ ID NO:843 through SEQ ID NO:1684) are sufficiently accurate and otherwise suitable for a variety of uses well known in the art and decribed further below. For instance, SEQ ID NO:X has uses including, but not limited to, in designing nucleic acid hybridization probes that will detect nucleic acid sequences contained in SEQ ID NO:X or the related cDNA clone contained in a library deposited with the ATCC. These probes will also hybridize to nucleic acid molecules in biological samples, thereby enabling immediate applications in chromosome mapping, linkage analysis, tissue identification and/or typing, and a variety of forensic and diagnostic methods of the invention. Similarly, polypeptides identified from SEQ ID NO:Y have uses that include, but are not limited to, generating antibodies which bind specifically to the cancer antigen polypeptides, or fragments thereof, and/or to the cancer antigen polypeptides encoded by the cDNA clones identified in Table 1.

Nevertheless, DNA sequences generated by sequencing reactions can contain sequencing errors. The errors exist as misidentified nucleotides, or as insertions or deletions of nucleotides in the generated DNA sequence. The erroneously inserted or deleted nucleotides cause frame shifts in the reading frames of the predicted amino acid sequence. In these cases, the predicted amino acid sequence diverges from the actual amino acid sequence, even though the generated DNA sequence may be greater than 99.9% identical to the actual DNA sequence (for example, one base insertion or deletion in an open reading frame of over 1000 bases).

Accordingly, for those applications requiring precision in the nucleotide sequence or the amino acid sequence, the present invention provides not only the generated nucleotide sequence identified as SEQ ID NO:X, the predicted translated amino acid sequence identified as SEQ ID NO:Y, but also a sample of plasmid DNA containing the related cDNA clone (deposited with the ATCC, as set forth in Table 1). The nucleotide sequence of each deposited clone can readily be determined by sequencing the deposited clone in accordance with known methods. Further, techniques known in the art can be used to verify the nucleotide sequences of SEQ ID NO:X.

The predicted amino acid sequence can then be verified from such deposits. Moreover, the amino acid sequence of the protein encoded by a particular clone can also be directly determined by peptide sequencing or by expressing the protein in a suitable host cell containing the deposited human cDNA, collecting the protein, and determining its sequence.

The present invention also relates to vectors or plasmids which include such DNA sequences, as well as the use of the DNA sequences. The material deposited with the ATCC on:

Table 2

ATCC Deposits	Deposit Date	ATCC Designation Number
LP01, LP02, LP03, LP04, LP05, LP06, LP07, LP08, LP09, LP10, LP11,	May-20-97	209059, 209060, 209061, 209062, 209063, 209064, 209065, 209066, 209067, 209068, 209069
LP12	Jan-12-98	209579
LP13	Jan-12-98	209578
LP14	Jul-16-98	203067
LP15	Jul-16-98	203068
LP16	Feb-1-99	203609
LP17	Feb-1-99	203610
LP20	Nov-17-98	203485
LP21	Jun-18-99	PTA-252
LP22	Jun-18-99	PTA-253
LP23	Dec-22-99	PTA-1081

each is a mixture of cDNA clones derived from a variety of human tissue and cloned in either a plasmid vector or a phage vector, as shown in Table 5. These deposits are referred to as "the deposits" herein. The tissues from which the clones were derived are listed in Table 5, and the vector in which the cDNA is contained is also indicated in Table 5. The deposited material includes the cDNA clones which were partially sequenced and are related to the SEQ ID NO:X described in Table 1 (column 9). Thus, a clone which is isolatable from the ATCC Deposits by use of a sequence listed as SEQ ID NO:X may include the entire coding region of a human gene or in other cases such clone may include a substantial portion of the coding region of a human gene. Although the sequence listing lists only a portion of the DNA sequence in a clone included in the ATCC Deposits, it is well within the ability of one skilled in the art to complete the sequence of the DNA included in a clone isolatable from the

ATCC Deposits by use of a sequence (or portion thereof) listed in Table 1 by procedures hereinafter further described, and others apparent to those skilled in the art.

Also provided in Table 5 is the name of the vector which contains the cDNA clone. Each vector is routinely used in the art. The following additional information is provided for convenience.

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., *Nucleic Acids Res. 16*:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., *Nucleic Acids Res. 17*:9494 (1989)) and pBK (Alting-Mees, M. A. et al., *Strategies 5*:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Phagemid pBS may be excised from the Lambda Zap and Uni-Zap XR vectors, and phagemid pBK may be excised from the Zap Express vector. Both phagemids may be transformed into *E. coli* strain XL-1 Blue, also available from Stratagene.

Vectors pSport1, pCMVSport 1.0, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, also available from Life Technologies. See, for instance, Gruber, C. E., et al., *Focus 15*:59 (1993). Vector lafmid BA (Bento Soares, Columbia University, New York, NY) contains an ampicillin resistance gene and can be transformed into *E. coli* strain XL-1 Blue. Vector pCR®2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into *E. coli* strain DH10B, available from Life Technologies. See, for instance, Clark, J. M., *Nuc. Acids Res. 16*:9677-9686 (1988) and Mead, D. *et al., Bio/Technology 9*: (1991).

The present invention also relates to the genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the cDNA contained in a deposited cDNA clone. The corresponding gene can be isolated in accordance with known methods using the sequence information disclosed herein. Such methods include, but are not limited to, preparing probes or primers from the disclosed sequence and identifying or amplifying the corresponding gene from appropriate sources of genomic material.

Also provided in the present invention are allelic variants, orthologs, and/or species homologs. Procedures known in the art can be used to obtain full-length genes, allelic variants, splice variants, full-length coding portions, orthologs, and/or species homologs of genes corresponding to SEQ ID NO:X, SEQ ID NO:Y, and/or the cDNA contained in the related cDNA clone in the deposit, using information from the sequences disclosed herein or the clones deposited with the ATCC. For example, allelic variants and/or species homologs may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source for allelic variants and/or the desired homologue.

The present invention provides a polynucleotide comprising, or alternatively consisting of, the nucleic acid sequence of SEQ ID NO:X, and/or the related cDNA clone (See, e.g., columns 1 and 9 of Table 1). The present invention also provides a polypeptide comprising, or alternatively, consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library. Polynucleotides encoding a polypeptide comprising, or alternatively consisting of, the polypeptide sequence of SEQ ID NO:Y, a polypeptide encoded by SEQ ID NO:X, and/or a polypeptide encoded by the the dDNA in the related cDNA clone contained in a deposited library, are also encompassed by the invention. The present invention further encompasses a polynucleotide comprising, or alternatively consisting of, the complement of the nucleic acid sequence of SEQ ID NO:X, and/or the complement of the coding strand of the related cDNA clone contained in a deposited library.

Many polynucleotide sequences, such as EST sequences, are publicly available and accessible through sequence databases and may have been publicly available prior to conception of the present invention. Preferably, such related polynucleotides are specifically excluded from the scope of the present invention. To list every related sequence would unduly burden the disclosure of this application. Accordingly, for each "Contig Id" listed in the first column of Table 3, preferably excluded are one or more polynucleotides comprising a nucleotide sequence described in the second column of Table 3 by the general formula of a-b, each of which are uniquely defined for the SEQ ID NO:X corresponding to that Contig Id in Table 1. Additionally, specific embodiments are directed to polynucleotide sequences excluding at least one, two, three, four, five, ten, or more of the specific polynucleotide sequences referenced by the Genbank Accession No. for each Contig Id which may be

included in column 3 of Table 3. In no way is this listing meant to encompass all of the sequences which may be excluded by the general formula, it is just a representative example.

Table 3.

Sequence/ Contig ID	General formula	Genbank Accession No.
507291	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 542 of SEQ ID NO:1, b is an integer of 15 to 556, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:1, and where b is greater than or equal to a + 14.	
508000	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2648 of SEQ ID NO:2, b is an integer of 15 to 2662, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:2, and where b is greater than or equal to a + 14.	T40333, T41194, T66286, T66339, T73997, T86453, T87207, R17614, R19835, R43336, R45934, R48920, R53521, R43336, R45934, R61813, R75928, R75937, H30115, H42959, H39114, H43825, AA028010, AA028107, AA028148, AA031964, AA032046, AA035668, AA190570, AA233781, AA461489, AA460726, AA460898
518325	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 324 of SEQ ID NO:3, b is an integer of 15 to 338, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:3, and where b is greater than or equal to a + 14.	
523111	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 799 of SEQ ID NO:4, b is an integer of 15 to 813, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:4, and where b is greater than or equal to a + 14.	
526869	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 887 of SEQ ID NO:5, b is an integer of 15 to 901, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:5, and where b is greater than or equal to a + 14.	AA459771
532211	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 717 of SEQ ID NO:6, b is an integer of 15 to 731, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:6, and where b is greater than or equal to a + 14.	H30209, H92182, W95693, W95692, AA196967
532247	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	R14583, R93797, H52942, H75493, H78857, W17094, W38705, W81551, W90159, N90874, AA010244,

	where a is any integer between 1 to 2760 of SEQ ID NO:7, b is an integer of 15 to 2774, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:7, and where b is greater than or equal to a + 14.	AA029093, AA126501, AA147066
537932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2599 of SEQ ID NO:8, b is an integer of 15 to 2613, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:8, and where b is greater than or equal to a + 14.	T91131, T84801, T85952, R59198, R59256, H43456, H59480, H79111, N26560, N35676, N64506, N66078, N76033, N78705, W07594, W70111, W70169, N90844, AA026910, AA026911, AA057689, AA079631, AA079805, AA131257, AA136081, AA165115, AA210764, AA211886, AA232838, AA262352
540117	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1087 of SEQ ID NO:9, b is an integer of 15 to 1101, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:9, and where b is greater than or equal to a + 14.	T49371, T49372, T49850, T61568, T64892, N39534, W57682, AA031859
547710	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1359 of SEQ ID NO:10, b is an integer of 15 to 1373, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:10, and where b is greater than or equal to a + 14.	R11154, R11155, R61204, R61205, R82674, H06105, R88575, R88638, H89977, H97031, N20224, W01143, W39387, W90318, W90788, AA001027, AA045864, AA045839, AA070190, AA070357, AA070481, AA074270, AA099007, AA099084, AA100370, AA112324, AA113319, AA158425, AA161510, AA171909, AA172133, AA173087, AA181768, AA188815, AA188874, AA190370, AA226831, AA252143
551747	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3790 of SEQ ID NO:11, b is an integer of 15 to 3804, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:11, and where b is greater than or equal to a + 14.	
552799	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2143 of SEQ ID NO:12, b is an integer of 15 to 2157, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:12, and where b is greater than or equal to a + 14.	
553243	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1103 of SEQ ID NO:13, b is an integer of 15 to 1117, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:13, and where b is	H63183, W61352, AA151059

	greater than or equal to a + 14.	
553368	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 871 of SEQ ID NO:14, b is an integer of 15 to 885, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:14, and where b is greater than or equal to a + 14.	
554349	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1010 of SEQ ID NO:15, b is an integer of 15 to 1024, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:15, and where b is greater than or equal to a + 14.	
558491	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 531 of SEQ ID NO:16, b is an integer of 15 to 545, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:16, and where b is greater than or equal to a + 14.	
558983	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 609 of SEQ ID NO:17, b is an integer of 15 to 623, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:17, and where b is greater than or equal to a + 14.	
572943	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 545 of SEQ ID NO:18, b is an integer of 15 to 559, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:18, and where b is greater than or equal to a + 14.	
585892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1341 of SEQ ID NO:19, b is an integer of 15 to 1355, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:19, and where b is greater than or equal to a + 14.	
589390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1266 of SEQ ID NO:20, b is an integer of 15 to 1280, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:20, and where b is greater than or equal to a + 14.	T47628, T49403, T49829, T49830, T50800, T50963, T51976, T55846, T55860, T55896, T55911, T58744, T58811, T58891, T59252, T59279, T59293, T59615, T59690, T59727, T59826, T60434, T60514, T60584, T61357, T40352, T62559, T62688, T62839, T63122, T64603, T64640.

		T67682, T67756, T68181, T68439, T68506, T68606, T68718, T68783, T68839, T68849, T68976, T69049, T71223, T71347, T71509, T71853, T71858, T71938, T72197, T72264, T72414, T72471, T72923, T73204, T73259, T73283, T73446, T73607, T73621, T73645, T73713, T73744, T73772, T73796, T74114, T74545, T74599, T87829, T90307, T90394, T91481, T92437, T92617, T81767, T82080, R27059, R27060, R31693, R31735, R50548, R50646, R64321, R64322, R75660, R75768, R75866, R76038, R79765, R79766, H22209, H24391, H25902, H27236, H28585, H29860, H29954, H41994, H42226, H42298, H43069, H43893, H43934, R83465, R84983, R94905, R94988, R96360, R96403, R97059,.R98674, R98900, R99186, R99187, H50701, H50801, H57754, H62182, H63649, H63650, H64755, H64756, H69075, H70056, H70057, H70855, H70856, H71581, H75758, H75893, H80974, H80975, H83141, H83142, H83271, H85046, H84668, H91780, H92207, H92350, H94891, H94943, H94966, H95486, H99418, N52264, N58261, N74184, N77638, N81021, N92261, N99137, W04350, W07850, W16893, W39467, W45038, W47174, W47433, W52853, W63782, W67635, W67759, W67868, W67881, W93706, W94183, W96351, W96352, N89587, AA012898, AA019884, AA020863, AA025865, AA025866, AA056092, AA057434, AA070445, AA192155, AA192879, AA226741, AA227477
596882	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1177 of SEQ ID NO:21, b is an integer of 15 to 1191, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:21, and where b is greater than or equal to a + 14.	
616289	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 839 of SEQ ID NO:22, b is an integer of 15 to 853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:22, and where b is greater than or equal to a + 14.	
622140	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	W39497, W52751, AA099814, AA128882, AA173072, AA226739

	sequence described by the general formula of a-b, where a is any integer between 1 to 460 of SEQ ID NO:23, b is an integer of 15 to 474, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:23, and where b is greater than or equal to a + 14.	
623566	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2266 of SEQ ID NO:24, b is an integer of 15 to 2280, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:24, and where b is greater than or equal to a + 14.	
647714	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1047 of SEQ ID NO:25, b is an integer of 15 to 1061, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:25, and where b is greater than or equal to a + 14.	
647752	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1558 of SEQ ID NO:26, b is an integer of 15 to 1572, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:26, and where b is greater than or equal to a + 14.	
651774	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1991 of SEQ ID NO:27, b is an integer of 15 to 2005, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:27, and where b is greater than or equal to a + 14.	T69901, T69949, T70775, R20554, R33030, R33917, R48406, H58331, H58720, H67041, H68124, H93586, H94430, H94513, H97468, H99219, N23459, N26334, N35428, N49203, N50256, N64246, N93349, W19550, W19996, W25330, W73940, W77984, W93791, W94028, N90424, AA025537, AA025680, AA025371, AA026317, AA026318, AA084549, AA086048, AA086130, AA098995, AA099068, AA115309, AA136486, AA151843, AA149689, AA148825, AA150406, AA150425, AA173377
651995	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1394 of SEQ ID NO:28, b is an integer of 15 to 1408, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:28, and where b is greater than or equal to a + 14.	
652156	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 903 of SEQ ID NO:29, b is an integer of 15 to 917, where both a and	T40364, R22492, R49907, R49908, R62310, R62311, R65652, R67030, R81699, R81700, H18589, H20024, H20099, H20123, H20797, H22404, H22615, H25816, H27051, H42294,

	b correspond to the positions of nucleotide residues shown in SEQ ID NO:29, and where b is greater than or equal to a + 14.	H44827, H49661, H51422, H51465, H56482, H56483, H70295, H86037, H93528, H93860, H96113, H96114, N22715, N31188, N33831, N54495, N70601, N70623, N76607, N78626, W04920, W05505, W07305, W15350, W39442, W60859, W60860, W72726, W76452, AA017463, AA024543, AA024544, AA026421, AA026498, AA027270, AA034429, AA046316, AA046142, AA053920, AA056230, AA063244, AA062885, AA085305, AA128171, AA126216, AA149890, AA150552, AA187825, AA188597, AA417004, AA417190
653010	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 563 of SEQ ID NO:30, b is an integer of 15 to 577, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:30, and where b is greater than or equal to a + 14.	
655904	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2045 of SEQ ID NO:31, b is an integer of 15 to 2059, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:31, and where b is greater than or equal to a + 14.	T61561, T90265, T90707, R09280, R17627, R43348, R54854, R54658, H20872, H27229, H64571, H64673, H64571, N47495, N54722, N75461, W73679, AA010711, AA010712, AA082107, AA130516, AA132052, AA132156, AA147852, AA147908, AA148276, AA148277, AA181933, AA187549, AA187845, AA186675, AA188310, AA193212
657852	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 535 of SEQ ID NO:32, b is an integer of 15 to 549, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:32, and where b is greater than or equal to a + 14.	
666414	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 827 of SEQ ID NO:33, b is an integer of 15 to 841, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:33, and where b is greater than or equal to a + 14.	
667847	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 849 of SEQ ID NO:34, b is an integer of 15 to 863, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:34, and where b is greater than or equal to a + 14.	T47009, T47010, T55133, T55301, T57663, T57702, T59664, T59797, T59800, T49370, T72020, T26631, R22343, R46325, R48879, R50151, R50204, R55208, R71485, R71535, R72144, R72362, R72553, R74062, H13587, H16167, H18121, H20172, H20361, H22514, H40774, H40775,

		H42435. H42865. H43100. H43164, H45140. H45441. H46013. H46083, H46159, R97084. R97131. H56498, H60260, H60567. H67238. H71802, H77325. H77338. H81556. H87775, H87825. H91889. H92057. H93187, H96056. H96420. H81556. H99575, N21484. N23829, N24221. N26831, N27079, N27278. N27582. N30213, N30255. N31642. N31989. N31996, N32655, N32790, N35515. N38983, N39859, N40012: N40488. N41792, N41978, N54988. N57097. N70071, N77176, N78930, N80037. N80573, N81058. N92768, N93810, W07000, W07659, W07868. W44961, W44962, W58175, W58263. W58182, AA001206. AA017579. AA026640, AA026706, AA057605. AA058758, AA082491, AA084088. AA086460, AA100968, AA112029. AA121337, AA121500, AA130704. AA130790, AA152420, AA156094. AA156123, AA181929, AA182575, AA182617, AA186931. AA195982. AA253952, AA283976, AA426098. AA425122, AA428823. AA429359
670188	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1216 of SEQ ID NO:35, b is an integer of 15 to 1230, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:35, and where b is greater than or equal to a + 14.	
670279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 626 of SEQ ID NO:36, b is an integer of 15 to 640, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:36, and where b is greater than or equal to a + 14.	T50781, T51265, T55324, T56327
670729	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 583 of SEQ ID NO:37, b is an integer of 15 to 597, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:37, and where b is greater than or equal to a + 14.	
674123	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 610 of SEQ ID NO:38, b is an integer of 15 to 624, where both a and b correspond to the positions of nucleotide residues	

	shown in SEQ ID NO:38. and where b is greater than or equal to a + 14.	
676496	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1015 of SEQ ID NO:39. b is an integer of 15 to 1029, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:39, and where b is greater than or equal to a + 14.	
678162	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1093 of SEQ ID NO:40, b is an integer of 15 to 1107, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:40, and where b is greater than or equal to a + 14.	T40233, T40521, T41098, T47133, T47529, T49156, T49157, T51636, T55352, T55402, T55422, T57649, T59314, T62530, T62806, T62954, T72271, T73592, T89655, T78884, R19194, R89249, R93164, H57861, H93645, N22493, N26661, N32984, N63146, N66448, N67443, N69984, N72141, N77952, N78933, N81091, N95826, W02074, W24850, W24972, W38365, W44897, W57997, W58080, W65414, W65435, W74634, AA007562, AA009767, AA022918, AA022939, AA025169, AA029717, AA029656, AA032096, AA040581, AA046091, AA070493, AA070646, AA070707, AA071405, AA071414, AA074752, AA075706, AA075696, AA079282, AA085620, AA100126, AA126795, AA128838, AA136579, AA143069, AA143200, AA146637, AA147370, AA147705, AA156001, AA157342, AA161090, AA164798, AA179749, AA187235, AA188048, AA187029, AA188384, AA192271, AA196973, AA235468, AA243180, AA459416, AA459642
678248	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1037 of SEQ ID NO:41, b is an integer of 15 to 1051, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:41, and where b is greater than or equal to a + 14.	
683668	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2178 of SEQ ID NO:42, b is an integer of 15 to 2192, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:42, and where b is greater than or equal to a + 14.	T49549, T49550, T49700, T49912, T49937, T50912, T51558, T53285, T53375, T53376, T53721, T54314, T54840, T55217, T56413, T99069, T99669, R01522, R31653, R32820, R32921, R35743, R50997, R64077, R65723, R69349, R71009, R72798, R72824, R76854, R77142, R79240, R79511, R80194, R80295, R81155, H39823, H39824, R84909, R85592, R91193, H50793, H52341, H53594, H53916, H92997, N26572, N32090,

		N32406, N34179, N36271, N45401, N49216, N50267, N67233, N67568, N72254, N75478, N93355, N94504, W00543, W05288, W05816, W23954, W24625, W24650, W25354, W49666, W52302, AA121852, AA121851, AA128593, AA128712, AA136731, AA136688, AA167235, AA167584, AA173693, AA176648, AA176804, AA179999, AA181456, AA181457, AA256158, AA256215, AA256247, AA458729, AA458778, AA464936, AA464937
693172	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 339 of SEQ ID NO:43, b is an integer of 15 to 353, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:43, and where b is greater than or equal to a + 14.	T49005, T50129, T54766, T59468, T71241, T89633, R66699, R67578, H25853, H26090, H41256, H43182, H45273, N58288, N95319, AA054338, AA057604, AA084261
694303	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3476 of SEQ ID NO:44, b is an integer of 15 to 3490, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:44, and where b is greater than or equal to a + 14.	
695042	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 767 of SEQ ID NO:45, b is an integer of 15 to 781, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:45, and where b is greater than or equal to a + 14.	
699799	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1417 of SEQ ID NO:46, b is an integer of 15 to 1431, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:46, and where b is greater than or equal to a + 14.	T50599, R25615, R31078, R68513, R70896, R75848, R76864, R76865, H01087, H26949, H63077, H75713, H75642, H95014, H98885, N24938, N33815, N47174, N47897, N51152, N53997, N59590, N62387, N63017, N67836, N69948, N78655, N79355, N94343, N98329, W01767, W03440, W15144, W19292, W25534, W37911, W42857, W42912, W48630, W72791, W76438, W81113, W80546, W80525, W80526, W84575, W84645, AA010674, AA011261, AA026981, AA031662, AA039737, AA039810, AA040524, AA040523, AA046308, AA046396, AA099365, AA101915, AA129310, AA129354, AA131951, AA186409
702216	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	T64167, T64355, T68409, T68475, T73691, T73717, T97735, T97840,

	sequence described by the general formula of a-b, where a is any integer between 1 to 1899 of SEQ ID NO:47, b is an integer of 15 to 1913, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:47, and where b is greater than or equal to a + 14.	T98899, T99491, R00460, R01214, R01326, H45786, R93124, R96609, H61118, H61119, H61454, H62460, H64003, H64052, H91078, H91378, N58480, N64695, N65991, N74260, N78070, N79244, N91708, N95101, W03761, W04301, N90479, AA130077, AA130076, AA152275, AA150441
703015	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1747 of SEQ ID NO:48, b is an integer of 15 to 1761, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:48, and where b is greater than or equal to a + 14.	R72819, R73270, H43839, W47195, W52204, AA242894, AA424584, AA424629
706391	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 942 of SEQ ID NO:49, b is an integer of 15 to 956, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:49, and where b is greater than or equal to a + 14.	T48974, H26922, H30342, H44743, H45233, R88178, H81778, H92363, N29006, N44860, N46515, AA079547, AA158434, AA160590, AA428285
706892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 549 of SEQ ID NO:50, b is an integer of 15 to 563, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:50, and where b is greater than or equal to a + 14.	
706924	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3201 of SEQ ID NO:51, b is an integer of 15 to 3215, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:51, and where b is greater than or equal to a + 14.	T68892, T68966, T75421, R15205, R16398, R41650, R42339, R52995, R52996, R41650, H12000, H16753, H16861, H27652, H27653, H27982, H28497, H29323, H29416, H85752, H98511, N22580, N24339, N28586, N42727, N50084, N75803, N78815, W07245, W21306, W23840, W57924, W58128, W72277, W76304, W86460, AA002243, AA002080, AA025565, AA025683, AA026606, AA026718, AA150696, AA150801
707642	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 612 of SEQ ID NO:52, b is an integer of 15 to 626, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:52, and where b is greater than or equal to a + 14.	
710369	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 906 of SEQ ID NO:53, b is an integer of 15 to 920, where both a and	T48815, T60685, T91108, T99835, AA150217, AA157340, AA157240, AA171947

	b correspond to the positions of nucleotide residues shown in SEQ ID NO:53, and where b is greater than or equal to a + 14.	
718826	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1076 of SEQ ID NO:54, b is an integer of 15 to 1090, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:54, and where b is greater than or equal to a + 14.	
719790	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1450 of SEQ ID NO:55, b is an integer of 15 to 1464, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:55, and where b is greater than or equal to a + 14.	T47380, T47538, T47539, T53445, T53446, T54910, T55077, T59959, T60032, T62504, T62649, T63049, T63297, T63382, T65688, T71591, T71742, T93094, T93187, T94131, T94222, T91210, T84959, T99044, T99045, R26119, R26148, R33224, R35866, R36526, R53923, R53924, R69596, R69684, R76209, R76210, R79249, R79521, H03427, H03507, H12529, H13501, H19016, H19310, H21587, H21652, H21653, H30119, H39693, H42698, H46635, R93371, R98210, R99855, H54120, H54786, H54837, H58991, H65355, H65566, H67613, H72632, H74102, H95312, N48235, N58029, N64226, N66907, N70763, N78303, N93848, N94316, N95432, N98433, W01816, W02218, W05772, W21419, W24044, W24297, W30823, W32382, W37228, W37317, W40321, W42528, W46445, W49731, W51944, W53011, W53012, W60051, W60129, W60154, W68332, W68216, W72730, W74593, W92813, W93310, AA010985, AA011307, AA031435, AA035708, AA037040, AA053073, AA053374, AA055567, AA069724, AA069690, AA069682, AA069900, AA069951, AA070693, AA071421, AA074606, AA075555, AA075673, AA075544, AA081017, AA081251, AA081428, AA082119, AA082022, AA082213, AA082241, AA082247, AA082400, AA082365, AA082438, AA082679, AA083225, AA083266, AA083508, AA083411, AA083637, AA084202, AA099623, AA102015, AA099659, AA100102, AA100163, AA100429, AA100430, AA100455, AA100456, AA100711, AA100764, AA100906, AA100919, AA100963, AA101118, AA102494, AA101184, AA112123, AA122359, AA122360, AA126882, AA127103, AA128195, AA128674, AA128686, AA128741,

		AA128747, AA128785, AA133488, AA133489, AA130006, AA130007, AA134211, AA130492, AA130507, AA134345, AA134346, AA134457, AA134458, AA134461, AA134462, AA130907, AA131020, AA131973, AA132141, AA132493, AA132601, AA134904, AA135121, AA135182, AA135348, AA136318, AA143066, AA143256, AA143278, AA143386, AA146650, AA146835, AA146836, AA146860, AA146861, AA146870, AA146871, AA146918, AA147716, AA147707, AA147868, AA148130, AA148090, AA148091, AA152422, AA148435, AA148867, AA148492, AA148702, AA151453, AA151452, AA151828, AA155801, AA155886, AA156025, AA156044, AA156053, AA156155, AA156222, AA157080, AA157168, AA157325, AA157423, AA157434, AA157471, AA157605, AA157631, AA157546, AA157775, AA157826, AA158157, AA158273, AA158888, AA158887, AA159153, AA159250, AA160104, AA159856, AA161278, AA161301, AA160817, AA164741, AA165616, AA165606, AA173037, AA173038, AA176229, AA176317, AA179185, AA179190, AA179200, AA181043, AA181262, AA181342, AA181834, AA181989, AA182794, AA187247, AA187342, AA187379, AA187470, AA187528, AA187740, AA187911, AA188028, AA186378, AA186424, AA186441, AA186442, AA186568, AA186653, AA186661, AA186703, AA186910, AA187081, AA187087, AA187078, AA187135, AA188313, AA188330, AA188342, AA190473, AA193219
720222	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 971 of SEQ ID NO:56, b is an integer of 15 to 985, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:56, and where b is greater than or equal to a + 14.	AA056718, AA428747
724033	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1232 of SEQ ID NO:57, b is an integer of 15 to 1246, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:57, and where b is greater than or equal to a + 14.	N50855, AA076233, AA076232

724767	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1952 of SEQ ID NO:58, b is an integer of 15 to 1966, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:58, and where b is greater than or equal to a + 14.	
727065	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1597 of SEQ ID NO:59, b is an integer of 15 to 1611, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:59, and where b is greater than or equal to a + 14.	T26554, R31862, R31869, R67140, R70861, H00137, H23051, H23350, H60670, N28391, N28646, AA081571
727246	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1835 of SEQ ID NO:60, b is an integer of 15 to 1849, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:60, and where b is greater than or equal to a + 14.	
727932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 219 of SEQ ID NO:61, b is an integer of 15 to 233, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:61, and where b is greater than or equal to a + 14.	
731167	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2319 of SEQ ID NO:62, b is an integer of 15 to 2333, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:62, and where b is greater than or equal to a + 14.	
732514	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1456 of SEQ ID NO:63, b is an integer of 15 to 1470, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:63, and where b is greater than or equal to a + 14.	
734080	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 925 of SEQ ID NO:64, b is an integer of 15 to 939, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:64, and where b is greater than or equal to a + 14.	
734288	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2054 of SEQ ID NO:65, b is an integer of 15 to 2068, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:65, and where b is greater than or equal to a + 14.	
739448	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1377 of SEQ ID NO:66, b is an integer of 15 to 1391, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:66, and where b is greater than or equal to a + 14.	T53676, T53677, T54741, T55855, T55906, T56935, T57622, T58975, T58979, T61059, T61143, T90498, T90594, T93775, R07734, R07735, R40067, R75954, R75978, R76790, R76809, R77290, R77315, R77348, R79433, R79434, R97814, H50168, H70091, H77406, H80889, H82088, H82195, N33576, N39028, N48219, N49421, N52598, N66328, N67208, N73788, N78932, N92856, N99411, W07071, W17213, W24422, W25582, W47407, W47574, W49651, W49725, W68140, W68467, AA025829, AA025972, AA074731, AA074835, AA075316, AA081368, AA081369, AA082652, AA082810, AA101054, AA102495, AA115718, AA115719, AA127079, AA127080, AA127200, AA127199, AA128645, AA128813, AA133732, AA130465, AA130466, AA132111, AA143233, AA143289, AA146780, AA147706, AA148134, AA151491, AA157062, AA157046, AA157630, AA165124, AA165123, AA164625, AA165420, AA165583, AA173407, AA173462, AA179910, AA179911, AA180198, AA181087, AA181556, AA182450, AA182951, AA186670, AA188289, AA192925, AA193075, AA464823
739668	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 645 of SEQ ID NO:67, b is an integer of 15 to 659, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:67, and where b is greater than or equal to a + 14.	
740060	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2967 of SEQ ID NO:68, b is an integer of 15 to 2981, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:68, and where b is greater than or equal to a + 14.	
741560	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 589 of SEQ ID NO:69, b is an integer of 15 to 603, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:69, and where b is greater than or equal to a + 14.	
742543	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1087 of SEQ ID NO:70, b is an integer of 15 to 1101, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:70, and where b is greater than or equal to a + 14.	
742831	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 700 of SEQ ID NO:71, b is an integer of 15 to 714, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:71, and where b is greater than or equal to a + 14.	
745327	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2876 of SEQ ID NO:72, b is an integer of 15 to 2890, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:72, and where b is greater than or equal to a + 14.	
745695	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2474 of SEQ ID NO:73, b is an integer of 15 to 2488, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:73, and where b is greater than or equal to a + 14.	T56303, T58644, T58694, R48815, R48816, R68140, R74376, R78015, R81014, H00852, H01233, H17193, H17969, H25101, H27005, H30607, H41236, H42218, H42290, H42904, H42977, H45271, H45342, R83816, R98855, R98939, H53696, H62059, H82544, H83097, N40713, N92791, W19377, AA025571, AA053695, AA053675, AA069167, AA069166, AA076604, AA076603, AA079426, AA100088, AA099771, AA130265, AA158402, AA179641, AA235643, AA253454, AA250758, AA458951, AA458978, AA459194, AA419280, AA419329, AA425117, AA430664
750316	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 697 of SEQ ID NO:74, b is an integer of 15 to 711, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:74, and where b is greater than or equal to a + 14.	
750522	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 892 of SEQ ID	

	NO:75. b is an integer of 15 to 906. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:75, and where b is greater than or equal to a + 14.	
750583	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 257 of SEQ ID NO:76, b is an integer of 15 to 271. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:76. and where b is greater than or equal to a + 14.	
751020	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 659 of SEQ ID NO:77. b is an integer of 15 to 673. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:77, and where b is greater than or equal to a + 14.	N80268, N95387, W57806, W63590, AA182782, AA187759, AA199806, AA262640, AA262111, AA262106, AA460214
752196	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 353 of SEQ ID NO:78, b is an integer of 15 to 367, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:78, and where b is greater than or equal to a + 14.	R67541
753084	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1330 of SEQ ID NO:79, b is an integer of 15 to 1344, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:79, and where b is greater than or equal to a + 14.	T93791, T93840, R77826, R78199, R99272, H54274, H65600, H67128, H75533, H75532, H81433, N57836, N58786, N72699, N77475, W02480, W78743, W80625, W90276, AA007397, AA127528, AA127529, AA130419, AA147733, AA150095, AA195008, AA195060
754957	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3734 of SEQ ID NO:80, b is an integer of 15 to 3748, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:80, and where b is greater than or equal to a + 14.	
756557	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1877 of SEQ ID NO:81, b is an integer of 15 to 1891, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:81, and where b is greater than or equal to a + 14.	
756712	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1940 of SEQ ID NO:82, b is an integer of 15 to 1954, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:82, and where b is greater than or equal to a + 14.	
757414	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 922 of SEQ ID NO:83, b is an integer of 15 to 936, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:83, and where b is greater than or equal to a + 14.	T49651, T49652, T92946, T93013, H02307, H02419, N42072, AA169576
757614	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1499 of SEQ ID NO:84, b is an integer of 15 to 1513, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:84, and where b is greater than or equal to a + 14.	T93709, T96172, H00439, H00480, R85176, H51264, H51834, H53645, H57470, H57991, H73334, N33138, N42318, N94987, AA028955, AA081550, AA082013, AA113225, AA113810, AA133619, AA133522, AA132699, AA132810, AA151877, AA149662, AA157324, AA157422, AA159905, AA165014, AA165442, AA165443, AA167837, AA166621, AA166924, AA195339, AA195338, AA252790
757815	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1284 of SEQ ID NO:85, b is an integer of 15 to 1298, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:85, and where b is greater than or equal to a + 14.	
759878	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1995 of SEQ ID NO:86, b is an integer of 15 to 2009, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:86, and where b is greater than or equal to a + 14.	
760227	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 520 of SEQ ID NO:87, b is an integer of 15 to 534, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:87, and where b is greater than or equal to a + 14.	
760312	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4288 of SEQ ID NO:88, b is an integer of 15 to 4302, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:88, and where b is greater than or equal to a + 14.	
766051	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	T57753, T60650, R11036, R11084, R00826, R01482, H87221, N25112,

	sequence described by the general formula of a-b, where a is any integer between 1 to 2768 of SEQ ID NO:89, b is an integer of 15 to 2782, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:89, and where b is greater than or equal to a + 14.	N33451, N42424, N47338, N48186, N62628, N68902, N71490, N78399, N99533, W16943, W78948, W85915, W95743, N89568, AA039230, AA039231, AA047564, AA047582, AA047702, AA047752, AA120926, AA126453, AA135549, AA135529, AA429718
767593	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1023 of SEQ ID NO:90, b is an integer of 15 to 1037, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:90, and where b is greater than or equal to a + 14.	T51635, T57709, T61468, T63793, T63818, T92894, T92984, T94396, T75475, T75508, T87575, T79848, T85949, R25644, R27489, R70702, R78772, H44836, H44835, R84349, R86157, R89703, R99494, H48567, H48836, H57859, H83579, H86373, H86690, H88284, H97937, H98241, H99117, H99249, N24363, N24573, N26374, N27129, N31662, N36546, N40064, N45098, N45108, N53503, N59526, N63219, N64179, N64178, N66660, N70536, N72298, N98943, W02894, W19364, W60295, W60386, W72691, W77806, W93582, W93631, W92326, W92382, N90765, AA001997, AA013356, AA017023, AA017221, AA018780, AA026639, AA026705, AA029569, AA029496, AA029736, AA035387, AA035694, AA044958, AA055558, AA063564, AA100726, AA100744, AA134118, AA130301, AA151965, AA233192, AA253060, AA253117
768053	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1038 of SEQ ID NO:91, b is an integer of 15 to 1052, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:91, and where b is greater than or equal to a + 14.	
768055	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1220 of SEQ ID NO:92, b is an integer of 15 to 1234, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:92, and where b is greater than or equal to a + 14.	T68053, R09316, R09788, T84929, R24826, R66259, R68879, R80029, H00967, H89841, H96162, N39802, N44634, N68319, N70487, N71145, N72732, W01594, W52285, W73342, W85800, AA022906, AA022975, AA031962, AA032044, AA032163, AA037604, AA043694, AA043695, AA044134, AA074287, AA081041, AA081042, AA082218, AA082461, AA082475, AA083977, AA100460, AA155926, AA167365, AA171958, AA173534, AA187036, AA224429
769685	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1557 of SEQ ID	

	NO:93. b is an integer of 15 to 1571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:93, and where b is greater than or equal to a + 14.	
771920	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1858 of SEQ ID NO:94, b is an integer of 15 to 1872, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:94, and where b is greater than or equal to a + 14.	
772790	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1502 of SEQ ID NO:95, b is an integer of 15 to 1516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:95, and where b is greater than or equal to a + 14.	
772916	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1756 of SEQ ID NO:96, b is an integer of 15 to 1770, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:96, and where b is greater than or equal to a + 14.	
773225	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 924 of SEQ ID NO:97, b is an integer of 15 to 938, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:97, and where b is greater than or equal to a + 14.	
773632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 297 of SEQ ID NO:98, b is an integer of 15 to 311, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:98, and where b is greater than or equal to a + 14.	
774364	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 606 of SEQ ID NO:99, b is an integer of 15 to 620, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:99, and where b is greater than or equal to a + 14.	W01405, AA172322
775355	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2497 of SEQ ID NO:100, b is an integer of 15 to 2511, where both a	T49285, T61774, T68350, T68396, T94414, T69842, T81078, R01216, R05674, R21522, R21626, R23745, R23797, R24081, R24137, R24753, R32662, R36359, R45484, R45484,

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:100. and where b is greater than or equal to a + 14.	R63380. R63433. R70942. R70995. R73973. R78964. H08973. H09543. H16712. H16713. H20846, H20896. R99241. H82276. H82382. H84715. H85367. H85516. H89615, H95047. H96450. H97881. N20953, N21537. N22201, N25769. N29477, N30442. N37087. N42334. N42354, N66424. N66864, N67873. N71242, N73740. N94555, N99903. W45394, W46993. W46961, W46960. W46881, W73247. W90778, AA026678, AA026215. AA043908. AA044414, AA042828, AA062957, AA076063, AA121145, AA121476, AA195131, AA234043, AA234044, AA426421
775844	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2967 of SEQ ID NO:101. b is an integer of 15 to 2981. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:101. and where b is greater than or equal to a + 14.	T73286. T66741. T66742. R12147. R15080. R19321. R39271. R42973. R44589. R44589. H06197. H08725. R94752. H71652. H71653. H79764. H79765. H79770. H79762. H79761. H79771. H92246. H96184. N45199. W93244. W93245. W93258. W93257. W94615. W94654. AA001180. AA039582. AA039689. AA082198. AA157370. AA157869. AA253368
777760	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2790 of SEQ ID NO:102, b is an integer of 15 to 2804. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:102. and where b is greater than or equal to a + 14.	
779837	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 708 of SEQ ID NO:103, b is an integer of 15 to 722, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:103, and where b is greater than or equal to a + 14.	T67628. T72838, H59238, H84693, N80048. W07009, W37555, W39191, N90251. AA057629
780769	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1622 of SEQ ID NO:104, b is an integer of 15 to 1636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:104, and where b is greater than or equal to a + 14.	T66609, T66610, T83560, R15983. R15984, R35702, R49338. R49338, H11613, R94244, H87098, H87745, W60710, W60772. W94034, AA258151, AA258913, AA425943
781445	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1547 of SEQ ID NO:105. b is an integer of 15 to 1561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:105, and where b is	

	greater than or equal to a + 14.	
781531	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 472 of SEQ ID NO:106, b is an integer of 15 to 486, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:106, and where b is greater than or equal to a + 14.	
783018	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 786 of SEQ ID NO:107, b is an integer of 15 to 800, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:107, and where b is greater than or equal to a + 14.	R18976
783097	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1044 of SEQ ID NO:108, b is an integer of 15 to 1058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:108, and where b is greater than or equal to a + 14.	
784198	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1062 of SEQ ID NO:109, b is an integer of 15 to 1076, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:109, and where b is greater than or equal to a + 14.	
784868	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1185 of SEQ ID NO:110, b is an integer of 15 to 1199, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:110, and where b is greater than or equal to a + 14.	
785428	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3616 of SEQ ID NO:111, b is an integer of 15 to 3630, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:111, and where b is greater than or equal to a + 14.	T47751, T39348, T39359, T98137, T79193, T95760, R16653, R16654, R24052, R24245, R33230, R44846, R50794, R50912, R44846, R60930, R61049, R71116, R71620, R77888, R80860, H00109, H04333, H04688, H05041, H09555, H30257, H30320, H47931, R94218, R99062, R99260, H50702, H50803, H52629, H52628, H54000, H67115, H70269, H83460, H83572, H84911, H99358, N21482, N21632, N24626, N33762, N41609, N67949, N69593, N70188, N71452, N71818, N77888, N79031, N99501, W02150, W03072, W05781, W19647, W19972, W20125, W30896, W33043.

		W33197, W35407, W37262, W39072, W47654, W52846, W56143, W60064, W60074, W65501, W67522, W67591, W69745, W69926, W80811, W94093, W94156, N90996, AA039462, AA040857, AA043084, AA043810, AA053423, AA053042, AA064625, AA064709, AA115540, AA115051, AA120833, AA129500, AA129499, AA146736, AA148602, AA152314, AA150343, AA150620, AA150790, AA157282, AA160296, AA173937, AA173969, AA181340, AA188207, AA186354, AA188646, AA190484, AA199676, AA199677, AA243342, AA250981, AA459647, AA459773, AA460227
785845	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1512 of SEQ ID NO:112, b is an integer of 15 to 1526, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:112, and where b is greater than or equal to a + 14.	
785854	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 571 of SEQ ID NO:113, b is an integer of 15 to 585, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:113, and where b is greater than or equal to a + 14.	T85881, W45204
786705	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 487 of SEQ ID NO:114, b is an integer of 15 to 501, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:114, and where b is greater than or equal to a + 14.	R09422
787186	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1951 of SEQ ID NO:115, b is an integer of 15 to 1965, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:115, and where b is greater than or equal to a + 14.	
787279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1046 of SEQ ID NO:116, b is an integer of 15 to 1060, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:116, and where b is greater than or equal to a + 14.	T62081, T97170, R17585, R42923, R48789, R48896, R54561, R54562, R54721, R54722, R42923, R72984, R73595, H23901, H43508, H46275, H46348, H47255, H47254, R83475, R89352, R91048, R93150, R93669, R94520, R98839, H48417, H48899, H48900, H50560, H54157, H58936,

		H58983, H67630, H69455, H72554, H72955, H89822, N23388, N33070, N35168, N40256, N44641, N52556, N59706, N68387, N80806, N92514, W17007, W19578, W20217, W38835, W49822, W56061, W65416, W65285, N90575, AA002190, AA045344, AA045446, AA052950, AA053432, AA082245, AA083753, AA102071, AA099961, AA101574, AA112070, AA125782, AA125931, AA135139, AA135268, AA146635, AA151603, AA149484, AA149981, AA152120, AA171975, AA172123, AA181805, AA181821, AA188148, AA188225, AA186556, AA186917, AA460297, AA461585
789002	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 695 of SEQ ID NO:117, b is an integer of 15 to 709, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:117, and where b is greater than or equal to a + 14.	
789008	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2039 of SEQ ID NO:118, b is an integer of 15 to 2053, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:118, and where b is greater than or equal to a + 14.	T47492, T47493, T47900, T48303, T48445, T48456, T49007, T49079, T49080, T49218, T49310, T49311, T49913, T49914, T49941, T51256, T51337, T51371, T51423, T51604, T51757, T52271, T52400, T53326, T53327, T54148, T54244, T54295, T54330, T54402, T54407, T55485, T55733, T56237, T56379, T56414, T56565, T39384, T40546, T40551, T40552, T40824, T89603, T79470, T79561, R01378, R12635, R20536, R21209, R21238, R21239, R22062, R22119, R22190, R22241, R22534, R22535, R22823, R23625, R23881, R24090, R25741, R26431, R26587, R28327, R28328, R28330, R31619, R32132, R32349, R33134, R33286, R35454, R36658, R39739, R50498, R50581, R20536, R56656, R65717, R65777, R65870, R67856, R67857, R68076, R69399, R69531, R69752, R69920, R71289, R72350, R74061, R77148, R77149, R80495, R80640, R82550, H00862, H01301, H01472, H01571, H02637, H02893, H03072, H03073, H03443, H03525, H03812, H03836, H23457, H23458, H26513, H26583, H26584, R86226, R86227, R87053, R91130, R91174, R92513, R92642, R93418, R93468, R93700, R94462, R94463, R94793, R95110,

		R96330, R96329, R96675, R96943, R97000, R98195, R99857, H48277, H48366, H48451, H53119, H54247, H54246, H57144, H57217, H58791, H59276, H59324, H59614, H59654, H62873, H62997, H66302, H67109, H67468, H67594, H67634, H67646, H67685, H67891, H67935, H68007, H68476, H72996, H73208, H73882, H74057, H74076, H74196, H75522, H75366, H77704, H77705, H78593, H79262, H79373, H81287, H81343, H82036, H82218, H82313, H87010, H87011, H90552, H90551, H93198, H94403, N28269, N30773, N34862, N38975, N38989, N39317, N43935, N45164, N48122, N48136, N50666, N50756, N52570, N53559, N53589, N55006, N55026, N57654, N58258, N58340, N58627, N58738, N70218, N72552, N72649, N77216, N77511, N77635, N80637, W01074, W58701, W68231, W68232, W68700, W72561, W72580, W72399, W76223, W85725, W92304, W92318, W92144, W92354, AA004478, AA004551, AA009715, AA009825, AA024464, AA024465, AA025660, AA039523, AA039522, AA040081, AA040128, AA040033, AA040827, AA045744, AA053323, AA099152, AA099250
789555	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1810 of SEQ ID NO:119, b is an integer of 15 to 1824, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:119, and where b is greater than or equal to a + 14.	T85669, H62189, H62190, H73963, H73295, N74147, W04314, W23625, W35215, AA040573, AA040671
789631	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 592 of SEQ ID NO:120, b is an integer of 15 to 606, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:120, and where b is greater than or equal to a + 14.	
789779	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 824 of SEQ ID NO:121, b is an integer of 15 to 838, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:121, and where b is greater than or equal to a + 14.	N69694, AA151932
790387	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	H19654, H87102, H87749, N29354, N34298, N44187, N57052, W69612,

	sequence described by the general formula of a-b, where a is any integer between 1 to 642 of SEQ ID NO:122, b is an integer of 15 to 656, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:122, and where b is greater than or equal to a + 14.	W93844, W93865, AA027893, AA029638, AA058317, AA058495, AA179870, AA232827, AA233881, AA235809
790461	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1372 of SEQ ID NO:123, b is an integer of 15 to 1386, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:123, and where b is greater than or equal to a + 14.	R66275, R76171, R82537, AA054476, AA056199, AA127010, AA143025, AA151006, AA150976
790931	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 831 of SEQ ID NO:124, b is an integer of 15 to 845, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:124, and where b is greater than or equal to a + 14.	T92052, R10686, T84927, R21818, R22331, R22332, R22401, R23139, R23140, R23369, R32153, R32154, R63527, R63575, R68799, R68901, R80768, H12779, H12836, H56522, H56704, H94832, H96055, H96058, H96422, H96418, N26715, N27088, N31910, N32532, N33383, N34596, N42693, N42748, W32121, W37432, W44577, W44627, W51792, W61294, W65390, AA026773, AA026774
791176	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1642 of SEQ ID NO:125, b is an integer of 15 to 1656, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:125, and where b is greater than or equal to a + 14.	T51708, T51919, T69384, R50942, R73632, R73706, H28125, N22822, N78772
791983	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 823 of SEQ ID NO:126, b is an integer of 15 to 837, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:126, and where b is greater than or equal to a + 14.	
792539	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1203 of SEQ ID NO:127, b is an integer of 15 to 1217, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:127, and where b is greater than or equal to a + 14.	H53623, H53662, N23079, N69293, N89689, AA034518, AA035409, AA035410, AA046490, AA046762, AA085037, AA085105, AA134976, AA135078, AA459951, AA460040
792749	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1335 of SEQ ID NO:128, b is an integer of 15 to 1349, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:128, and where b is greater than or equal to a + 14.	R13058, R13951, R40011, R51765, R51766, R40011, R67629, R67630, H01808, H29310, H29403, R99196, H52742, H52788, H61636, H71767, H71768, N20919, N27779, N36030, N41741, N47900, N55480, N76967, W21551, W44410, W44331, W46458, W46528, W46810, W46928, W51766,

		W57869, W58140, W86456, N90422, AA029174, AA029253, AA031374, AA031375, AA062913, AA082549, AA133965, AA167773, AA166872, AA176295, AA176395, AA428235
792961	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2304 of SEQ ID NO:129, b is an integer of 15 to 2318, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:129, and where b is greater than or equal to a + 14.	
793206	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2135 of SEQ ID NO:130, b is an integer of 15 to 2149, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:130, and where b is greater than or equal to a + 14.	
793249	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1006 of SEQ ID NO:131, b is an integer of 15 to 1020, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:131, and where b is greater than or equal to a + 14.	T48358, T48359, T71001, T71063, T72193, T72972, T67531, T69528, T86709, T86804, T89854, T90890, T91159, T85694, T85895, T95466, T95467, R00007, R00008, R12353, R23932, R23933, R37279, R63973, R64080, R73825, R73826, R76905, R77073, R77445, R77538, R79797, R79808, R79894, R79908, H11925, H11926, H15192, H16754, H16862, H19737, H20072, H21725, H22675, H24523, H26125, H26391, H39766, H41271, H41373, H41374, H43544, H43545, H44881, H45180, H45181, R92671, R94833, H57801, H58122, H58123, H62248, H62337, H69587, H69586, H80840, H80930, H85462, H85747, H86829, H86902, H96591, H96708, H97829, H99614, N25266, N26147, N27161, N29792, N33452, N33767, N33906, N36535, N38816, N39177, N40101, N42935, N42425, N44530, N45252, N45445, N57801, N59012, N78685, N79046, N91819, N98480, W02726, W04566, W15191, W15596, W17335, W24253, W25723, W30937, W31253, W31429, W31674, W39685, W44989, W46619, W46654, W57768, W57804, W57841, W57622, W67135, W67136, W73878, W73364, W73441, W77815, W80810, W80903, W92682, W92512, W92513, W96375, W96526, AA001447, AA001482, AA021374, AA021375, AA037268, AA037489, AA037569, AA039708, AA040262, AA040417, AA057011,

		AA074646, AA074679, AA075303, AA088467, AA098947, AA100987, AA126026, AA126122, AA126778, AA128010, AA128034, AA136619, AA136750, AA143234, AA143291, AA143564, AA143565, AA146915, AA151446, AA151447, AA156218, AA157383, AA159151, AA173294, AA179768, AA180442, AA181155, AA181156, AA181722, AA186611, AA188254, AA190686, AA191758, AA191547, AA195441, AA223540, AA223587
793626	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2305 of SEQ ID NO:132, b is an integer of 15 to 2319, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:132, and where b is greater than or equal to a + 14.	
794417	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1359 of SEQ ID NO:133, b is an integer of 15 to 1373, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:133, and where b is greater than or equal to a + 14.	
795197	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1643 of SEQ ID NO:134, b is an integer of 15 to 1657, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:134, and where b is greater than or equal to a + 14.	
795251	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2346 of SEQ ID NO:135, b is an integer of 15 to 2360, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:135, and where b is greater than or equal to a + 14.	T89826, T74514, T89080, R24028, H03686, H97493, N54611, W94797, W94798, AA129537, AA190765, AA191357, AA256363, AA425151, AA429405
795752	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1028 of SEQ ID NO:136, b is an integer of 15 to 1042, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:136, and where b is greater than or equal to a + 14.	
796261	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1023 of SEQ ID	

	NO:137. b is an integer of 15 to 1037, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:137, and where b is greater than or equal to a + 14.	
796933	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1476 of SEQ ID NO:138. b is an integer of 15 to 1490, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:138, and where b is greater than or equal to a + 14.	
799424	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1670 of SEQ ID NO:139, b is an integer of 15 to 1684, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:139, and where b is greater than or equal to a + 14.	
799698	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 413 of SEQ ID NO:140, b is an integer of 15 to 427, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:140, and where b is greater than or equal to a + 14.	
800351	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 875 of SEQ ID NO:141, b is an integer of 15 to 889, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:141, and where b is greater than or equal to a + 14.	
800573	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1491 of SEQ ID NO:142, b is an integer of 15 to 1505, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:142, and where b is greater than or equal to a + 14.	
805815	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1221 of SEQ ID NO:143, b is an integer of 15 to 1235, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:143, and where b is greater than or equal to a + 14.	
806445	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1406 of SEQ ID NO:144, b is an integer of 15 to 1420, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:144, and where b is greater than or equal to a + 14.	
810309	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1905 of SEQ ID NO:145, b is an integer of 15 to 1919, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:145, and where b is greater than or equal to a + 14.	
811022	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1365 of SEQ ID NO:146, b is an integer of 15 to 1379, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:146, and where b is greater than or equal to a + 14.	
811023	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 500 of SEQ ID NO:147, b is an integer of 15 to 514, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:147, and where b is greater than or equal to a + 14.	
811143	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2044 of SEQ ID NO:148, b is an integer of 15 to 2058, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:148, and where b is greater than or equal to a + 14.	
811381	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1767 of SEQ ID NO:149, b is an integer of 15 to 1781, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:149, and where b is greater than or equal to a + 14.	
811595	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1695 of SEQ ID NO:150, b is an integer of 15 to 1709, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:150, and where b is greater than or equal to a + 14.	T51013, T51104, T54094, T54185, T68577, T68655, T90261, T90702, T92691, R34639, R49168, R51392, R49168, R84952, R84994, H84723, H84890, N29820, N42512, N64677, N67206, N73458, N80110, N92710, W02861, W20327, W23680, W76675, AA031294, AA062736, AA062781, AA070243, AA070244, AA084464, AA100714, AA100767, AA136726, AA136684, AA191613, AA223541, AA223589, AA252636
813000	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 908 of SEQ ID NO:151, b is an integer of 15 to 922, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:151, and where b is greater than or equal to a + 14.	
813288	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 621 of SEQ ID NO:152, b is an integer of 15 to 635, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:152, and where b is greater than or equal to a + 14.	
813431	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2314 of SEQ ID NO:153, b is an integer of 15 to 2328, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:153, and where b is greater than or equal to a + 14.	T94237, T89464, T89552, R09285, T78198, R14453, R15241, R15311, R21130, R33140, R33292, R40972, R46726, R42211, R40972, R46726, R66207, R67085, R73679, R73770, H12485, H19135, H22930, H24111, H26774, H26884, R89854, R89894, R92012, R92057, H53798, H61991, H61992, H64854, H65452, H73213, H74063, H79753, H79754, H80620, H80654, H81209, H81210, H84019, H84020, N35581, N68664, N73792, N91681, N92730, N99417, W20349, W46901, W52684, W60422, W61136, W61108, W61174, W68119, W73989, W79021, W79231, W80414, W80777, W80930, AA040315, AA045023, AA045024, AA045188, AA045352, AA181735, AA181799, AA223229, AA223428, AA464186, AA464780, AA428152, AA430305
813450	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1254 of SEQ ID NO:154, b is an integer of 15 to 1268, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:154, and where b is greater than or equal to a + 14.	T90954, T84401, T85262, R22109, R48652, R72000, R73453, H14261, H27403, H42017, H42018, H38149, H38150, H69302, H69397, N98775, AA148803, AA150212
813478	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4285 of SEQ ID NO:155, b is an integer of 15 to 4299, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:155, and where b is greater than or equal to a + 14.	
813505	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 992 of SEQ ID NO:156, b is an integer of 15 to 1006, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:156, and where b is greater than or equal to a + 14.	
815552	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1672 of SEQ ID NO:157, b is an integer of 15 to 1686, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:157, and where b is greater than or equal to a + 14.	
815606	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4133 of SEQ ID NO:158, b is an integer of 15 to 4147, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:158, and where b is greater than or equal to a + 14.	T69152, T69213, T80080, T80327, R19043, R27520, R38534, R38898, R44031, R44031, R67769, H11493, H11852, H13644, H22161, H28042, H39529, H42500, H43488, N32678, N50022, N51861, N54126, N54677, W16972, W32896, W35293, W38598, N89624, N90277, AA027830, AA027892, AA035739, AA055806, AA069223, AA078890, AA078891, AA099437, AA099478, AA101431, AA112543, AA121794, AA129629, AA136251, AA143110, AA150576, AA157125, AA158242, AA158709, AA159976, AA160357, AA159491, AA160534, AA160629, AA165150, AA165151, AA164643, AA166799, AA169647, AA169822, AA173082, AA187009, AA224150, AA224303, AA224514, AA224513, AA224488, AA226779, AA227396, AA227518, AA232104, AA232580, AA256938, AA255494, AA429442
816048	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1228 of SEQ ID NO:159, b is an integer of 15 to 1242, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:159, and where b is greater than or equal to a + 14.	T54940, T59322, R35627, R46514, R48419, R48536, R48537, R48569, R48582, R48668, R48683, R49781, R49827, R53111, R53210, R66870, R67958, R69435, R69517, R70414, R71907, R71948, R72113, R72818, R73269, R75924, R75959, R79565, R79566, R80393, H25645, H26211, H29817, H29904, H39626, H39738, H39881, H40715, H42210, H42281, H42354, H42710, H43124, R83615, R86066, R92103, R92104, R96726, R96727, H54075, H54232, H54233, H62253, H62342, H80441, H80442, H91114, H97541, H99927, N27357, N27665, N93636, W19226, W19703, W25418, W25514, W44404, W63554, W78078, N89960, AA027093, AA027132, AA045021, AA045022, AA045721, AA045720, AA046247, AA046280, AA058624, AA074786, AA074787, AA082394, AA085101, AA085282, AA100996, AA127562, AA127729, AA127784, AA128372,

		AA134954, AA143611, AA148145, AA150570, AA161257, AA182028, AA188387, AA232423, AA464270, AA464381, AA421219, AA425804, AA428372
822978	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2215 of SEQ ID NO:160, b is an integer of 15 to 2229, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:160, and where b is greater than or equal to a + 14.	R28400, R82355, R82411, H01338, H01388, N24952, N33829, AA043471, AA043472, AA125807, AA128280, AA129405, AA133871, AA129367, AA133179, AA133312, AA131385, AA428408
823616	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1906 of SEQ ID NO:161, b is an integer of 15 to 1920, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:161, and where b is greater than or equal to a + 14.	
823981	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2605 of SEQ ID NO:162, b is an integer of 15 to 2619, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:162, and where b is greater than or equal to a + 14.	
824364	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1405 of SEQ ID NO:163, b is an integer of 15 to 1419, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:163, and where b is greater than or equal to a + 14.	R21933, H39733, N69879, AA027031, AA100964, AA157234, AA173338
824423	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3796 of SEQ ID NO:164, b is an integer of 15 to 3810, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:164, and where b is greater than or equal to a + 14.	
825279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 803 of SEQ ID NO:165, b is an integer of 15 to 817, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:165, and where b is greater than or equal to a + 14.	R06729, R61520, R86829, H51131, N57993, W93696, AA423827
825442	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1564 of SEQ ID	

	NO:166, b is an integer of 15 to 1578, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:166, and where b is greater than or equal to a + 14.	
825548	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1680 of SEQ ID NO:167, b is an integer of 15 to 1694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:167, and where b is greater than or equal to a + 14.	
825725	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1622 of SEQ ID NO:168, b is an integer of 15 to 1636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:168, and where b is greater than or equal to a + 14.	
826639	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 653 of SEQ ID NO:169, b is an integer of 15 to 667, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:169, and where b is greater than or equal to a + 14.	
827079	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3584 of SEQ ID NO:170, b is an integer of 15 to 3598, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:170, and where b is greater than or equal to a + 14.	
827153	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 926 of SEQ ID NO:171, b is an integer of 15 to 940, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:171, and where b is greater than or equal to a + 14.	
827351	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1444 of SEQ ID NO:172, b is an integer of 15 to 1458, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:172, and where b is greater than or equal to a + 14.	R14710, H92769, H92882, AA195498, AA242878, AA242884, AA252152, AA251967, AA465181, AA465542, AA481105, AA481210, AA492206, AA732326
827503	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2695 of SEQ ID NO:173, b is an integer of 15 to 2709, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:173, and where b is greater than or equal to a + 14.	
827563	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 999 of SEQ ID NO:174, b is an integer of 15 to 1013, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:174, and where b is greater than or equal to a + 14.	
827565	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1683 of SEQ ID NO:175, b is an integer of 15 to 1697, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:175, and where b is greater than or equal to a + 14.	
827893	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1395 of SEQ ID NO:176, b is an integer of 15 to 1409, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:176, and where b is greater than or equal to a + 14.	
828072	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1489 of SEQ ID NO:177, b is an integer of 15 to 1503, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:177, and where b is greater than or equal to a + 14.	R20502, R45322, R45322, H29062, H29165, N36388, N39601, AA043930, AA044003, AA115568, AA115087, AA232982, AA234020, AA251431, AA251432, AA459761, AA768137, AA830696, AA918618, AA977409
828228	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1364 of SEQ ID NO:178, b is an integer of 15 to 1378, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:178, and where b is greater than or equal to a + 14.	T76992, T83862, R37649, R68086, R68125, H05325, H05379, H11520, H60866, N27826, N59149, N71661, AA004459, AA004512, AA026983, AA031653, AA045803, AA045870, AA127220, AA126199, AA129772, AA133788, AA131742, AA166788, AA216416, AA229513, AA469120, AA469189, AA503687, AA516488, AA522741, AA542827, AA614664, AA847108, AA876618, AA886579, AA887825, AA888263, AA888262, AA934459, N31217, D79619, N55800, AA026982, AA031743
828241	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2237 of SEQ ID NO:179, b is an integer of 15 to 2251, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:179, and where b is greater than or equal to a + 14.	R09047, H71262, N28995, W07805, W89157, AA007537, AA203119

828287	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 986 of SEQ ID NO:180, b is an integer of 15 to 1000, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:180, and where b is greater than or equal to a + 14.	R00158, R34699, R34806, R55812, R55897, H02931, H04234, H38596, H38841, H38877, R84345, R84762, R85507, H51401, N22910, N31298, N36027, N64463, N70710, N80820, N94519, N99846, W15234, W15579, W15620, W23968, W24669, W30920, W31655, W37399, W37400, W39182, W45512, W44342, W45653, W44569, W44608, W47630, W47631, W52183, W52421, W57603, W58189, W58466, W60614, W73715, W78044, W90451, W90258, W92042, W91902, AA012954, AA013060, AA013459, AA013460, AA018132, AA018050, AA021226, AA021359, AA021556, AA021640, AA033802, AA040580, AA040552, AA047883, AA054092, AA055181, AA055893, AA082252, AA082502, AA099128, AA099165, AA100988, AA131285, AA136296, AA136178, AA151469, AA151470, AA156144, AA158033, AA158325, AA164422, AA164402, AA167105, AA182609, AA182541, AA187289, AA187406, AA523678, AA582094, AA570257, AA573999, AA574305, AA579097, AA661683, AA662869, AA664665, AA736798, AA770689, AA865267, AA902336, AA923648, AA933570, AA939196, AA988468, AI000226, AI089764, D79059, N84733, W73650, N86290, N88454, C04677, C06015, AA033803, R29541, AA089664, AA089996, C17096, C17255, C19033, AA093458
828364	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1415 of SEQ ID NO:181, b is an integer of 15 to 1429, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:181, and where b is greater than or equal to a + 14.	R55711, R55921, R68105, R68149, R72479, R72941, N70480, W72759
828371	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2711 of SEQ ID NO:182, b is an integer of 15 to 2725, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:182, and where b is greater than or equal to a + 14.	T62048, T62112, T91683, T92364, T92416, T93284, N49690, N49793, N64329, N80813, W15549, W15404, W31643, W53039, W92220, W92342, AA055521, AA055520, AA149883, AA150063, AA148836, AA150436
828403	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1737 of SEQ ID NO:183, b is an integer of 15 to 1751, where both a	AA485171, AA515218, AA603721, AA612760, AA838541, AA970526, C18512

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:183, and where b is greater than or equal to a + 14.	
828501	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2186 of SEQ ID NO:184, b is an integer of 15 to 2200, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:184, and where b is greater than or equal to a + 14.	H19145, N75547, AA044653, AA128979, AA159576, AA423963, AA523306, H62675, H97872, AA610503, AA010941, AA011327, AA043344
828520	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1973 of SEQ ID NO:185, b is an integer of 15 to 1987, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:185, and where b is greater than or equal to a + 14.	H70392, N30525, N30537, AA010769, AA463668, AA927343, AA091744
828527	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1723 of SEQ ID NO:186, b is an integer of 15 to 1737, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:186, and where b is greater than or equal to a + 14.	T39306, T40514, R08857, R08964, R00734, R00735, R13824, R20172, R37684, R44959, R44959, H05503, H17017, H17018, H54295, H54372, H54503, H67654, H67974, H87993, N33311, N37017, N44843, N55182, N75469, N75534, N77241, N93004, W05278, W05327, W45465, W88760, W88865, AA010623, AA010624, AA234956, AA235130, AA424457, AA282705, AA283023, AA283109, AA481529, AA481595, AA490727, AA491218, AA554176, AA614573, AA665370, AA687964, AA736921, AA765107, AA767430, AA809487, AA865595, N88052
828538	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1118 of SEQ ID NO:187, b is an integer of 15 to 1132, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:187, and where b is greater than or equal to a + 14.	
828541	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:188, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:188, and where b is greater than or equal to a + 14.	
828549	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3773 of SEQ ID NO:189, b is an integer of 15 to 3787, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:189. and where b is greater than or equal to a + 14.	
828562	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 540 of SEQ ID NO:190. b is an integer of 15 to 554, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:190, and where b is greater than or equal to a + 14.	
828576	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 860 of SEQ ID NO:191, b is an integer of 15 to 874, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:191, and where b is greater than or equal to a + 14.	
828602	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2089 of SEQ ID NO:192. b is an integer of 15 to 2103, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:192, and where b is greater than or equal to a + 14.	
828628	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1303 of SEQ ID NO:193, b is an integer of 15 to 1317, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:193, and where b is greater than or equal to a + 14.	
828667	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1238 of SEQ ID NO:194, b is an integer of 15 to 1252, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:194, and where b is greater than or equal to a + 14.	
828684	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1674 of SEQ ID NO:195, b is an integer of 15 to 1688, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:195, and where b is greater than or equal to a + 14.	R11676, R12284, N68621, N71575, N99448, W02008, W58632, W74361, W76341, W78934. W85701, AA070898, AA070787, AA102636, AA102661, AA102678. AA190864, AA190957, AA197279, AA251577, AA464994, AA421724, AA470741, AA505341, AA506137. AA583780, AA579967, AA714136, AA743352, AA747903, AA814422, AA826755, AA836633, AA837944, AA936844, AI004160, C00265. AA641021
828727	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	R35925, R35954, R49443, R49468, R49443, R49468, N74960, AA083678, AA086366, AA100585, AA111863,

	where a is any integer between 1 to 742 of SEQ ID NO:196. b is an integer of 15 to 756. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:196. and where b is greater than or equal to a + 14.	AA156573. AA159175. AA192611. AA195925. AA195976. AA418567. AA418582
828734	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1457 of SEQ ID NO:197. b is an integer of 15 to 1471. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:197. and where b is greater than or equal to a + 14.	
828750	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 678 of SEQ ID NO:198. b is an integer of 15 to 692. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:198. and where b is greater than or equal to a + 14.	
828842	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1559 of SEQ ID NO:199, b is an integer of 15 to 1573, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:199, and where b is greater than or equal to a ÷ 14.	R31695, R31737, R86919, R86763, H66952, N30849, N41376, N95538, W03782, W24227, N90171, AA020001, AA046039, AA046149, AA099753, AA489705, AA552582, AA580818, AA584291, AA730113, AA910268
828843	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2728 of SEQ ID NO:200, b is an integer of 15 to 2742, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:200, and where b is greater than or equal to a + 14.	T57326, T57387, T94838, T94837, T94879, T94925, T74456, R11995, R15234, R19543, R21728, R36670, R39752, R39834, R40808, R40808, R43895, R70936, R70988, R74057, R74152, R79967, R80062, H02983, H04277, H08966, H09537, H25298, H25343, H25449, H25495, H29439, H29438, H29887, H29987, R86318, H65676, H87966, H88350, H97859, N20316, N26629, N27590, N39724, N52972, W39188, W45099, W45149, N90248, AA004834, AA033776, AA039900, AA039901, AA041524, AA044928, AA082729, AA085742, AA112974, AA128343, AA133157, AA171997, AA418609, AA418664, AA421626, AA430065, AA230107, AA230108, AA513630, AA521134, AA622056, AA635868, AA639882, AA714929, AA715480, AA715556, AA729814, AA731061, AA811597, AA830222, AA873240, AA886078, AA886270, AA907208, AA932201, AA977447, AA989000, D81476, N56281, C21262, AA089709
828851	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1403 of SEQ ID NO:201, b is an integer of 15 to 1417, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:201, and where b is greater than or equal to a + 14.	
828856	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1498 of SEQ ID NO:202, b is an integer of 15 to 1512, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:202, and where b is greater than or equal to a + 14.	
828862	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 405 of SEQ ID NO:203, b is an integer of 15 to 419, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:203, and where b is greater than or equal to a + 14.	AA021223
828870	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2819 of SEQ ID NO:204, b is an integer of 15 to 2833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:204, and where b is greater than or equal to a + 14.	
828873	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 5816 of SEQ ID NO:205, b is an integer of 15 to 5830, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:205, and where b is greater than or equal to a + 14.	
828892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 741 of SEQ ID NO:206, b is an integer of 15 to 755, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:206, and where b is greater than or equal to a + 14.	R54649, W46198
828893	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1982 of SEQ ID NO:207, b is an integer of 15 to 1996, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:207, and where b is greater than or equal to a + 14.	
828897	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1654 of SEQ ID NO:208, b is an integer of 15 to 1668, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:208, and where b is greater than or equal to a + 14.	
828910	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2236 of SEQ ID NO:209, b is an integer of 15 to 2250, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:209, and where b is greater than or equal to a + 14.	T91595, T65436, T65518, T70584, T70847, T75377, R09159, R09261, R09950, T96365, T96446, R12590, R13068, R18120, R21193, R22430, R22480, R22810, R25025, R26742, R26976, R32026, R32079, R33017, R33904, R36588, R39200, R40499, R45972, R40499, R45972, R56330, R64494, R65591, R67446, R70974, R74477, R74579, R77932, R78301, R78497, R78547, R80142, R80143, H00643, H00729, H03024, H04306, H06614, H07124, H09643, H09677, H28706, H28835, H42802, H47310, R92010, H65658, H65657, H67068, H68151, H71685, H72248, H72786, H72785, H73342, H75583, H75514, H77433, H98557, N20087, N22979, N23822, N28617, N29593, N32509, N33262, N40705, N42724, N44752, N45195, N57760, N58105, N59101, N59726, N64423, N66868, N71993, N73995, N99375, W01801, W02025, W19280, W19667, W19930, W25451, W25645, W31475, W31938, W32153, W32005, W37711, W37710, W46758, W46905, W49818, W56089, W57771, W57844, W61375, W61376, W60415, W60416, W61142, W61190, W67942, W67941, W74649, W84332, W84393, W86146, W94323, AA016041, AA015933, AA022593, AA022594, AA030003, AA043309, AA069392, AA069393, AA069775, AA069812, AA102392, AA112674, AA112673, AA135337, AA135336, AA143448, AA152405, AA152459, AA149804, AA149829, AA149849, AA149856, AA156559, AA157731, AA159045, AA160734, AA173662, AA173661, AA235812, AA242974, AA243081, AA242998, AA252146, AA460003, AA460542, AA428205, AA429142, AA285041, AA283758, AA283993, AA480305, AA506566, AA524852, AA631324, AA575859, AA658502, AA766717, AA808234, AA837876, AA866075, AA877425, AA879058, AA886608, AA902179, AA904000, AA928667, AA937136, AA962263, AA995987, AI024986, W25995, W26229, W27231, W26246, W28106,

		W28807, W48809, C01974, AA640952, C14885, C15137
828927	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 824 of SEQ ID NO:210, b is an integer of 15 to 838, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:210, and where b is greater than or equal to a + 14.	
828932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1199 of SEQ ID NO:211, b is an integer of 15 to 1213, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:211, and where b is greater than or equal to a + 14.	T50679, T51209, T78077, R42605, R48768, R42605, R91277, H61157, W38635, W44738, W46899, W80700, AA017684, AA017707, AA018069, AA019662, AA040254, AA053989, AA054041, AA070137, AA070138, AA074661, AA086354, AA158859, AA223111, AA224210, AA224315, AA232155, AA471047, AA588037, AA720832, AA872503
828933	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 955 of SEQ ID NO:212, b is an integer of 15 to 969, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:212, and where b is greater than or equal to a + 14.	
828941	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1680 of SEQ ID NO:213, b is an integer of 15 to 1694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:213, and where b is greater than or equal to a + 14.	
828957	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1196 of SEQ ID NO:214, b is an integer of 15 to 1210, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:214, and where b is greater than or equal to a + 14.	R09987, R16645, R16734, R81727, H58067, H58066, H59815, H59816, H64860, H65458, N70923, W81647, W81187, AA052891, AA053046, AA251319, AA251723, AA262259, AA262870, AA463359, AA463865, AA417918, AA418169, AA480203, AA521273, AA836429, AA858135, AA888105, AA917914, AA937591, AA947712, AA961752, AA973797, AI085881
828963	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1762 of SEQ ID NO:215, b is an integer of 15 to 1776, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:215, and where b is greater than or equal to a + 14.	
828964	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1404 of SEQ ID NO:216, b is an integer of 15 to 1418, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:216, and where b is greater than or equal to a + 14.	
828966	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2186 of SEQ ID NO:217, b is an integer of 15 to 2200, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:217, and where b is greater than or equal to a + 14.	T57322, T57383, R07432, R07433, R24183, R37889, R64196, R64212, H10798, H16281, H96182, N24864, N31801, N31897, N51466, N53607, N71323, N71374, N71696, N78973, N91801, N99595, N99806, W17338, W38617, W44695, W52815, W93325, W95029, AA027074, AA031625, AA031706, AA034522, AA101476, AA101477, AA156927, AA157179, AA173234, AA196758, AA506558, AA541561, AA552220, AA573198, AA687807, AA732065, AA769029, AA804914, AA858375, AA931935, AA995830, AI075078, AI075079, AA641307
828967	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1839 of SEQ ID NO:218, b is an integer of 15 to 1853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:218, and where b is greater than or equal to a + 14.	T86194, T99270, R00981, R21065, R28076, R28291, R46245, R46245, R61751, R61752, H20415, H41325, H46347, H46354, W01107, W96450, W96548, AA082920, AA192528, AA494252, AA507548, AA604189, AA604361, AA614008, AA622126, AA573865, AA578191, AA568157, AA780392, AA812241, AA830010, AA836096, AA876742, C21216
828977	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1079 of SEQ ID NO:219, b is an integer of 15 to 1093, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:219, and where b is greater than or equal to a + 14.	T54853, T55018, T61617, T61701, T71718, T71787, R43855, R43855, H79047, W23509, W78022, AA028959, AA028960, AA035641, AA035749, AA040562, AA042827, AA044641, AA150059, AA459301, AA459532, AA419054, AA532924, AA603462, AA573839, AA863332, AA877269, AI016670, AI083871, AI085531
828978	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2141 of SEQ ID NO:220, b is an integer of 15 to 2155, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:220, and where b is greater than or equal to a + 14.	
828979	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1250 of SEQ ID NO:221, b is an integer of 15 to 1264, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:221, and where b is greater than or equal to a + 14.	

829001	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2071 of SEQ ID NO:222, b is an integer of 15 to 2085, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:222, and where b is greater than or equal to a + 14.	
829003	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2907 of SEQ ID NO:223, b is an integer of 15 to 2921, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:223, and where b is greater than or equal to a + 14.	T56900, T56901, T57894, T57976, T58709, T83854, T83994, T83995, T85283, T85493, T85938, T98545, T98546, R23866, R51491, R51492, R70815, H06524, H06579, H21400, H22212, H26306, H26465, H40800, H42803, H44004, H45104, H45577, R84544, R85933, R95902, R98186, R98187, R99129, H51499, H62734, H62818, H67266, H67280, H67971, H72027, H72028, H86532, H86617, H97834, N22060, N22322, N22927, N23444, N23843, N27358, N27627, N31797, N53099, N55505, N55527, N62760, N76278, N76994, N81072, N99969, W07363, W15385, W30908, W32209, W32266, W37612, W39341, W45721, W44369, W60688, W60728, W74331, W79764, W79508, AA010902, AA011007, AA013382, AA013383, AA017180, AA018376, AA021435, AA128552, AA128295, AA161229, AA160487, AA236095, AA259037, AA458538, AA428449, AA491943, AA492101, AA501898, AA505736, AA551906, AA552335, AA554636, AA564579, AA588897, AA593936, AA595710, AA610733, AA612690, AA569349, AA570259, AA570263, AA573856, AA579746, AA658849, AA721609, AA743280, AA743326, AA808972, AA831035, AA836900, AA887420, AA887859, AA970292, AA994943, AA994947, AI014465, F19724, N36447, D78889, N75198, W37467, W79607, C03008, C04753
829016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4381 of SEQ ID NO:224, b is an integer of 15 to 4395, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:224, and where b is greater than or equal to a + 14.	
829027	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3021 of SEQ ID	

	NO:225, b is an integer of 15 to 3035, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:225, and where b is greater than or equal to a + 14.	
829028	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1497 of SEQ ID NO:226, b is an integer of 15 to 1511, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:226, and where b is greater than or equal to a + 14.	
829031	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2225 of SEQ ID NO:227, b is an integer of 15 to 2239, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:227, and where b is greater than or equal to a + 14.	T52373, T52446, T65540, T91789, R10959, T84998, R06717, R28502, R48288, R48390, R48442, R54616, R54879, R55311, R55316, R55413, R55418, R72602, R72669, R72946, H15595, H27333, H41543, H37781, R84976, R85050, R88513, R88514, H49052, H49116, H96219, H96754, H97979, N23664, N25056, N26150, N32997, N51857, N54122, W65281, W65277, W72409, W76488, W92510, N91031, AA045475, AA056943, AA057662, AA057806, AA126670, AA127032, AA136891, AA137001, AA158595, AA158989, AA279342, AA604130, AA604929, AA631863, C01812
829034	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2332 of SEQ ID NO:228, b is an integer of 15 to 2346, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:228, and where b is greater than or equal to a + 14.	
829036	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2232 of SEQ ID NO:229, b is an integer of 15 to 2246, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:229, and where b is greater than or equal to a + 14.	W19899, W56172, N91246, AA053015, AA258943, AA508101, AA557537, AA744258, C06034, AA053503
829049	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1988 of SEQ ID NO:230, b is an integer of 15 to 2002, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:230, and where b is greater than or equal to a + 14.	
829073	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 980 of SEQ ID	N71827, W07562, W79070, W94296, AA026190, AA215725, AA279902, AA832099

	NO:231, b is an integer of 15 to 994, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:231, and where b is greater than or equal to a + 14.	
829075	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 472 of SEQ ID NO:232, b is an integer of 15 to 486, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:232, and where b is greater than or equal to a + 14.	
829076	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2067 of SEQ ID NO:233, b is an integer of 15 to 2081, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:233, and where b is greater than or equal to a + 14.	
829080	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 502 of SEQ ID NO:234, b is an integer of 15 to 516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:234, and where b is greater than or equal to a + 14.	
829087	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1115 of SEQ ID NO:235, b is an integer of 15 to 1129, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:235, and where b is greater than or equal to a + 14.	
829092	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1031 of SEQ ID NO:236, b is an integer of 15 to 1045, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:236, and where b is greater than or equal to a + 14.	
829095	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 676 of SEQ ID NO:237, b is an integer of 15 to 690, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:237, and where b is greater than or equal to a + 14.	T98739, T98740, R53404, R72484, H09731, H16600, H21795, H25680, N79773, N93472, AA812105, AA826523, AA954170, AI084914
829096	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1859 of SEQ ID NO:238, b is an integer of 15 to 1873, where both a	T40001, T40939, R53257, R62981, R62980, R63036, H15127, H15187, H24078, H24188, H81472, H88927, H88927, H99390, N32032, N47835, N66666, N98950, AA022842,

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:238, and where b is greater than or equal to a + 14.	AA022965, AA024917, AA024918, AA035721, AA062907, AA102646, AA101299, AA223395, AA419511, AA421963, AA421964, AA524699, AA532380, AA614315, AA570194, AA742712, AA865440, AA887301, AA987486, AA988144, AA091175
829118	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 891 of SEQ ID NO:239, b is an integer of 15 to 905, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:239, and where b is greater than or equal to a + 14.	
829152	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1470 of SEQ ID NO:240, b is an integer of 15 to 1484, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:240, and where b is greater than or equal to a + 14.	T72498, T73568, T74363, T86984, R10378, R10477, T85969, R05924, R06022, H58205, H65999, H66000, N68870, N92084, N92944, AA188651, AA188754, N72345
829160	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1507 of SEQ ID NO:241, b is an integer of 15 to 1521, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:241, and where b is greater than or equal to a + 14.	R19077, R24890, R70937, R70989, R75822, R75823, H13581, R88030, H97197, H97205, H97610, H97622, H97640, H99011, N22163, N22211, N25706, N31618, N31627, N34096, N35586, N57066, N57078, N57083, N63961, N71248, N71530, N79638, W23686, W25345, W80523, W80524, AA027117, AA044025, AA044347, AA056543, AA056646, AA082122, AA120870, AA120871, AA129173, AA129197, AA173547, AA173713, AA190689, AA252595, AA258865, AA259007, AA576323, AA768606, N55993, N84224
829163	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1130 of SEQ ID NO:242, b is an integer of 15 to 1144, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:242, and where b is greater than or equal to a + 14.	R27150, H50951, N39917, N41848, N41877
829176	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 920 of SEQ ID NO:243, b is an integer of 15 to 934, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:243, and where b is greater than or equal to a + 14.	T46875, T53785, T62036, T73807, R11065, R11122, T84299, T85183, R01714, R02656, R02737, R02738, H41134, H64904, H79712, H79713, N68598, N71315, N71366, N99798, W01984
829204	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	R50489, R50573, R74498, R74499, AA234014, AA535362, AA554207, AA847239

	where a is any integer between 1 to 901 of SEQ ID NO:244, b is an integer of 15 to 915, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:244, and where b is greater than or equal to a + 14.	
829207	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1262 of SEQ ID NO:245, b is an integer of 15 to 1276, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:245, and where b is greater than or equal to a + 14.	
829228	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3352 of SEQ ID NO:246, b is an integer of 15 to 3366, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:246, and where b is greater than or equal to a + 14.	T40764, T49773, T49774, H05098, H49148, H51985, H52105, N36154, N51490, N52526, N53635, AA054314, AA074167, AA152473, AA152472, AA188950, AA278366, AA281330, AA468930, AA469004, AA482010, AA542938, AA554491, AA565215, AA579406, AA741363, AA807139, AA832066, AA836995, AA876036, AA995854
829252	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2134 of SEQ ID NO:247, b is an integer of 15 to 2148, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:247, and where b is greater than or equal to a + 14.	
829254	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2211 of SEQ ID NO:248, b is an integer of 15 to 2225, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:248, and where b is greater than or equal to a + 14.	
829269	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1190 of SEQ ID NO:249, b is an integer of 15 to 1204, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:249, and where b is greater than or equal to a + 14.	
829277	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1300 of SEQ ID NO:250, b is an integer of 15 to 1314, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:250, and where b is greater than or equal to a + 14.	
829290	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1145 of SEQ ID NO:251, b is an integer of 15 to 1159, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:251, and where b is greater than or equal to a + 14.	
829294	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2474 of SEQ ID NO:252, b is an integer of 15 to 2488, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:252, and where b is greater than or equal to a + 14.	
829299	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1540 of SEQ ID NO:253, b is an integer of 15 to 1554, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:253, and where b is greater than or equal to a + 14.	T82894, H25618, N48726, W52191, AA037331, AA223798, AA224330, AA635842, AA748884, AA826495, AA864458, AA903250, AA908466, AA931986, D81481, N56293, C02225
829308	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1492 of SEQ ID NO:254, b is an integer of 15 to 1506, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:254, and where b is greater than or equal to a + 14.	R13979, R17378, R40039, R42616, R42616, R40039, R56257, R56346, H05467, H07018, R86778, H99527, H99526, H99763, N24571, N25539, N25635, N28490, N30121, N34013, N34136, N34233, N35730, N49189, N50244, N92737, W20356, AA255602, AA262707, AA255576, AA262183, AA279758, AA570002, AA572777, AA721016, AA814424, AA864521, AA902860, AA948310, AI024777, AI056401
829349	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 640 of SEQ ID NO:255, b is an integer of 15 to 654, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:255, and where b is greater than or equal to a + 14.	T39288, T47082, T50451, T50586, T59000, T59073, T59535, T59586, T63704, T63861, T69920, T69974, T71240, T72474, T72943, T90268, T90710, T83786, T95048, R31368, R33435, R34369, R34489, R73911, R80467, R80667, R94351, R97310, R97345, H57329, H57376, H62783, H64845, H65444, H82981, H83214, H93955, H93956, N29780, N42940, N45379, N57200, N80805, W06876, W15396, W47162, W47283, W52164, W52024, W52758, W73045, W73275, W73604, W73643, W86783, W87274, AA009954, AA010849, AA011288, AA022621, AA022757, AA025805, AA025929, AA025968, AA046835, AA054475, AA058513, AA063327, AA075215, AA075451, AA088739, AA088740, AA099371, AA099457, AA112397, AA113053, AA121065, AA121066, AA132025, AA132147, AA132237, AA132357, AA146935,

		AA147721, AA147756, AA147602, AA148113, AA156063, AA157120, AA157223, AA157610, AA165107, AA164710, AA173741, AA173185, AA187331, AA187332, AA187293, AA187393, AA187741, AA188097, AA187033, AA188455, AA188457, AA188467, AA216356, AA228668, AA229001, AA228993, AA229108, AA397406, AA482922, AA483319, AA483431, AA491567, AA501502, AA507889, AA508445, AA513947, AA515053, AA522563, AA523140, AA525478, AA524922, AA526106, AA534088, AA535846, AA548219, AA552477, AA555012, AA558315, AA564882, AA565458, F16817, F16991, F17527, AA582793, AA587225, AA588487, AA595626, AA602055, AA602240, AA603392, AA631634, AA638971, AA639988, AA640535, AA576051, AA576894, AA566049, AA655021, AA659001, AA661609, AA662354, AA664631, AA664721, AA664980, AA665338, AA688035, AA714993, AA715012, AA720861, AA730373, AA730633, AA742678, AA742934, AA746812, AA747153, AA747192, AA747959, AA808437, AA836880, AA837645, AA838637, AA872341, AA876822, AA922665, AA961515, AA968734, AA970649, AA978219, AA988051, AA988404, AA991418, AA994111, AI002489, AI053409, AI053609, AI053760, AI082351, AI083631, N83854, N83948, N85971, N86260, N86628, N87758, AA641679, AA642097, AA642839, C20758, AA092159, AA092465, AA094493
829354	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1978 of SEQ ID NO:256, b is an integer of 15 to 1992, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:256, and where b is greater than or equal to a + 14.	
829388	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2259 of SEQ ID NO:257, b is an integer of 15 to 2273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:257, and where b is greater than or equal to a + 14.	
829540	Preferably excluded from the present invention are	N26408, N28830, N28838, N31522,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1490 of SEQ ID NO:258, b is an integer of 15 to 1504, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:258, and where b is greater than or equal to a + 14.	W15157, W81560, W81561, AA126749, AA126756, AA126772, AA187148
829626	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1778 of SEQ ID NO:259, b is an integer of 15 to 1792, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:259, and where b is greater than or equal to a + 14.	
829730	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2034 of SEQ ID NO:260, b is an integer of 15 to 2048, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:260, and where b is greater than or equal to a + 14.	
829892	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1268 of SEQ ID NO:261, b is an integer of 15 to 1282, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:261, and where b is greater than or equal to a + 14.	R84306, N99830, N90467, AA113938, AA192541, AA243317, L44546, AA713588
829933	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 585 of SEQ ID NO:262, b is an integer of 15 to 599, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:262, and where b is greater than or equal to a + 14.	AA121059, AA429187
829938	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1247 of SEQ ID NO:263, b is an integer of 15 to 1261, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:263, and where b is greater than or equal to a + 14.	AA001837, AA142857, AA235114, AA235222, AA614412, AA687460, AA857702, AA857893, AA962131, AA962521
829969	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1006 of SEQ ID NO:264, b is an integer of 15 to 1020, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:264, and where b is greater than or equal to a + 14.	R22931, R23036, H09755, H47088, N38971, N38985, N57545, AA075344, AA075597, AA136299, AA136180, AA279124, AA279243, AA279928, AA279929, AA909786, AI000293, N48117, N48131
829982	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	H40097, N80803, N93871, W07650, W15482, W40363, W42635, W45238,

	sequence described by the general formula of a-b, where a is any integer between 1 to 557 of SEQ ID NO:265, b is an integer of 15 to 571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:265, and where b is greater than or equal to a + 14.	W67482, W67483, W70331, W72456, W73235, W73290, W76515, W78220, AA040927, AA040928, AA074829, AA075095, AA083686, AA166708, AA167049, AA228843, AA468686, AA469044, AA505509, AA548788, AA564157, AA595572, AA622149, AA633298, AA576799, AA746697, AA807946, AA873193, AA903706, AA919114, AA932502, AA938506, AA974058, AA977996, AI000750, N85073, N86741, N87037, N88197, N88746, AA090569
830007	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1336 of SEQ ID NO:266, b is an integer of 15 to 1350, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:266, and where b is greater than or equal to a + 14.	
830019	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1305 of SEQ ID NO:267, b is an integer of 15 to 1319, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:267, and where b is greater than or equal to a + 14.	T61424, T53868, T61391, T63785, R23153, R23154, R23905, R64468, R65575, R69390, R69523, R79153, R79154, H14532, H14533, H47318, H47402, H53647, H61347, H93017, H94242, N29789, N42932, W57927, W58148, W67701, W68160, W74342, W81702, W81703, W94692, W95218, W95440, W95785, AA043712, AA056570, AA114073, AA133633, AA133634, AA151774, AA149729, AA149782, AA149795, AA425861, AA425990, AA428095, AA428642, AA494401, AA515475, AA523534, AA548827, AA552032, AA564916, F16977, AA593645, AA613557, AA617694, AA618542, AA576565, AA576574, AA746168, AA766359, AA833956, AA837906, AA857421, AA857877, AA903383, AA903849, AA903888, AA916517, AA922889, AA962544, AA970534, AA974964, AA975402, AA976089, AA983583, AA992448, F18477, C04429, C17306
830073	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3680 of SEQ ID NO:268, b is an integer of 15 to 3694, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:268, and where b is greater than or equal to a + 14.	T93694, T96159, H04182, H04181, H15428, H48586, N74976, W05676, W44928, AA085826, AA085971, AA126446, AA425304, AA425408, AA280817, AA280995, AA287270, AA287417, AA668788, AA836455, AA977754
830130	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1228 of SEQ ID	

	NO:269, b is an integer of 15 to 1242, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:269, and where b is greater than or equal to a + 14.	
830134	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2043 of SEQ ID NO:270, b is an integer of 15 to 2057, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:270, and where b is greater than or equal to a + 14.	
830135	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 946 of SEQ ID NO:271, b is an integer of 15 to 960, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:271, and where b is greater than or equal to a + 14.	
830148	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1153 of SEQ ID NO:272, b is an integer of 15 to 1167, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:272, and where b is greater than or equal to a + 14.	R15244, R31943, R31992, H06853, H06894, H13355, H30882, R84410, R84411, R94120, H53381, H97695, H99925, N46996, N69023, N77897, W00690, W19694, W38937, W74721, W74795, N89822, N89950, AA009490, AA009904, AA031349, AA031350, AA035629, AA035719, AA046140, AA062845, AA062905, AA079564, AA079636, AA116062, AA116046, AA126968, AA148568, AA159591, AA160429, AA161272, AA161273, AA160576, AA179774, AA180491, AA179635, AA182631, AA182727, AA179634, AA192371, AA192282, AA199831, AA251312, AA256883, AA255477, AA430121, AA533720, AA551694, AA552307, AA552661, AA582138, AA586611, AA587906, AA594387, AA602977, AA605299, AA633388, AA573941, AA574038, AA579715, AA687647, AA741352, AA838339, AA857603, AA858082, AA866081, AA865003, AA875861, AA910672, AA927563, AI076918, W21962
830149	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2757 of SEQ ID NO:273, b is an integer of 15 to 2771, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:273, and where b is greater than or equal to a + 14.	R60249, R60762, R63751, R67526, H95029, H95095, N59347, N77158, W19778, AA047615, AA047555, AA047687, AA047738, AA056453, AA070880, AA112293, AA113105, AA112550, AA112614, AA158015, AA158228, AA160995, AA160996, AA190555, AA191131, AA224574, AA227422, AA255563, AA255586, AA418477, AA424689, AA470392, AA515485, AA515507, AA583475,

		AA588210, AA602533, AA573902, AA568354, AA746111, AA766146, AA804893, N83302
830154	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1875 of SEQ ID NO:274, b is an integer of 15 to 1889, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:274, and where b is greater than or equal to a + 14.	
830183	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 590 of SEQ ID NO:275, b is an integer of 15 to 604, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:275, and where b is greater than or equal to a + 14.	
830194	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1367 of SEQ ID NO:276, b is an integer of 15 to 1381, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:276, and where b is greater than or equal to a + 14.	T51023, T51115, T52795, T53595, T56300, T56767, T59691, T59827, T59904, T63354, T72200, T72269, T92900, T92990, R07165, R07217, R44334, R49609, R44334, R49609, H11106, H20800, H22618, H42472, H43453, H50320, H50321, H69947, N20118, N21306, N26128, N63140, N67225, N67232, W45407, W56419, W56420, W72419, W76279, W94626, W94710, AA029459, AA029524, AA034511, AA035053, AA035563, AA039819, AA041465, AA053002, AA055974, AA056002, AA070356, AA070320, AA074029, AA074039, AA074189, AA074336, AA075645, AA075646, AA076380, AA084435, AA084465, AA084453, AA085290, AA086454, AA099172, AA101922, AA101959, AA099618, AA102011, AA112794, AA126226, AA126304, AA128510, AA129955, AA133875, AA128443, AA133328, AA133403, AA134003, AA130990, AA131028, AA132940, AA135158, AA135628, AA143273, AA146730, AA151853, AA155641, AA155696, AA155726, AA157967, AA158903, AA158902, AA158943, AA158944, AA159293, AA159526, AA161206, AA160558, AA160739, AA160740, AA165357, AA167787, AA169218, AA169512, AA169691, AA176365, AA179272, AA179388, AA180903, AA181001, AA181325, AA181508, AA182781, AA173899, AA187757, AA188120, AA186725, AA187070, AA187152, AA190896, AA199819, AA223210,

		AA223254. AA227038. AA232399, AA233288. AA243192. AA252285, AA492525. AA420611. AA420688. AA492171. AA492254. AA503950, AA507398. AA513704. AA513757, AA515944. AA525799. AA558212, AA563863. AA565107. F17110. AA582829. AA586678. AA603895, AA604163. AA568617. AA617883, AA622814. AA635987. AA569079, AA570078. AA570258. AA570419, AA573205. AA573965. AA574048, AA566065. AA748781. AA834135, AA837022. AA838454. AA838636, AA838049. AA838058. AA856831, AA909853. AA910298. AA927706, AA932101. AA937900. AA953604, AA969555. AA973234. AA978074, AA985430. AA985432. AA988742, AA994207. AI002611. AI014411, N84537. N85082. W22113. W22114, W22431. W22639. W23207. W23271, W29046. N88675. AA640915, AA092777
830207	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1135 of SEQ ID NO:277, b is an integer of 15 to 1149, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:277, and where b is greater than or equal to a + 14.	R51744, R88177. W05323. AA746479, AA761644. AA826038. W27619, AA642452
830242	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 797 of SEQ ID NO:278, b is an integer of 15 to 811, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:278, and where b is greater than or equal to a + 14.	
830328	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1246 of SEQ ID NO:279, b is an integer of 15 to 1260, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:279, and where b is greater than or equal to a + 14.	
830340	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1654 of SEQ ID NO:280, b is an integer of 15 to 1668, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:280, and where b is greater than or equal to a + 14.	
830341	Preferably excluded from the present invention are	T62985, T63236, T71911, T66677,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2314 of SEQ ID NO:281, b is an integer of 15 to 2328, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:281, and where b is greater than or equal to a + 14.	T66678, T80777, T81178, R16218, R16219, R67281, H15642, H15643, R96139, R96356, H61487, H61952, H62021, H62022, H62510, H62577, H62887, H63016, H65659, H65660, H72388, H72834, H80906, H97768, N30162, N35776, N52509, N66853, W44421, AA004323, AA004410, AA025214, AA026003, AA040205, AA040849, AA079158, AA079159, AA137066, AA137080, AA137137, AA136971, AA193479, AA532656, AA602312, AA828635, AA872751, AA934418, D80729, C15337
830351	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 942 of SEQ ID NO:282, b is an integer of 15 to 956, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:282, and where b is greater than or equal to a + 14.	
830358	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1388 of SEQ ID NO:283, b is an integer of 15 to 1402, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:283, and where b is greater than or equal to a + 14.	
830390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 661 of SEQ ID NO:284, b is an integer of 15 to 675, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:284, and where b is greater than or equal to a + 14.	
830400	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1325 of SEQ ID NO:285, b is an integer of 15 to 1339, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:285, and where b is greater than or equal to a + 14.	T40239, T41103, T60782, T61153, T92326, T95403, R16530, R16587, R46049, R49231, R49231, R46049, H26122, H26387, H67872, H67872, H97917, N23194, N29748, N57652, N64158, N67587, N77509, N80178, W03502, W23838, W57929, W72584, AA011087, AA011088, AA070667, AA074878, AA075068, AA075019, AA076166, AA079857, AA082235, AA099016, AA099093, AA100754, AA113152, AA126886, AA128207, AA126932, AA128546, AA130882, AA136302, AA136408, AA143052, AA143693, AA148079, AA149931, AA151001, AA151091, AA155761, AA157290, AA160781, AA165535, AA173281, AA179903, AA180211, AA181162, AA181673, AA181986,

		AA187551, AA191657, AA192202, AA196746, AA196944, AA223166, AA224485, AA242866, AA397377, AA468734, AA514807, AA523669, AA534165, AA534195, AA565551, AA565552, H67199, AA581627, AA588734, AA588752, AA593857, AA595407, AA595555, AA603965, AA610486, AA614617, AA631563, AA635960, AA636057, AA576256, AA577470, AA580124, AA580480, AA714208, AA728790, AA729276, AA729361, AA744895, AA745002, AA746940, AA746948, AA747346, AA804602, AA810873, AA833970, AA836938, AA838563, AA858405, AA872330, AA922975, AA946823, AA954185, AA962678, AA978008, AA985504, AA987717, AI004904, AI017374, AI075264, F19611, AI089951, N83301, AA082282, AA091465, AA093298, AA094459
830437	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1384 of SEQ ID NO:286, b is an integer of 15 to 1398, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:286, and where b is greater than or equal to a + 14.	
830458	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 912 of SEQ ID NO:287, b is an integer of 15 to 926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:287, and where b is greater than or equal to a + 14.	T47583, T47584, T49761, T50148, T50203, T47161, R11382, R14878, H18220, H18258, R92715, N78687, W20222, W58210, W58319, W72115, W77801, W79332, W79431, W79487, W79631, W94437, N90582, AA043441, AA043442, AA148009, AA147947, AA150837, AA224863, AA225964, AA226110, AA259194, AA259193, AA420769, AA420829, AA470787, AA493672, AA501962, AA502082, AA506908, AA528607, AA588435, AA603500, AA603814, AA627229, AA627233, AA627240, AA632058, AA632689, AA639239, AA579023, AA580698, AA662633, AA661967, AA665215, AA729443, AA730546, AA737851, AA745424, AA745526, AA747036, AA878568, AA879157, AA886627, AA902180, AA922294, AA933050, AA962580, AA977360, AA985679, AA996058, AA996145, AI053546, AI085892, N83274, W15194, N88934, C04128, AA640839, AA091328, AA093116, AA094048, AA094287
830466	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3080 of SEQ ID NO:288, b is an integer of 15 to 3094, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:288, and where b is greater than or equal to a + 14.	
830497	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1969 of SEQ ID NO:289, b is an integer of 15 to 1983, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:289, and where b is greater than or equal to a + 14.	T47088, T47089, T58430, T58462, R00971, H42144, N77388, W51953, W52502, AA036671, AA114976, AA593693, AA575857, C01052
830511	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1284 of SEQ ID NO:290, b is an integer of 15 to 1298, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:290, and where b is greater than or equal to a + 14.	
830512	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2445 of SEQ ID NO:291, b is an integer of 15 to 2459, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:291, and where b is greater than or equal to a + 14.	
830513	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 556 of SEQ ID NO:292, b is an integer of 15 to 570, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:292, and where b is greater than or equal to a + 14.	
830540	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2454 of SEQ ID NO:293, b is an integer of 15 to 2468, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:293, and where b is greater than or equal to a + 14.	T66458, T98908, R15832, R21916, R22565, H12306, R99043, H57499, H82961, AA046203, AA046283, AA055081, AA055141, AA173411, AA173467, AA173996, AA176693
830550	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1066 of SEQ ID NO:294, b is an integer of 15 to 1080, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:294, and where b is greater than or equal to a + 14.	R50040, R60172, R71512, H09125, H09475, H21789, R84538, R85928, R94762, R96633, R96680, R97580, H53135, H53241, H82960, H83191, N68166, N68684, N77903, N80174, N80625, N92442, N93242, N93314, N98261, W03498, W05839, W20000, W25100, W31279, W37087, W60751, W67554, W67583, W73877, W77814, W80412, W95868, W95954, N91343,

		AA026891, AA026892, AA033547, AA034170, AA069175, AA088435, AA151307, AA161037, AA237097, AA251326, AA251729, AA428848, AA429940, AA287366, AA287504, AA470593, AA470594, AA514493, AA564438, H67293, AA582501, AA583172, AA587111, AA602517, AA603483, AA569955, AA732412, AA737913, AA810504, AA832193, AA857743, AA915872, AA915896, AA915992, AA948498, AA983538, AA991546, AI052409, AI053921
830567	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2681 of SEQ ID NO:295, b is an integer of 15 to 2695, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:295, and where b is greater than or equal to a + 14.	R69708, R75813, R75814, N22294, N47088, N50300, N50983, N81194, N93236, AA074258, AA083867, AA083973, AA195801, AA196063, AA252500, AA252415, AA258014, AA287593, AA291332, AA492017, AA522597, AA617684, AA713960, AA740158, AA749386, AA808100, AA808680, AA814350, AA826203, AA831453, AA887306, AA918645, AA972761, N88184
830586	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1380 of SEQ ID NO:296, b is an integer of 15 to 1394, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:296, and where b is greater than or equal to a + 14.	R99131, H81094, W01508, AA045861, AA085947, AA102188, AA146772, AA148854, AA233843, AA424679, AA491204, AA514459, AA532818, AA809984, AA838521, AA954880, AI089939
830632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 984 of SEQ ID NO:297, b is an integer of 15 to 998, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:297, and where b is greater than or equal to a + 14.	T47818, R21519, R21621, R22056, R22112, R31393, R32890, R48823, R48824, R66656, R67377, R71682, H25037, H25038, H25842, H26215, H26515, H26994, H28312, H28313, H29756, H30178, H41920, H41966, H42490, H43473, R83733, R85464, R88798, R89058, R93321, H52733, H59363, H60020, H73314, H73513, H80831, H80832, H82603, H86794, H86795, H86853, H86852, H92710, H96832, H98741, N23451, N23463, N26478, N26861, N31350, N31593, N35529, N39970, N42652, N62104, N74283, N76446, N78334, N92771, W04383, W19424, W20392, W24569, W35168, W60060, W60111, W84373, W84420, AA025658, AA029558, AA062705, AA062707, AA063390, AA062771, AA081934, AA126557, AA136019, AA151638, AA192245, AA194655, AA470430, AA493634, AA552261, AA552348, AA565278, AA565462, AA583788, AA593646, AA594277, AA604853, AA613755,

		AA632449, AA632505, AA657974, AA730677, AA730804, AA748100, AA765824, AA857805, AA954102, AA961763, AA962500, AA974525, AA983564, AA987422, AA987934, AA989423, AI000235, F19140, N84058, N84994, C03222, AA091370, AA091545
830645	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1652 of SEQ ID NO:298, b is an integer of 15 to 1666, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:298, and where b is greater than or equal to a + 14.	
830652	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2430 of SEQ ID NO:299, b is an integer of 15 to 2444, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:299, and where b is greater than or equal to a + 14.	
830659	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1012 of SEQ ID NO:300, b is an integer of 15 to 1026, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:300, and where b is greater than or equal to a + 14.	T65101, T66494, T66636, T84051, T86086, R05580, R13805, R15868, R16050, H05221, H05222, H13512, H16069, H18275, H21247, H44169, R83705, R92365, H48479, H48643, H54436, H54526, H73472, H73726, H97495, N29822, N30479, N31551, N32563, N39176, N39961, N45251, N68667, N91684, W07693, W32510, W32607, W38017, W74179, W79849, AA018138, AA028191, AA033572, AA033571, AA042915, AA043002, AA053878, AA054501, AA058344, AA099556, AA101993, AA134643, AA143525, AA176419, AA424269, AA555196, AA769107, AA987653, AI076212, N84624, N85006, AI084132, AI084154, AA094327
830696	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 816 of SEQ ID NO:301, b is an integer of 15 to 830, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:301, and where b is greater than or equal to a + 14.	
830706	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3286 of SEQ ID NO:302, b is an integer of 15 to 3300, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:302, and where b is	

	greater than or equal to a + 14.	
830743	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 461 of SEQ ID NO:303, b is an integer of 15 to 475, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:303, and where b is greater than or equal to a + 14.	N30323, N56655, N69079, N69946, N80244, N98327, W07371, W42660, W45185, W55989, W56279, W68387, W68503, W72685, W74708, W74677, W77791, W80647, AA010723, AA011171, AA033537, AA034221, AA035773, AA056334, AA062820, AA132021, AA132124, AA135594, AA135681, AA151293, AA151292, AA181331, AA186392, AA187084, AA228662, AA228680, AA229819, AA468802, AA470869, AA483684, AA491891, AA514852, AA533423, AA548946, AA563674, AA564612, AA594511, AA600707, AA622053, AA635767, AA639353, AA662887, AA664589, AA729365, AA747035, AA747774, AA814124, AA873167, AA886626, AA903495, AA903981, AA922807, AA969768, AA973174, AA974282, AA976458, AA977143, AA983332, AI025140, AI066527, F19035, F19464, C03984, C13986, C14221, C14299, C14336, C14341, C14380, C14385, C14396, C14434, C14483, C14504, C14513, C15788
830770	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2888 of SEQ ID NO:304, b is an integer of 15 to 2902, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:304, and where b is greater than or equal to a + 14.	
830830	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1539 of SEQ ID NO:305, b is an integer of 15 to 1553, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:305, and where b is greater than or equal to a + 14.	
830838	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1973 of SEQ ID NO:306, b is an integer of 15 to 1987, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:306, and where b is greater than or equal to a + 14.	
830851	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 771 of SEQ ID NO:307, b is an integer of 15 to 785, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:307, and where b is greater than or equal to a + 14.	
830853	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2164 of SEQ ID NO:308, b is an integer of 15 to 2178, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:308, and where b is greater than or equal to a + 14.	
830856	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 861 of SEQ ID NO:309, b is an integer of 15 to 875, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:309, and where b is greater than or equal to a + 14.	
830862	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 742 of SEQ ID NO:310, b is an integer of 15 to 756, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:310, and where b is greater than or equal to a + 14.	T46908, T46909, T46921, T46922, T50921, T52918, T53038, T56001, T59028, T94115, T94204, R53898, R53908, H02747, H27523, H77792, H88026, H88248, H90255, H96065, H88248, N21994, N64072, N73723, N74262, N75815, N77939, W03894, W23887, AA081082, AA113423, AA115852, AA143290, AA143335, AA146868, AA157054, AA157208, AA179118, AA187792, AA188385, AA468513, AA468983, AA501970, AA523481, AA528461, AA533759, AA533618, AA535287, AA541570, AA558529, L44430, AA604961, AA568927, AA659814, AA661481, AA661996, AA731036, AA748135, AA847331, AA878667, AA885549, AA935403, AA938035, AI001062, F19242, N83489, N83646, N84328, N85002, N85167, N85223, N85325, N85833, N85949, N86287, N86329, N87923, N83150, AA642852, AA091775, AA093919
830879	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 837 of SEQ ID NO:311, b is an integer of 15 to 851, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:311, and where b is greater than or equal to a + 14.	T62074, T62130, T67747, T67857, R44816, R48904, R44816, H13822, H29311, W37451, N90567, AA128266, AA164552, AA235044, AA236012, AA746229, AA962194, AA987868, AA994828, AI000188, AI015557
830919	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1321 of SEQ ID NO:312, b is an integer of 15 to 1335, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:312, and where b is	

	greater than or equal to a + 14.	
830969	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 502 of SEQ ID NO:313, b is an integer of 15 to 516, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:313, and where b is greater than or equal to a + 14.	
830991	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1819 of SEQ ID NO:314, b is an integer of 15 to 1833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:314, and where b is greater than or equal to a + 14.	
831002	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1340 of SEQ ID NO:315, b is an integer of 15 to 1354, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:315, and where b is greater than or equal to a + 14.	
831003	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2407 of SEQ ID NO:316, b is an integer of 15 to 2421, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:316, and where b is greater than or equal to a + 14.	T64373, N48387, W52748, W52754, W70187, AA029541, AA034463, AA058497, AA082001, AA082284, AA085967, AA088397, AA133444, AA133477, AA149568, AA187408, AA226818, AA226855
831021	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1078 of SEQ ID NO:317, b is an integer of 15 to 1092, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:317, and where b is greater than or equal to a + 14.	
831036	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1366 of SEQ ID NO:318, b is an integer of 15 to 1380, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:318, and where b is greater than or equal to a + 14.	
831071	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2598 of SEQ ID NO:319, b is an integer of 15 to 2612, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:319, and where b is greater than or equal to a + 14.	

831094	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 929 of SEQ ID NO:320, b is an integer of 15 to 943, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:320, and where b is greater than or equal to a + 14.	
831099	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2945 of SEQ ID NO:321, b is an integer of 15 to 2959, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:321, and where b is greater than or equal to a + 14.	T58120, T90056, T90158, T94290, T94639, R69200, R69590, R69678, R76031, H65424, H65425, N32273, N40465, N47619, N48504, N66482, N67212, N67243, N67881, N71915, N72302, N92538, N94512, W03004, W06930, W20370, W23962, W38380, W38525, W38716, W39486, W42582, W42594, W44824, W48665, W51898, W52474, W53040, W60142, N90075, N90423, AA025009, AA024962, AA029382, AA029726, AA031500, AA031546, AA037283, AA037749, AA039259, AA044145, AA044261, AA065061, AA070027, AA082386, AA083544, AA083757, AA088692, AA088829, AA099577, AA100236, AA100245, AA100517, AA112739, AA112091, AA116055, AA130509, AA130510, AA132145, AA135909, AA136308, AA136413, AA136528, AA136751, AA146853, AA146852, AA148049, AA156943, AA159808, AA165022, AA173867, AA181803, AA182563, AA182776, AA186553, AA186858, AA192463, AA194658, AA255837, AA261995, AA423999, AA493599, AA228337, AA228348, AA506755, AA506420, AA513968, AA514542, AA522900, AA524125, AA551485, AA553912, AA563900, AA594966, AA602651, AA610339, AA610361, AA614772, AA618333, AA576828, AA665045, AA714493, AA729997, AA738153, AA768641, AA804931, AA806122, AA827914, AA857664, AA876216, AA877173, AA877646, AA894385, AA922728, AA947835, AA977110, AA984009, AA988275, AA988567, N84005, N84600, N84939, N85553, AI084028, N86141, N88049, N89450, N89451, C02877, C02980, C03631, C05243, C05332, C05993, AA642453, AA090838, AA089614, AA091652, AA093130, AA093851
831113	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	AA122085, AA147371, AI005336

	where a is any integer between 1 to 788 of SEQ ID NO:322. b is an integer of 15 to 802. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:322. and where b is greater than or equal to a + 14.	
831120	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1710 of SEQ ID NO:323. b is an integer of 15 to 1724. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:323. and where b is greater than or equal to a + 14.	
831172	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2247 of SEQ ID NO:324, b is an integer of 15 to 2261. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:324, and where b is greater than or equal to a + 14.	
831178	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1199 of SEQ ID NO:325, b is an integer of 15 to 1213, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:325, and where b is greater than or equal to a + 14.	
831184	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2750 of SEQ ID NO:326, b is an integer of 15 to 2764, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:326, and where b is greater than or equal to a + 14.	
831203	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1750 of SEQ ID NO:327, b is an integer of 15 to 1764, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:327, and where b is greater than or equal to a + 14.	
831210	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 557 of SEQ ID NO:328, b is an integer of 15 to 571, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:328, and where b is greater than or equal to a + 14.	AA057014, AA059289
831228	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 459 of SEQ ID	

	NO:329, b is an integer of 15 to 473, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:329, and where b is greater than or equal to a + 14.	
831256	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1321 of SEQ ID NO:330, b is an integer of 15 to 1335, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:330, and where b is greater than or equal to a + 14.	R17500, R48877, H12160, R84358, H90367, N33987, AA161057
831257	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1032 of SEQ ID NO:331, b is an integer of 15 to 1046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:331, and where b is greater than or equal to a + 14.	T49922, T85470, R37545, H03610, AA005184, AA045346
831277	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1297 of SEQ ID NO:332, b is an integer of 15 to 1311, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:332, and where b is greater than or equal to a + 14.	
831317	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1430 of SEQ ID NO:333, b is an integer of 15 to 1444, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:333, and where b is greater than or equal to a + 14.	T39850, T47708, T47709, T47863, T51491, T52507, T53819, T53951, T55884, T60330, T60359, T60364, T60380, T60480, T60634, T61198, T61280, T61878, T62028, T67704, T67742, T67780, T67853, T67910, T68010, T68058, T68132, T68154, T68379, T68998, T68999, T69078, T69079, T69119, T69177, T69442, T70496, T71707, T72285, T72505, T72998, T73123, T73679, T73756, T73761, T73837, T74031, T74383, T74405, T74655, T74784, T74798, T74892, T85320, T85533, R83453, R88738, R90989, R90995, H58528, H59441, H60092, H60282, H60589, H67401, H67458, H72811, H79422, H80518, H80570, H91775, H91816, N57814, W60714, W60741, AA034367, AA040550, AA040667, AA242768, AA424551, AA424642, R29495, R29660, R29089, C21224
831339	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1016 of SEQ ID NO:334, b is an integer of 15 to 1030, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:334, and where b is	

	greater than or equal to a + 14.	
831363	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2113 of SEQ ID NO:335, b is an integer of 15 to 2127, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:335, and where b is greater than or equal to a + 14.	T58736, T58803, T61766, T64470, T64610, T67816, T68878, T68952, T72450, T72511, T72968, T73613, T73939, H41914, H41957, N75040, W05718, AA043436, AA043416, AA045231, AA058807, AA484773, AA502762, AA503811, AA527553, AA744171, AA902935, AA903099, AI002033
831367	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 833 of SEQ ID NO:336, b is an integer of 15 to 847, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:336, and where b is greater than or equal to a + 14.	
831379	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 688 of SEQ ID NO:337, b is an integer of 15 to 702, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:337, and where b is greater than or equal to a + 14.	R26001, R26804, R82629, R82630, H21598, H27310, H27309, H38082, H38083, H44451, H44494, H47613, R83356, R83791, R96066, R96103, H72512, H72910, H80449, H80450, H90511, H90607, N71766, N94349, W16956, W23496, W24351, W46455, W46523, W48658, W70263, W73002, W76239, W92963, W92964, AA157329, AA157426, AA458665, AA229554, AA280810, AA280936, AA490898, AA491084, AA493730, AA527336, AA534762, AA535794, F17720, AA603439, AA568655, AA659071, AA826699, AA872867, AA876999, AA932403, AA953149, AA953343, AI000023, AI017353, AI094807, N95548, C02063, C04109
831385	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 861 of SEQ ID NO:338, b is an integer of 15 to 875, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:338, and where b is greater than or equal to a + 14.	
831390	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1434 of SEQ ID NO:339, b is an integer of 15 to 1448, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:339, and where b is greater than or equal to a + 14.	T53890, T54037, T81546, T81973, R20470, R21066, R45288, R46246, R45288, R46246, H13340, H17537, H30523, R85229, R85230, R94643, R94685, R94686, H52010, H52125, H71328, H71376, N25973, N28794, N30891, N36603, N41703, N62205, N63213, N76503, W45706, W44353, W52126, W74523, W79862, AA033566, AA034468, AA099015, AA099092, AA100315, AA129588, AA167137, AA194961, AA226935, AA226943, AA418898, AA428909,

		AA485083, AA485195, AA505107, AA506087, AA516109, AA525370, AA617946, AA627402, AA573848, AA574063, AA809830, AA834509, AA837985, AA862394, AA862989, AA974789, AA988779, AI000171, AI094917, W24010, N88026, C20972
831391	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 829 of SEQ ID NO:340, b is an integer of 15 to 843, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:340, and where b is greater than or equal to a + 14.	
831405	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1279 of SEQ ID NO:341, b is an integer of 15 to 1293, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:341, and where b is greater than or equal to a + 14.	T54632, T54714, T55384, T55812, T56220, T60613, T69578, R08164, R08219, T78003, T78164, R01577, R12676, R16414, H60551, N21984, N25878, N25887, N75352, W01648, W72541, W76166, W86984, W86811, W88909, W88788, AA022691, AA022784, AA193302, AA194256, AA235873, AA425660, AA573463, AA953249, R29055
831442	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1259 of SEQ ID NO:342, b is an integer of 15 to 1273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:342, and where b is greater than or equal to a + 14.	
831476	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1779 of SEQ ID NO:343, b is an integer of 15 to 1793, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:343, and where b is greater than or equal to a + 14.	R48303, R48405, R73778, H30456, H81254, W02773, W24831, W73089, W73194, AA034015, AA151153, AA151154, AA418429, AA424672, AA593592, AA910532, AA987246, AI001017, C02335, C04320
831488	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1658 of SEQ ID NO:344, b is an integer of 15 to 1672, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:344, and where b is greater than or equal to a + 14.	
831518	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2095 of SEQ ID NO:345, b is an integer of 15 to 2109, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:345, and where b is greater than or equal to a + 14.	

831519	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1700 of SEQ ID NO:346, b is an integer of 15 to 1714, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:346, and where b is greater than or equal to a + 14.	
831521	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1658 of SEQ ID NO:347, b is an integer of 15 to 1672, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:347, and where b is greater than or equal to a + 14.	
831550	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1469 of SEQ ID NO:348, b is an integer of 15 to 1483, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:348, and where b is greater than or equal to a + 14.	
831560	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1828 of SEQ ID NO:349, b is an integer of 15 to 1842, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:349, and where b is greater than or equal to a + 14.	T56438, R22852, R46063, R52365, R81781, R81879, H02958, H04256, H05743, H05849, H23235, H23349, H43210, H43260, H87699, H91571, W00708, W56717, W56762, W70251, W70252, AA026841, AA027043, AA041261, AA041495, AA043451, AA043452, AA054505, AA054366, AA055050, AA055129, AA147629, AA147667
831562	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2994 of SEQ ID NO:350, b is an integer of 15 to 3008, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:350, and where b is greater than or equal to a + 14.	
831570	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2742 of SEQ ID NO:351, b is an integer of 15 to 2756, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:351, and where b is greater than or equal to a + 14.	
831593	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1631 of SEQ ID NO:352, b is an integer of 15 to 1645, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:352, and where b is	

	greater than or equal to a + 14.	
831596	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1623 of SEQ ID NO:353, b is an integer of 15 to 1637, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:353, and where b is greater than or equal to a + 14.	
831627	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1105 of SEQ ID NO:354, b is an integer of 15 to 1119, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:354, and where b is greater than or equal to a + 14.	AA147578, AA156449, AA588796, AA863066, D80116
831649	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 724 of SEQ ID NO:355, b is an integer of 15 to 738, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:355, and where b is greater than or equal to a + 14.	R21047
831664	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1952 of SEQ ID NO:356, b is an integer of 15 to 1966, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:356, and where b is greater than or equal to a + 14.	R35205, H13039, R84255, W24589, W93157, AA186436, AA188774, AA227246, AA658889, AA838204, W22056, W25833, W28198, W28494, AA090436, AA089530, AA089667
831674	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1548 of SEQ ID NO:357, b is an integer of 15 to 1562, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:357, and where b is greater than or equal to a + 14.	
831684	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1917 of SEQ ID NO:358, b is an integer of 15 to 1931, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:358, and where b is greater than or equal to a + 14.	T64083, R54664, R54665, W52888, W60096, W60162, AA009843, AA009870, AA236225, AA236291, AA459452, AA465675, AA554776, AA563899, AA583755, AA593849, AA596013, AA627978, AA573921, AA747840, AA828086, AA830260, AA837593, AA996154, C01662
831687	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 855 of SEQ ID NO:359, b is an integer of 15 to 869, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:359, and where b is greater than or equal to a + 14.	T49489, R05976, R55046, N21648, N31054, N48001, AA464953, AA426224, AA430556, AA600829, AA744708, AA747361, AA976473, AI097658

831726	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 547 of SEQ ID NO:360, b is an integer of 15 to 561, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:360, and where b is greater than or equal to a + 14.	
831736	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1666 of SEQ ID NO:361, b is an integer of 15 to 1680, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:361, and where b is greater than or equal to a + 14.	T60384, T93026, T83297, R17403, R17423, R21319, H65765, N94506, W23956, W24344, W45068, W57786, W57860, W81343, AA058929, AA151788, AA151833
831762	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 726 of SEQ ID NO:362, b is an integer of 15 to 740, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:362, and where b is greater than or equal to a + 14.	
831801	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1310 of SEQ ID NO:363, b is an integer of 15 to 1324, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:363, and where b is greater than or equal to a + 14.	T39530, T64430, R36089, H12597, H12647, H19534, H20096, H26648, H26663, W15192, W45569, W45621, AA018144, AA018145, AA018470, AA039510, AA039529, AA047549, AA047837, AA057785, AA074201, AA075686, AA079138, AA135599, AA135658, AA147502, AA147931, AA156715, AA156811, AA188215, AA186362, AA425996, AA283917, AA514670, AA522463, AA714301, AA742700, AA872728, AA887841, AA971644, AI015637, AI053971, AI054233, AI074507, AI084901, W28363
831848	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2839 of SEQ ID NO:364, b is an integer of 15 to 2853, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:364, and where b is greater than or equal to a + 14.	T77112, R13655, R19353, R19511, R24780, R35812, R36752, R38177, R43861, R44629, R45511, R43861, R45511, R44629, R71248, R71299, R82784, H00629, H01917, H04479, H45706, H45757, H94039, H94125, N30574, N57220, AA033684, AA114107, AA253260, AA461547, AA460619, AA715125, AI096588, C03714, AA092127
831861	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1823 of SEQ ID NO:365, b is an integer of 15 to 1837, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:365, and where b is greater than or equal to a + 14.	T57456, T58038, T58104, R08156, R27046, R28341, R28340, N32411, N56831, N78961, W16984, W16954, W17352, W74522, W79861, AA025882, AA025883, AA084109, AA100121, AA100060, AA132713

831866	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1809 of SEQ ID NO:366, b is an integer of 15 to 1823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:366, and where b is greater than or equal to a + 14.	
831878	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 884 of SEQ ID NO:367, b is an integer of 15 to 898, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:367, and where b is greater than or equal to a + 14.	
831899	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1103 of SEQ ID NO:368, b is an integer of 15 to 1117, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:368, and where b is greater than or equal to a + 14.	AA159048, AA768390, AA806956
831913	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2212 of SEQ ID NO:369, b is an integer of 15 to 2226, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:369, and where b is greater than or equal to a + 14.	
831972	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3622 of SEQ ID NO:370, b is an integer of 15 to 3636, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:370, and where b is greater than or equal to a + 14.	
831985	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4025 of SEQ ID NO:371, b is an integer of 15 to 4039, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:371, and where b is greater than or equal to a + 14.	
831986	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1585 of SEQ ID NO:372, b is an integer of 15 to 1599, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:372, and where b is greater than or equal to a + 14.	
832010	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 450 of SEQ ID NO:373. b is an integer of 15 to 464, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:373, and where b is greater than or equal to a + 14.	
832016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 876 of SEQ ID NO:374, b is an integer of 15 to 890, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:374, and where b is greater than or equal to a + 14.	
832041	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1860 of SEQ ID NO:375, b is an integer of 15 to 1874, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:375, and where b is greater than or equal to a + 14.	R63637, R92994, N30838, N30844, N41366, N41372, AA639771
832044	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2004 of SEQ ID NO:376, b is an integer of 15 to 2018, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:376, and where b is greater than or equal to a + 14.	T56668, R09616, R20197, R44983, R52998, R52997, R44983, H06485, H06543, H09799, H09885, H24790, N57987, N62197, N76494, W02915, W78217, AA041290, AA041323, AA074236, AA075127, AA075212, AA075847, AA088708, AA088793, AA112359, AA121803, AA151677, AA166711, AA167069, AA181608, AA188478, AA194067, AA194182, AA221025, AA221037, AA228036, AA228145, AA557397, AA564567, AA582681, AA582151, AA601549, AA613841, AA832393, AA846987, AA865356, AA866164, AA872667, AA862962, AA911092, AA937359, AI000072, D83877
832049	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 804 of SEQ ID NO:377, b is an integer of 15 to 818, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:377, and where b is greater than or equal to a + 14.	
832122	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2551 of SEQ ID NO:378, b is an integer of 15 to 2565, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:378, and where b is greater than or equal to a + 14.	
832148	Preferably excluded from the present invention are	T78202, R37864, R62706, R78737,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1666 of SEQ ID NO:379, b is an integer of 15 to 1680, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:379, and where b is greater than or equal to a + 14.	R78736, H62109, N50394, N51659, N67973, N80394, W33108, W33107, AA016055, AA074831, AA075097, AA256793, AA256472, AA418825, AA418922, AA430755, AA280663, AA281049, AA467867, AA502148, H71558, AA721278, AA748880, AA809767, AA810852, AA832174, AA911263, AA938484, AA975282, D80672, D81573, D81746, AI096900, C02375
832197	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1253 of SEQ ID NO:380, b is an integer of 15 to 1267, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:380, and where b is greater than or equal to a + 14.	
832237	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1017 of SEQ ID NO:381, b is an integer of 15 to 1031, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:381, and where b is greater than or equal to a + 14.	R36943, R42259, R53230, R42259, H09607, AA150724, AA831055
832246	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1583 of SEQ ID NO:382, b is an integer of 15 to 1597, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:382, and where b is greater than or equal to a + 14.	H13698, H13750, R91283, R91322, H97506, N64810, N75659, W61290, W65386, H54890, AA568261, AA830860, AA863239, AA873329, AA938701, D82264, C18047
832256	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 161 of SEQ ID NO:383, b is an integer of 15 to 175, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:383, and where b is greater than or equal to a + 14.	
832280	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2157 of SEQ ID NO:384, b is an integer of 15 to 2171, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:384, and where b is greater than or equal to a + 14.	H09977, H09978, R89392, R94438, H93033, H93466, H93904, N29334, N53767, N57027, N71868, N71879, N73126, W24652, AA026682, AA047124, AA127259, AA224396, AA224473, AA227220, AA236734, AA236763, AA236910, AA236919
832285	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2350 of SEQ ID NO:385, b is an integer of 15 to 2364, where both a and b correspond to the positions of nucleotide	R12740, R14184, R15171, R26447, R28455, R34165, R35396, R39792, R40473, R49696, R41588, R40473, R49696, R70668, R70669, R79640, R79833, H02312, H08199, H08297, R99351, H84241, H84567, H85554,

	residues shown in SEQ ID NO:385, and where b is greater than or equal to a + 14.	N24354, N25230, N32462, N33863, N64676, N70374, N80109, W47526, W47527, W80678, W80934, W93668, AA082195, AA223758, AA243624, AA255527, AA256711, AA262387, AA281015, AA281094, AA281183, AA281203, AA287927, AA287991, AA505084, AA505086, AA525301, AA553559, AA564243, AA582189, AA737010, AA808271, AA872481, AA937541, AI015987, C01015, C20842
832294	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2850 of SEQ ID NO:386, b is an integer of 15 to 2864, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:386, and where b is greater than or equal to a + 14.	
832326	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2669 of SEQ ID NO:387, b is an integer of 15 to 2683, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:387, and where b is greater than or equal to a + 14.	
832333	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1432 of SEQ ID NO:388, b is an integer of 15 to 1446, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:388, and where b is greater than or equal to a + 14.	
832346	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 709 of SEQ ID NO:389, b is an integer of 15 to 723, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:389, and where b is greater than or equal to a + 14.	T88928, R12446, R37113, R42462, H15692, H18859, N34664, AA132220, AA224337, AA460720, AA492479
832370	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1032 of SEQ ID NO:390, b is an integer of 15 to 1046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:390, and where b is greater than or equal to a + 14.	
832381	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 685 of SEQ ID NO:391, b is an integer of 15 to 699, where both a	

	and b correspond to the positions of nucleotide residues shown in SEQ ID NO:391, and where b is greater than or equal to a + 14.	
832394	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1531 of SEQ ID NO:392, b is an integer of 15 to 1545, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:392, and where b is greater than or equal to a + 14.	
832454	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 735 of SEQ ID NO:393, b is an integer of 15 to 749, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:393, and where b is greater than or equal to a + 14.	T57094, T58711, T68990, T71879, R92183, H93778, N63977, N80768, AA034382, AA034383, AA057664, AA235744, AA425865, AA524693, AA551804, AA523604, AA614639, AA740316, AA872373, AA938571, AA947337, R28997, AA640968, C21135
832465	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 597 of SEQ ID NO:394, b is an integer of 15 to 611, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:394, and where b is greater than or equal to a + 14.	R36004, R36378, H71881, H96279, N50049, N63692, W74426, W79180, W87805, AA421015, AA527679, AA833773, AA987375, F19351, AA642491, C14893, C14937
832475	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1842 of SEQ ID NO:395, b is an integer of 15 to 1856, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:395, and where b is greater than or equal to a + 14.	
832495	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2637 of SEQ ID NO:396, b is an integer of 15 to 2651, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:396, and where b is greater than or equal to a + 14.	
832498	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2493 of SEQ ID NO:397, b is an integer of 15 to 2507, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:397, and where b is greater than or equal to a + 14.	T67126, T67127, R13516, R20638, H64071, N22361, N25516, N39506, N75609, N78204, W40313, W45344, AA074739, AA074803, AA143509, AA523999, AA552542, AA554032, N20483, AA588804, AA617733, AA577150, AA577309, AA579423, AA740813, AA835721, AA836640, AA909766, AA936979, AA947310, N26815, AI085484, D78707, W67520, W68152
832501	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1259 of SEQ ID NO:398, b is an integer of 15 to 1273, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:398, and where b is greater than or equal to a + 14.	
832505	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3760 of SEQ ID NO:399, b is an integer of 15 to 3774, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:399, and where b is greater than or equal to a + 14.	T50501, T50636, T92136, R52390, R59648, H06170, H28886, H28885, R96577, R96600, H84171, H94122, H98228, N36866, N36872, N46136, N46142, N63589, N66323, W48779, W49798, AA029033, AA054487, AA058524, AA084466, AA086177, AA098967, AA099485, AA100345, AA147008, AA147009, AA146910, AA146909, AA160346, AA159865, AA192832, AA203513, AA252521, AA252553, AA463513, AA463570, AA421250, AA425704, AA427774, AA278328, AA278999, AA280712, AA281733, AA281871, AA282407, AA282626, AA283639, AA542810, AA557893, AA568486, AA569759, AA577522, AA659517, AA659737, AA664537, AA713950, AA805488, AA835999, AA876619, AA931568, AA935758, AA946722, AI000603, D82640
832539	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1508 of SEQ ID NO:400, b is an integer of 15 to 1522, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:400, and where b is greater than or equal to a + 14.	H72563, AA160114, AA159654, AA161261, AA165097, AA223618, AA243203
832554	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1356 of SEQ ID NO:401, b is an integer of 15 to 1370, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:401, and where b is greater than or equal to a + 14.	
832569	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1398 of SEQ ID NO:402, b is an integer of 15 to 1412, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:402, and where b is greater than or equal to a + 14.	
832578	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1736 of SEQ ID NO:403, b is an integer of 15 to 1750, where both a and b correspond to the positions of nucleotide	R09545, R09658, R09967, R11471, R16714, R16910, R16965, R19372, R80788, R80988, H28725, H63085, H63169, H75499, H75500, N33554, N41536, N52961, N52966, N74070, W01039, W57770, W57843, W60109,

	residues shown in SEQ ID NO:403. and where b is greater than or equal to a + 14.	W91978. W92107. AA001984. AA004653. AA027155. AA418427. AA281395. AA532870. AA564737. AA588889. AA631841. AA639548. AA765363. AA877896. AA887900. AA974026. AI057270. AI084214. AI094490. AI096750. AI097632. AI096745
832615	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1325 of SEQ ID NO:404, b is an integer of 15 to 1339, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:404, and where b is greater than or equal to a + 14.	
832620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 468 of SEQ ID NO:405, b is an integer of 15 to 482, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:405, and where b is greater than or equal to a + 14.	
832632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1399 of SEQ ID NO:406, b is an integer of 15 to 1413, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:406, and where b is greater than or equal to a + 14.	
832633	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1679 of SEQ ID NO:407, b is an integer of 15 to 1693, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:407, and where b is greater than or equal to a + 14.	R69173, AA053085, AA053597, AA427705, AA730380, AA865757, AA911497, AI083906
833483	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1328 of SEQ ID NO:408, b is an integer of 15 to 1342, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:408, and where b is greater than or equal to a + 14.	
834574	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2403 of SEQ ID NO:409, b is an integer of 15 to 2417, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:409, and where b is greater than or equal to a + 14.	
834859	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1387 of SEQ ID NO:410, b is an integer of 15 to 1401, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:410, and where b is greater than or equal to a + 14.	
834861	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3002 of SEQ ID NO:411, b is an integer of 15 to 3016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:411, and where b is greater than or equal to a + 14.	
834890	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 944 of SEQ ID NO:412, b is an integer of 15 to 958, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:412, and where b is greater than or equal to a + 14.	T40255, T40256, T40770, T40778, T40803, T41118, T94280, T94627, R13201, R32388, R32389, R53769, H28669, H39502, H42532, H42533, R82957, R85205, R85206, R88749, R90730, R90754, R91006, R92221, H56130, H56210, H58500, H57659, H69479, H69882, N22547, N31579, N42592, N45537, N48687, N56654, N58050, N69059, N73728, N80748, N92927, N94545, W20471, W30838, W52039, W60171, W68292, W93085, W93140, N91563, AA010850, AA011289, AA054592, AA054780, AA081135, AA081214, AA081655, AA081936, AA082127, AA082262, AA088665, AA088804, AA102560, AA100239, AA114237, AA115714, AA115715, AA127304, AA127303, AA147789, AA148021, AA149821, AA152050, AA160878, AA169126, AA171659, AA172131, AA172285, AA194597, AA243129, AA419357, AA425135, AA426203, AA244212, AA505963, AA508221, AA527434, AA527878, AA565036, F17736, AA582605, AA582728, AA583851, AA586421, AA601920, AA570580, AA574367, AA577515, AA577538, AA565998, AA657417, AA659655, AA662658, AA665113, AA714991, AA770684, AA808865, AA826971, AA838507, AA876809, AA877842, AA878025, AA886042, AA886643, AA877950, AA937751, AA948428, AA947036, AA973473, AA983150, AA989361, AI082367, D78922, D82096, N83321, C04115, R29685, C17110, C18023, C18068, AA093539, AA094947, AA151399, AA654145, AA654136
835079	Preferably excluded from the present invention are	N25566, W00985, AA081340,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 486 of SEQ ID NO:413, b is an integer of 15 to 500, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:413, and where b is greater than or equal to a + 14.	AA152231, AA164282, AA171619, AA187113, AI073932
835554	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3383 of SEQ ID NO:414, b is an integer of 15 to 3397, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:414, and where b is greater than or equal to a + 14.	
835560	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2866 of SEQ ID NO:415, b is an integer of 15 to 2880, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:415, and where b is greater than or equal to a + 14.	
835723	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1602 of SEQ ID NO:416, b is an integer of 15 to 1616, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:416, and where b is greater than or equal to a + 14.	T71562, R11480, R19383, R25309, R46659, R48802, R48913, R50038, R50376, R54963, R46659, R70030, R70077, R70161, R71380, R72303, R72352, R72772, R72773, R73386, R73387, H15775, H15776, H25239, H27204, H30499, H42026, H42613, H43207, H43254, H44314, H44936, H44975, R98394, R98395, R99071, R99271, H58902, H58903, H73590, H73436, H75566, H80599, N40440, N48475, N59703, AA515035, AA515043, AA515450, AA515650, AA515746, AA551788, AA551943, AA554602, AA557281, AA581549, AA581554, AA587399, AA593890, AA593997, AA593998, AA568878, AA568962, AA622458, AA714206, AA728962, AA737738, AA738036, AA738486, AA847538, AA865069, AA872029, AA886612, AA903381, AA916458, AA916464, AA922563, AA928617, AA928314, AA934581, AA973769, AA973767, AA983480, AA991199, AA994932, AA995182, AA999704, AI028371, AA643041
835791	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1801 of SEQ ID NO:417, b is an integer of 15 to 1815, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:417, and where b is greater than or equal to a + 14.	

835817	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1952 of SEQ ID NO:418, b is an integer of 15 to 1966, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:418, and where b is greater than or equal to a + 14.	
835840	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2838 of SEQ ID NO:419, b is an integer of 15 to 2852, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:419, and where b is greater than or equal to a + 14.	T66583, R15957, R22860, R62339, R62341, R62856, AA210836, AA214633, AA256340, AA732582, AA740735
836048	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2691 of SEQ ID NO:420, b is an integer of 15 to 2705, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:420, and where b is greater than or equal to a + 14.	
836898	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1887 of SEQ ID NO:421, b is an integer of 15 to 1901, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:421, and where b is greater than or equal to a + 14.	
836927	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2463 of SEQ ID NO:422, b is an integer of 15 to 2477, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:422, and where b is greater than or equal to a + 14.	
837344	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 763 of SEQ ID NO:423, b is an integer of 15 to 777, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:423, and where b is greater than or equal to a + 14.	
837789	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1635 of SEQ ID NO:424, b is an integer of 15 to 1649, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:424, and where b is greater than or equal to a + 14.	
838549	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1594 of SEQ ID NO:425, b is an integer of 15 to 1608, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:425, and where b is greater than or equal to a + 14.	
838754	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1780 of SEQ ID NO:426, b is an integer of 15 to 1794, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:426, and where b is greater than or equal to a + 14.	
838768	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 756 of SEQ ID NO:427, b is an integer of 15 to 770, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:427, and where b is greater than or equal to a + 14.	
839486	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 498 of SEQ ID NO:428, b is an integer of 15 to 512, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:428, and where b is greater than or equal to a + 14.	
839561	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1456 of SEQ ID NO:429, b is an integer of 15 to 1470, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:429, and where b is greater than or equal to a + 14.	R61634, AA135004, AA159213
839816	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 420 of SEQ ID NO:430, b is an integer of 15 to 434, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:430, and where b is greater than or equal to a + 14.	
840068	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1809 of SEQ ID NO:431, b is an integer of 15 to 1823, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:431, and where b is greater than or equal to a + 14.	
840279	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 3377 of SEQ ID NO:432, b is an integer of 15 to 3391, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:432, and where b is greater than or equal to a + 14.	
840489	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2539 of SEQ ID NO:433, b is an integer of 15 to 2553, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:433, and where b is greater than or equal to a + 14.	
840538	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2518 of SEQ ID NO:434, b is an integer of 15 to 2532, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:434, and where b is greater than or equal to a + 14.	T47551, T47552, T64522, T65947, R70190, H97064, N25641, N34240, N48063, N53261, N67904, N92702, N98774, W16899, W20316, W31028, W40137, W45371, W48722, W48577, W68670, W68773, W74242, AA033573, AA033574, AA063270, AA063271, AA065213, AA064894, AA082200, AA083707, AA085441, AA085694, AA088302, AA088303, AA099844, AA099984, AA102604, AA111894, AA112981, AA115039, AA115800, AA115799, AA122221, AA126905, AA126955, AA127109, AA127548, AA127549, AA128933, AA129152, AA129743, AA133290, AA135251, AA151963, AA156321, AA156382, AA160182, AA165104, AA164688, AA173757, AA180038, AA182644, AA190866, AA190959, AA191561, AA191637, AA197348, AA195895, AA258593, AA258622, AA262173, AA464978, AA465047, AA417938, AA418116, AA292727, AA523585, AA525020, AA548516, AA551816, AA554642, AA581720, AA568802, AA579801, AA738216, AA832441, AA903391, AA938688, AA977201, AA987552, AI095102, AI084149, W27768, C05889, C06263, AA089556, AA652586, AA213999, AA213977, AA219123, AA219290, AA435695, D12383, D12389, AA451677, AA453222, AA485641, AA485768, AA488670, AA485947, AA486053, AA486197, AA489511, AA489512, AA489558, AA491452, AA489876, AA600130, AA608644, AA620481, AA664307, AA629754, AA629909, AA677148, AA722910, AA772440, AA773550, AI038219, AI075755, AI081932, AI084706, T10852, T24678, F00208, F00897

840545	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1808 of SEQ ID NO:435, b is an integer of 15 to 1822, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:435, and where b is greater than or equal to a + 14.	
840549	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1016 of SEQ ID NO:436, b is an integer of 15 to 1030, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:436, and where b is greater than or equal to a + 14.	R10733, T86298, R55182, R55183, H00476, H00530, H25856, H25909, H25910, N50923, W84600, W84452, AA227897, D78774, AA486440, AA629249
840551	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1618 of SEQ ID NO:437, b is an integer of 15 to 1632, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:437, and where b is greater than or equal to a + 14.	
840557	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1002 of SEQ ID NO:438, b is an integer of 15 to 1016, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:438, and where b is greater than or equal to a + 14.	
840561	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 580 of SEQ ID NO:439, b is an integer of 15 to 594, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:439, and where b is greater than or equal to a + 14.	
840562	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1566 of SEQ ID NO:440, b is an integer of 15 to 1580, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:440, and where b is greater than or equal to a + 14.	R08937, R09046, R14796, R18307, R31150, R42283, R51828, R54224, R42283, R72104, R72156, R73118, R73171, R73943, H25904, H27191, H27192, H30471, H72478, H72879, H88214, H98231, W45061, W45071, W49842, W67423, W67424, W93880, W94151, AA023007, AA022473, AA032224, AA032282, AA034411, AA035691, AA040428, AA046861, AA046994, AA046313, AA046139, AA053780, AA101657, AA101658, AA167298, AA227543, AA227684, AA458877, AA459067, AA463656, AA464047, AA464754, AA225370, AA225425, AA225400, AA558796, AA582089, AA565830, AA713907,

		AA864510, AA936117, C01002, N86320, C04277, AA652714, AA402391, AA402565, AA479073, AA621791, AA670200, AA456544, AA676732, AA707089, AI014599, AI022852, AI023739, AI091873, AI094288, Z39517, Z43438
840564	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1068 of SEQ ID NO:441, b is an integer of 15 to 1082, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:441, and where b is greater than or equal to a + 14.	
840572	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1227 of SEQ ID NO:442, b is an integer of 15 to 1241, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:442, and where b is greater than or equal to a + 14.	T87514, T87515, H84879, AA001503, AA506411, AA508167, AA715396, AA931268, AA292666, AA478036, AA478193, AA478194, AA707886, AA724969, AA725050, AA779127, AA843885
840600	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 954 of SEQ ID NO:443, b is an integer of 15 to 968, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:443, and where b is greater than or equal to a + 14.	R38172, AA226748, AA484320, AA831852
840604	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1346 of SEQ ID NO:444, b is an integer of 15 to 1360, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:444, and where b is greater than or equal to a + 14.	
840608	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1821 of SEQ ID NO:445, b is an integer of 15 to 1835, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:445, and where b is greater than or equal to a + 14.	
840620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1341 of SEQ ID NO:446, b is an integer of 15 to 1355, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:446, and where b is greater than or equal to a + 14.	R17303, R41982, R41982, H43756, N62762, AA053677, AA053697, AA084224, AA084019, AA084952, AA419123, AA419160, AA426014, AA425077, AA427847, AA524035, AA565019, AA632254, AA745726, AA835832, AA931712, AA932520, AA937139, AA961716, AA995607, AA453838, AA455030, AA476981, AA479615, AA482659, AA455837,

		AA488554, AA620470, AA781416, AA844227, AI090902, T19161
840625	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 361 of SEQ ID NO:447, b is an integer of 15 to 375, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:447, and where b is greater than or equal to a + 14.	
840626	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1379 of SEQ ID NO:448, b is an integer of 15 to 1393, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:448, and where b is greater than or equal to a + 14.	
840638	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1649 of SEQ ID NO:449, b is an integer of 15 to 1663, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:449, and where b is greater than or equal to a + 14.	H01158, H01159, H05751, H05858, H83341, H83695, N47512, N47513, W39756, W79733, W90027, W90155, AA047691, AA047741, AA086374, AA100549, AA159315, AA159414, AA282525, AA282633, AA595381, AA688093, AA744757, AA865203, AA933811, AA969838, AA975917, F18424, D12197, D12219, AA478596, AA665540, AA909221, AA969720, AI049820
840649	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1366 of SEQ ID NO:450, b is an integer of 15 to 1380, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:450, and where b is greater than or equal to a + 14.	R00133, R22651, R44356, R44356, R56353, R93194, N47106, N50316, N50780, N55139, AA010596, AA010597, AA012940, AA012888, AA013216, AA013313, AA017544, AA017417, AA047814, AA047792, AA235545, AA262268, AA262879, AA563873, AA570239, AA573586, AA827412, AA862337, AA902472, AA962409, AA971292, AA973596, AI056509, AI080455, AA410833, T23822, T16761
840651	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 912 of SEQ ID NO:451, b is an integer of 15 to 926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:451, and where b is greater than or equal to a + 14.	
840666	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1628 of SEQ ID NO:452, b is an integer of 15 to 1642, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:452, and where b is greater than or equal to a + 14.	N32778, N34353, N34537, N41780, N42818, N93337, W25190, AA035229, AA035230, AA044070, AA044162, AA195074, AA195174, AA419441, AA731906, AA761315, AA761330, AA766382, AA766593, AA769537, AA805515, AA806516, AA809893, AA814954, AA857917, N44554.

		AA393941, AI074651, T10618, Z35722
840681	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2240 of SEQ ID NO:453, b is an integer of 15 to 2254, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:453, and where b is greater than or equal to a + 14.	
840682	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1917 of SEQ ID NO:454, b is an integer of 15 to 1931, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:454, and where b is greater than or equal to a + 14.	
840684	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 757 of SEQ ID NO:455, b is an integer of 15 to 771, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:455, and where b is greater than or equal to a + 14.	
840697	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1155 of SEQ ID NO:456, b is an integer of 15 to 1169, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:456, and where b is greater than or equal to a + 14.	R00751, R02584, R02703, R69879, R69927, H13156, H29249, H29248, H41216, R83398, H54666, H54667, H73551, H73552, H90468, H91760, H97869, N31729, N31735, N51232, W32147, W32175, W44313, W45660, W57760, W57761, W68386, W68502, W68752, W68835, W72538, W76163, AA035740, AA043246, AA043585, AA044419, AA043053, AA047593, AA047601, AA088798, AA147253, AA155747, AA160105, AA165689, AA172386, AA173747, AA189005, AA189006, AA471066, AA507210, AA513086, AA516406, AA514685, AA635861, AA657400, AA668796, AA737126, AA768005, AA768358, AA887459, AA977176, D80509, D81008, D81471, D81800, D82666, N83795, AA643662, AA284937, AA290823, AA447984, AA448126, AA676807, AA709464, AA780333, AA843801, AA853391, AA868403, AA917460, T17166, T17177, T16671, T48481, T48507
840698	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3235 of SEQ ID NO:457, b is an integer of 15 to 3249, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:457, and where b is	

	greater than or equal to a + 14.	
840708	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1902 of SEQ ID NO:458, b is an integer of 15 to 1916, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:458, and where b is greater than or equal to a + 14.	R21272, R45362, R45362, H06049, H13385, AA082768, AA101114, AA131634, AA131718, AA152290, AA150232, AA418083, AA418230, AA422115, AA424919, AA426139, AA741277, AA749290, AA811505, AA836102, AA411231, AA453804, AA453890, AA758905, AA769817, AA770192, AA904708, AA905158, AA969156, AI093952, Z42470, Z41665, Z44053
840714	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2759 of SEQ ID NO:459, b is an integer of 15 to 2773, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:459, and where b is greater than or equal to a + 14.	
840716	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2017 of SEQ ID NO:460, b is an integer of 15 to 2031, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:460, and where b is greater than or equal to a + 14.	
840721	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1825 of SEQ ID NO:461, b is an integer of 15 to 1839, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:461, and where b is greater than or equal to a + 14.	
840735	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 765 of SEQ ID NO:462, b is an integer of 15 to 779, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:462, and where b is greater than or equal to a + 14.	T47277, T56085, T93319, T85388, H57620, H58465, N77902, N80219, N93978, W19715, W37380, W37643, W38508, W38722, W47048, W68079, W67976, W69349, W69350, AA025313, AA024560, AA063371, AA063370, AA463222, AA463223, AA424422, AA469264, AA480510, AA507733, AA524348, AA557233, AA602394, AA603318, AA631014, AA569554, AA575944, AA688112, AA911131, AA932225, AA937015, AA994856, AI077707, N92552, W00604, C00184, AA292823, AA401683, AA663906, AA664122, AA771943, AA779608, AA812529, AI028120, AI027559, AI032511, AI033880, AI034204, AI078458, AI041685, D31473, T64469
840738	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	

	sequence described by the general formula of a-b, where a is any integer between 1 to 1703 of SEQ ID NO:463, b is an integer of 15 to 1717, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:463, and where b is greater than or equal to a + 14.	
840745	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 814 of SEQ ID NO:464, b is an integer of 15 to 828, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:464, and where b is greater than or equal to a + 14.	
840747	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1159 of SEQ ID NO:465, b is an integer of 15 to 1173, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:465, and where b is greater than or equal to a + 14.	
840756	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 507 of SEQ ID NO:466, b is an integer of 15 to 521, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:466, and where b is greater than or equal to a + 14.	AA074254
840776	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1414 of SEQ ID NO:467, b is an integer of 15 to 1428, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:467, and where b is greater than or equal to a + 14.	T47069, T47068, T63511, T63587, T79637, T79722, R36141, R36419, R65831, R65934, R69612, R69701, H00464, H00514, H04572, H04575, H12602, H12652, H13166, H66218, H67195, H67868, H67868, N62959, W92249, W92250, W92609, W95234, AA007598, AA193373, AA195360, AA195359, AA425046, AA430627, AA428172, AA484871, AA557201, AA902998, AA927360, N79862, AA479674, AA477192, AA481418, AA481651, AA495983, AA496377, AA496655, AA912146, AA912181, AI049805, AA693485
840784	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3449 of SEQ ID NO:468, b is an integer of 15 to 3463, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:468, and where b is greater than or equal to a + 14.	
840788	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 607 of SEQ ID	

	NO:469, b is an integer of 15 to 621, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:469, and where b is greater than or equal to a + 14.	
840794	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1819 of SEQ ID NO:470, b is an integer of 15 to 1833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:470, and where b is greater than or equal to a + 14.	
840797	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3188 of SEQ ID NO:471, b is an integer of 15 to 3202, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:471, and where b is greater than or equal to a + 14.	
840799	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 927 of SEQ ID NO:472, b is an integer of 15 to 941, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:472, and where b is greater than or equal to a + 14.	
840818	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1265 of SEQ ID NO:473, b is an integer of 15 to 1279, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:473, and where b is greater than or equal to a + 14.	
840822	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3195 of SEQ ID NO:474, b is an integer of 15 to 3209, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:474, and where b is greater than or equal to a + 14.	T47621, T77305, T83423, R18484, R51973, R51974, R73192, H06082, H12940, H27135, H45895, H45904, N72089, W00342, W52213, W96404, AA045488, AA058907, AA062768, AA069032, AA081439, AA082427, AA084417, AA101216, AA234022, AA534011, AA565390, AA588319, AA588430, AA568701, AA635907, AA579930, AA827039, AA857519, AA872490, AA904077, AA995057, AI073336, N95359, C15883, AA781445, AA906492, AI037943, AI039428
840830	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 819 of SEQ ID NO:475, b is an integer of 15 to 833, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:475, and where b is	N33920, N33932, N49642, N49629, AA508747, AA514767, AA583465, AA805203, AA878968, U37231, T24573

	greater than or equal to a + 14.	
840846	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1127 of SEQ ID NO:476, b is an integer of 15 to 1141, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:476, and where b is greater than or equal to a + 14.	T68706, T68719, T68771, T68784, T73424, T73431, T73486, T73492, T73499, T73535, T89865, R11465, T79345, T79774, T81799, T82119, T82855, T96198, T96454, T96686, T96802, T96920, T97027, T99996, T99997, R00156, R00157, R83404, R85816, R91357, R93314, R94713, R94794, R97348, R99024, R99798, H48280, H48369, H48754, H54738, H54739, H55985, H55984, H56050, H56244, H57662, H57872, H57873, H58502, H60170, H60211, H62933, H69203, H69228, H69229, H71630, H73011, H73012, H81193, H81194, H90826, H91385, N33963, N49672, N49822, N52577, N54836, N58435, N64440, N66934, N69249, N69373, N74062, N75759, N78025, N78145, N94249, N95116, W03303, W01169, W01912, N91401, AA025243, AA026028, AA193126, AA194255, AA236507, AA242995, AA622239, AA575858, AA575872, AA576026, AA576150, AA576597, AA864932, AA877934, AA969761, AA994970, AI017867, D82634, C21067, AA431221, AA779655, AA782374, AA812640, AA923315, AA962377, AA993251, AI018445, AI025584, AI092470, T79311
840848	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1088 of SEQ ID NO:477, b is an integer of 15 to 1102, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:477, and where b is greater than or equal to a + 14.	R10066, R10163, T26606, R61067, R72646, H08322, H47858, H47859, R86048, H68866, H68867, H69098, H82364, N58491, N78080, W52876, W60083, AA043086, AA045865, AA045866, AA055712, AA057298, AA058743, AA079887, AA079888, AA099233, AA099234, AA102153, AA113213, AA115932, AA121000, AA131067, AA143412, AA146598, AA155632, AA155688, AA160447, AA173257, AA173248, AA195987, AA196375, AA233537, AA463552, AA503072, AA551794, AA586410, AA594814, AA613123, AA573356, AA580449, AA731195, AA742856, AA827930, AA863440, AA865529, AA876847, AA953614, AA976924, N84278, N88762, C17112, AA219765, AA284503, AA293437, AA293046, AA669435, AA722103, AI027785, AI073617, AI092707, T17392, F08770, D12026
840860	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	T89645, T89919, T93704, R21871, R22387, R78094, R78181, R78515,

	sequence described by the general formula of a-b, where a is any integer between 1 to 4187 of SEQ ID NO:478, b is an integer of 15 to 4201, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:478, and where b is greater than or equal to a + 14.	R78560, H40124, H41731, N28359, N42893, N62851, N64787, N67463, N76199, N77065, N77758, W67341, W68381, AA034244, AA044935, AA045056, AA057392, AA057684, AA071214, AA071442, AA081937, AA082360, AA082229, AA082230, AA082708, AA083297, AA083188, AA127585, AA149575, AA151791, AA167113, AA173360, AA191227, AA195437, AA223329, AA223614, AA243268, AA261939, AA262815, AA262816, AA422160, AA426276, AA225924, AA504466, AA504634, AA522823, AA554566, AA632813, AA576873, AA662886, AA730326, AA748669, AA828942, AA837197, AA857065, AA857683, AA862276, AA864246, AA873317, AI083733, D82604, D82635, N81179, N85023, N85166, N85712, C00193, C00199, C02425, N87331, N88683, N88852, N89408, C02916, C05151, C06382, AA642209, C21319, AA091285, AA091688, AA094300, AA205974, AA206268, AA206598, AA205324, AA649340, AA247212, AA404505, AA421263, AA421361, D11545, AA441853, AA441826, AA463350, AA463858, AA487271, AA487388, AA496439, AA496488, AA634627, AA663685, AA665466, AA456144, AA722996, AA772136, AA772153, AA774179, AA992418, AI076734, T10506, Z30218, Z38961, T16262, T48571, D31110, D45597, F06042, F00682
840861	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 773 of SEQ ID NO:479, b is an integer of 15 to 787, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:479, and where b is greater than or equal to a + 14.	T52180, T52256, T57048, T60934, T60993, T94137, T94228, T91060, T85924, R23216, R23292, R31316, R31576, R62640, R62693, H03198, H18231, H18269, H22414, H26112, H26116, H26378, H40754, H38895, H47721, H48072, R89134, R89141, R91829, R91836, R98452, H65626, H65627, H69728, H71913, H71914, H78844, H80090, H83062, H84585, H87467, H87577, H93457, H93458, N23179, N30549, N32644, N39052, N40455, N48060, N48244, N53258, N53755, N63557, N94559, N94883, N94981, N95791, N42987, W19445, W19573, W23831, W24902, W30850, W32700, W32701, W37523, W56867, W60497, W60972, W61219, W69268, W69346, W80426, W80556, W94817, W95832, W95966, W96035, W96092,

		N90310, AA010147, AA010148, AA025440, AA025757, AA027347, AA027822, AA027874, AA029650, AA029651, AA037779, AA039260, AA046801, AA046818, AA054707, AA058654, AA062684, AA063287, AA074876, AA074979, AA084381, AA085264, AA085328, AA085598, AA122190, AA120978, AA133892, AA129630, AA172403, AA172206, AA190489, AA190525, AA464455, AA464996, AA225769, AA259210, AA483109, AA483741, AA493542, AA502162, AA516183, AA522567, AA526813, AA557654, AA588882, AA593799, AA576216, AA659530, AA662308, AA688246, AA688254, AA687457, AA687516, AA689236, AA728852, AA729032, AA747479, AA747979, AA831447, AA887348, AA903105, AA916516, AA934714, AA953363, AA976759, AA991410, AA991434, AI002147, AI028033, N83338, C02469, R29174, AA090669, AA092066, AA648634, AA443968, AA444149, AA482243, AA482340, AA485406, AA598458, AA644566, AA664032, AA680199, AA676482, AA629708, AA630110, AA457100, AA431269, AA405296, AA405332, AA721997, AA724146, AA774657, AA781529, AA781641, AA781838, AA782849, AA813171, AA843229, AA846744, AA846814, AA854299, AA854765, AA789029, AA993047, AI023973, AI027725, AI031943, AI038463, AI041602, AI085085, AI086504, AI088189
840871	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 717 of SEQ ID NO:480, b is an integer of 15 to 731, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:480, and where b is greater than or equal to a + 14.	H42821, AA028094, AA099211, AA160368, AA223572, AA232552, AA252811
840874	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1105 of SEQ ID NO:481, b is an integer of 15 to 1119, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:481, and where b is greater than or equal to a + 14.	
840878	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	T40405, T41252, T47240, T47241, T50233, T52891, T57110, T58359, R19508, R43858, R43858, R75598,

	where a is any integer between 1 to 2042 of SEQ ID NO:482, b is an integer of 15 to 2056, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:482, and where b is greater than or equal to a + 14.	R75665, H13192, H13193, N25264, N31900, N42683, N72995, N93388, W25360, W47628, W47629, AA009691, AA009410, AA045777, AA045910, AA063040, AA063076, AA130044, AA149205, AA149206, AA191678, AA252698, AA464304, AA225264, AA514845, AA526726, AA548411, AA548704, AA552050, AA552558, AA568675, AA827017, AA834447, AA838450, AA886357, AA886653, AA887879, AA916602, AA928685, AA968793, AI005016, W28859, AA134038, AA455118, AA496380, AA496656, AA598830, AA653270, AA725217, AA733068, AI004394, AI023815, AI026954, AI040891, Z25388, Z28470, AA702322
840880	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 873 of SEQ ID NO:483, b is an integer of 15 to 887, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:483, and where b is greater than or equal to a + 14.	H02306, H02418, N48196, N53344, AA059013, AA506159, AA613938, AA662759, AA976725, AA854631
840884	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1864 of SEQ ID NO:484, b is an integer of 15 to 1878, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:484, and where b is greater than or equal to a + 14.	
840907	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1552 of SEQ ID NO:485, b is an integer of 15 to 1566, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:485, and where b is greater than or equal to a + 14.	
840926	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3032 of SEQ ID NO:486, b is an integer of 15 to 3046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:486, and where b is greater than or equal to a + 14.	
840932	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1890 of SEQ ID NO:487, b is an integer of 15 to 1904, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:487, and where b is	

	greater than or equal to a + 14.	
840940	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 813 of SEQ ID NO:488, b is an integer of 15 to 827, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:488, and where b is greater than or equal to a + 14.	
840947	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1912 of SEQ ID NO:489, b is an integer of 15 to 1926, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:489, and where b is greater than or equal to a + 14.	
840959	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1447 of SEQ ID NO:490, b is an integer of 15 to 1461, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:490, and where b is greater than or equal to a + 14.	
840964	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 791 of SEQ ID NO:491, b is an integer of 15 to 805, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:491, and where b is greater than or equal to a + 14.	R79226, H12332, H51062, H83364, H89523, N27508, N30527, N40233, N52503, N53855, N94367, AA055215, AA055306, AA188169, AA468498, AA470473, AA563662, AA622643, AA579613, AA668790, AA748160, AA765447, AA873430, AA879079, AA903275, AA970424, N73354, AA402259, AA883758, AA890505, AA906005, AI023931
840979	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2255 of SEQ ID NO:492, b is an integer of 15 to 2269, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:492, and where b is greater than or equal to a + 14.	
840984	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4094 of SEQ ID NO:493, b is an integer of 15 to 4108, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:493, and where b is greater than or equal to a + 14.	
840986	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2195 of SEQ ID NO:494, b is an integer of 15 to 2209, where both a and b correspond to the positions of nucleotide	H25393, H25394, H25511, H25512, R95750, R95794, H64076, H64131, H68715, H80548, H80604, H94681, H95039, H99481, N28293, N30167, N35782, W47389, W47262, W61304, W65368, AA054346, AA054383,

	residues shown in SEQ ID NO:494, and where b is greater than or equal to a + 14.	AA058320, AA058448, AA512954, AA558416, AA588459, AA935690, AI097565, N87339, AA993027, AA993568, AA701454, AA702350
840988	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1663 of SEQ ID NO:495, b is an integer of 15 to 1677, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:495, and where b is greater than or equal to a + 14.	T87048, R24473, R43337, R43337, N75007, W05750, AA182467, AA227466, AA504464, AA504538, AA923479, AA648887, AA663889, AI027636, AI028506, AI026720, Z42717
840990	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1688 of SEQ ID NO:496, b is an integer of 15 to 1702, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:496, and where b is greater than or equal to a + 14.	
840992	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2362 of SEQ ID NO:497, b is an integer of 15 to 2376, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:497, and where b is greater than or equal to a + 14.	
841009	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 826 of SEQ ID NO:498, b is an integer of 15 to 840, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:498, and where b is greater than or equal to a + 14.	T40334, T41195, T79150, T79231, T85615, T98895, T99485, R25796, H03311, H03312, H11314, H21245, R91754, R91755, R93025, R97834, R97886, R99577, R99583, R99683, R99689, H88057, H97799, H97870, N34019, N35363, N42786, N44738, N52502, N70158, N72884, N74746, N93542, N95357, N98354, W01181, W03108, W15165, W19587, W21350, W24700, W24805, W39226, W48682, W49637, W49739, W51977, W67546, W67528, W67665, W79731, W93828, W93829, AA025348, AA025356, AA024401, AA024402, AA029589, AA029588, AA099331, AA099865, AA121627, AA126717, AA126816, AA126817, AA133155, AA165162, AA165163, AA557332, AA640015, AA579505, AA665011, AA665221, AA738009, AA830748, AA918150, AA918992, AA947223, AA974955, AI083731, N56157, N89240, AA092060, AA094384, AA650291, AA292814, AA402491, F20671, F21115, D11655, D11564, D11605, D12048, AA634049, U54738, AA732766, AA782030, AA843638, AA860477, AA861482, AI018649,

		AI092171, Z28714, T23956, AA694568
841012	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 447 of SEQ ID NO:499, b is an integer of 15 to 461, where both a and b correspond to the positions of nucleotide . residues shown in SEQ ID NO:499, and where b is greater than or equal to a + 14.	
841016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2768 of SEQ ID NO:500, b is an integer of 15 to 2782, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:500, and where b is greater than or equal to a + 14.	R21854, R21868, R23349, R27518, R63726, R63775, R65731, R65957, R65958, R66192, R66977, R66978, R67072, R69600, R69690, H12415, H12416, N46541, N47260, N47778, N48572, N51984, N95008, W25613, W31713, W32142, W38029, W38650, W38655, AA034256, AA037658, AA037660, AA039268, AA042908, AA042921, AA063533, AA126558, AA130121, AA130157, AA137270, AA136020, AA232954, AA233044, AA429346, AA429872, AA565520, AA604780, AA610435, AA631349, AA631518, AA740206, AA770618, AA912228, AI079705, N84191, N85956, N92894, W38030, C00380, N83173, C03262, AA092010, U82782, AA247592, AA284977, AA283619, AA291890, AA293636, AA410312, AA410537, AA453566, AA487623, AA626442, AA628932, AA629190, AA629753, AA629916, AA719528, AA843073, AA844228, AA890492, AI024670, AI051881, AI061324, T11149
841017	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1235 of SEQ ID NO:501, b is an integer of 15 to 1249, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:501, and where b is greater than or equal to a + 14.	R21764, R21815, N71125, W17312, AA112660, AA179538, AA179507, AA902202, AA907419, AA913594, AA994481, AI049652
841021	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1344 of SEQ ID NO:502, b is an integer of 15 to 1358, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:502, and where b is greater than or equal to a + 14.	R23836, W38704, AA033686, AA176734, AA192268, AA525913, AA531505, AA532666, AA533781, AA533827, AA533949, AA554396, AA576754, AA906883, N24273, C14272, C14285, C14286, C18998
841032	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 487 of SEQ ID NO:503, b is an integer of 15 to 501, where both a and b correspond to the positions of nucleotide	T41136, T52990, T52991, T61494, T63001, T63145, T87321, T87328, T89480, T84361, R05264, N75935, W05120, W25352, AA191627, AA258512, AA418549, AA224774, AA225253, AA229538, AA229537,

	residues shown in SEQ ID NO:503, and where b is greater than or equal to a + 14.	AA229951, AA230318, AA468106, AA468170, AA482814, AA482855, AA482894, AA482906, AA483676, AA491563, AA491627, AA492175, AA501375, AA502205, AA505498, AA508058, AA508125, AA512979, AA513165, AA523347, AA528170, AA531497, AA542840, AA551430, AA553992, AA554420, AA582164, AA583205, AA593192, AA593362, AA602125, AA603378, AA603728, AA617691, AA622865, AA630937, AA631991, AA570802, AA569520, AA654990, AA664728, AA664864, AA665278, AA729616, AA729639, AA729652, AA730512, AA730705, AA730910, AA737300, AA737303, AA736808, AA736909, AA738098, AA740165, AA740553, AA742574, AA742885, AA746988, AA747057, AA747094, AA747099, AA747961, AA748108, AA804727, AA805835, AA834105, AA838466, AA864527, AA872303, AA875939, AA876612, AA876936, AA879219, AA885735, AA886033, AA888159, AA888528, AA888683, AA903652, AA935001, AA948734, AA947836, AA978250, AA994661, AI073926, AI085517, N83676, N86451, N87989, AA642538, AA090432, AA090481, AA092225, AA091643, AA094678, AA094818, AA095214, AA648652, AA649783, AA650377, AA401641, F21163, AA411822, AA442212, AA609798, AA679909, F22052, AA679265, AA722456, AI003421, AI028430, AI077884, AI086743, T89286, R05321, AA694044
841051	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1997 of SEQ ID NO:504, b is an integer of 15 to 2011, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:504, and where b is greater than or equal to a + 14.	AA427363
841064	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1975 of SEQ ID NO:505, b is an integer of 15 to 1989, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:505, and where b is greater than or equal to a + 14.	R95695, H49073, H61707, H61911, H68517, H89719, H89781, H89828, H90680, N76870, W88654, W88898, AA046748, AA053076, AA053592, AA127256, AA127257, AA187351, AA188218, H67307, AA602545, AA720701, AA742288, N87596, AA094084, AA204976, AA676787, AA703221, AA779414, AI038609, AI074626, AI088527, T17364,

		AA702787
841069	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1071 of SEQ ID NO:506, b is an integer of 15 to 1085, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:506, and where b is greater than or equal to a + 14.	
841072	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1471 of SEQ ID NO:507, b is an integer of 15 to 1485, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:507, and where b is greater than or equal to a + 14.	
841078	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1916 of SEQ ID NO:508, b is an integer of 15 to 1930, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:508, and where b is greater than or equal to a + 14.	T39937, T68962, T84426, R20697, R36425, R45643, R45643, R68137, R70943, R70957, R70996, R71011, H02222, H05658, H05659, H25177, H29362, H54732, H54733, H60311, H60310, H77561, H77562, H78245, H78446, H82436, H82699, N20477, N57742, N59418, N59709, N76617, AA029237, AA055009, AA055434, AA236337, AA425703, AA427773, AA482193, AA482287, AA612777, AA729757, AA737276, AA744359, AA872776, AA972581, C06045, AA446583, AA449748, AA707197, AA757691, AA774691, AA992571, AI003756, AI027513, AI039704, AI042272, AI052652, AI077380, AI083949, AA774036
841080	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1120 of SEQ ID NO:509, b is an integer of 15 to 1134, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:509, and where b is greater than or equal to a + 14.	
841088	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1368 of SEQ ID NO:510, b is an integer of 15 to 1382, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:510, and where b is greater than or equal to a + 14.	R00895, R21561, R42090, R42090, H05080, N79589, N94381, W16578, W42724, W42813, W46346, W46347, W47346, W57707, W57783, AA070469, AA490938, AA586820, AA580196, AA745683, AA809239, AA931405, D11601, AA725448, AA992145, AI023735, AI025359, AI031575, AI033697, AI038145, AI093535, F00072
841092	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1727 of SEQ ID	

	NO:511. b is an integer of 15 to 1741. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:511. and where b is greater than or equal to a + 14.	
841095	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1516 of SEQ ID NO:512, b is an integer of 15 to 1530, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:512, and where b is greater than or equal to a + 14.	W20114, AA255840, AA568302, AA406006, AA434170
841096	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2985 of SEQ ID NO:513, b is an integer of 15 to 2999, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:513, and where b is greater than or equal to a + 14.	
841102	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2034 of SEQ ID NO:514, b is an integer of 15 to 2048, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:514, and where b is greater than or equal to a + 14.	
841104	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3286 of SEQ ID NO:515, b is an integer of 15 to 3300, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:515, and where b is greater than or equal to a + 14.	T93851, R05295, R05354, R71097, R71445, R99396, N53129, W38359, W38417, W38418, W39384, W44785, W44786, W69719, W69847, W73703, AA134718, AA164646, AA164647, AA418958, AA420439, AA420440, AA548241, AA548224, AA558195, W73847, Z19840, AA707354, AA868898, AA917430, AI073454, F09131, F11469, AA700476
841108	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3411 of SEQ ID NO:516, b is an integer of 15 to 3425, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:516, and where b is greater than or equal to a + 14.	T89709, T89806, T91163, T93774, T93819, T95226, R06420, R06475, R23277, R23370, R32742, R32743, R52354, R52355, R64095, R64184, R65984, R65985, R70225, R70226, R76344, R76672, R80205, H00679, H00770, H04254, H24758, H24803, H40273, H38053, H38054, H47116, H47210, R92478, R94873, R94872, H57866, H57867, H59353, H61105, H63261, H63535, H63938, H67759, H67760, H77384, H77385, H82932, H87435, H87541, H88753, H88754, N59081, N59489, N63682, N63939, N66851, N70709, N92122, N99845, W32595, W88585, W90769, W90327, W93082, W93137, AA025425, AA041232, AA114914, AA114913, AA128525, AA235362, AA235944,

		AA235945, AA425197, AA636023, AA639557, AA729723, AA907495, AI056355, AI089809, AA448599, AA449742, AA476262, AA478567, AA478700, AA599706, AA634117, AA677126, AA716562, AA923333, AA948589, AI051569, AI073816, AI074666, AI080341, AI084428, AI090962, AI096407
841118	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1344 of SEQ ID NO:517, b is an integer of 15 to 1358, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:517, and where b is greater than or equal to a + 14.	R20815, R36529, R38448, R46586, R46586, R71122, R71625, R77658, R80438, R80643, H12595, H12644, H99733, N20132, N25939, N29738, N57157, N59874, N67154, N67834, W03438, W04625, W31524, AA044199, AA044996, AA135739, AA135782, AA146912, AA146911, AA173589, AA224431, AA232224, AA256600, AA256599, AA419270, AA419321, AA425195, AA484744, AA507823, AA513832, AA584296, AA600955, AA614813, AA807248, AA904059, AA937796, AA973678, AA983325, AA991604, W01284, C16969, AA476260, AA476318, AA476367, AA609550, AA678511, AA722726, AA904676, AA954468, AI001869, AI031538, Z41297
841119	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1354 of SEQ ID NO:518, b is an integer of 15 to 1368, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:518, and where b is greater than or equal to a + 14.	R18472, W39766, AA076303, AA985235
841124	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 919 of SEQ ID NO:519, b is an integer of 15 to 933, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:519, and where b is greater than or equal to a + 14.	
841137	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1416 of SEQ ID NO:520, b is an integer of 15 to 1430, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:520, and where b is greater than or equal to a + 14.	T65560, R52978, R59392, H24368, H25185, N33308, AA016160, AA019434, AA082036, AA099724, AA099725, AA101466, AA100553, AA100634, AA100635, AA143046, AA150250, AA151129, AA165491, AA172129, AA176104, AA176248, AA176272, AA197310, AA227454, AA232220, AA243156, AA261904, AA262541, AA458854, AA459044, AA481155, AA493247, AA514323, AA522820, AA558368, AA582973, AA604489, AA640528, AA569125,

		AA569824, AA737640, AA743846, AA808232, AA812222, AA847813, AA865060, AA872242, AA872353, AA922866, AA933823, AA988358, AI056397, AI085865, AI088865, AA205921, AA205923, AA205997, AA204887, AA205731, D11887, AA634040, AA703823, AA703893, Z20424, AA707344, AA707416, AA716243, AA683201, AA890456, AI003274, AI076618, AI090177, T10877, Z28746, T25145, Z40353, F11026, F09670, AA699695, AA701137
841143	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1155 of SEQ ID NO:521, b is an integer of 15 to 1169, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:521, and where b is greater than or equal to a + 14.	T52948, T57468, T59332, T91403, T84637, R69314, R69315, R77481, R77675, R77676, H30692, H70576, N24036, N24905, N26173, N35858, N36029, W39771, W45303, W80648, W80649, AA029895, AA029983, AA036639, AA036850, AA043430, AA043431, AA046109, AA046196, AA076106, AA076107, AA083131, AA083181, AA083285, AA083293, AA147761, AA147804, AA155831, AA155741, AA430082, AA581553, AA593886, AA594233, AA604399, AA576339, AA715836, AA730946, AA737298, AA768251, AA872423, AA888276, AA961744, AA962699, AA975874, AI000132, R29417, AA640954, AA094702, AA398483, AA402600, AA489817, AA489948, AA496290, AA663953, AA663986, AA725581, AA771972, AA781165, AA845829, AA772618, AA773208, AA907551, AI003883, AI004593, AI031669, AI052123, AI085380
841148	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2148 of SEQ ID NO:522, b is an integer of 15 to 2162, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:522, and where b is greater than or equal to a + 14.	
841149	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 785 of SEQ ID NO:523, b is an integer of 15 to 799, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:523, and where b is greater than or equal to a + 14.	AA812937
841151	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b,	

	where a is any integer between 1 to 1708 of SEQ ID NO:524. b is an integer of 15 to 1722, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:524, and where b is greater than or equal to a + 14.	
841155	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 548 of SEQ ID NO:525, b is an integer of 15 to 562, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:525, and where b is greater than or equal to a + 14.	
841161	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2009 of SEQ ID NO:526, b is an integer of 15 to 2023, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:526, and where b is greater than or equal to a + 14.	H81836, AA015599, AA099033, AA099034, AA211818, AA741499, AA748367, AA768854, AA805297, AA804217, AI000120, AI090415, D79280, D79875, AA628397, AA628438, AA889584, Z36757
841162	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2833 of SEQ ID NO:527, b is an integer of 15 to 2847, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:527, and where b is greater than or equal to a + 14.	T54529, T54568, T39916, T40885, T64421, T64740, T94433, T94519, T94763, T94764, T67443, T67536, T69533, R08782, R08783, T84049, T86084, R18023, R19657, R33054, R33948, R52119, R52216, R53248, R53249, R71311, H04393, H04418, H23196, H23309, H47118, R95161, H54791, H54843, H66487, H66488, H87522, H87523, H92220, H97204, H97637, H98041, N25008, N27036, N32850, N32940, N41677, N41803, N52911, N55243, N55603, N59425, N62367, N67146, N67527, N68040, N68109, N69439, N79136, W03264, W02511, W16533, W16511, W16949, W19590, W20032, W25683, W56022, W57870, W58141, W84752, W84757, W96458, W96558, N89892, N91494, AA035714, AA040577, AA040675, AA043889, AA052991, AA053277, AA053702, AA062923, AA063530, AA074314, AA074909, AA074744, AA076274, AA098982, AA099025, AA146894, AA146893, AA160127, AA160126, AA160195, AA160196, AA169764, AA169385, AA179301, AA223348, AA233558, AA235471, AA460676, AA420533, AA506563, AA523418, AA527621, AA528362, AA531060, AA532619, AA541282, AA552184, AA564466, AA564790, H98795, AA583450, AA613483, AA622733, AA627809, AA577550, AA578980, AA579413, AA714153, AA721494, AA721786, AA737104,

		AA738062, AA745852, AA746662, AA748113, AA814512, AA814515, AA848156, AA858182, AA877787, AA886219, AA886814, AA908510, AA919073, AA953828, AA971838, AA974669, AA974937, AA975070, AA978156, AA985412, AA985429, AA989103, AA989168, AA975750, AI053418, AI053736, AI053892, AI053967, AI053988, AI054073, AI054111, F18748, AI096767, W16689, F17979, W26593, W74635, R29761, AA090571, AA090284, AA092279, AA092676, AA174176, AA206002, AA206857, AA206939, AA204847, AA204862, AA205665, AA205777, C17805, AA215924, AA284942, AA285094, AA292514, AA293872, AA398296, AA401676, AA412021, AA450108, AA450173, AA477960, AA478675, AA479216, AA482218, AA608548, AA634838, AA634910, AA634951, AA644321, AA664196, AA665979, AA668238, AA668579, AA669764, AA669856, AA676279, AA630300, Z20366, AA716371, AA716380, Z19906, AA777040, AA778451, AA781061, AA845834, T25435, Z21568, AA772588, AA917780, AI003327, AI016140, AI024969, AI032559, AI056850, AI088269, AI090536, AI092597, AI093387, T15364, D29035, T27400, T27473, F02321, F06069, T69476, AA773898, AA694154
841163	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 802 of SEQ ID NO:528, b is an integer of 15 to 816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:528, and where b is greater than or equal to a + 14.	T70512, W58177, W58266, AA027003, AA047260, AA057146, AA076110, AA150122, AA150030, AA424246, AA425670, AA523788, AA554661, AA582491, AA587000, AA633476, AA578397, AA662364, AA687611, AA729856, AA741041, AA806947, AA894899, AA922687, AA934486, AA946779, AA954606, AA962108, AA988276, AI054171, AA436000, AA436099, AA442324, AA451996, AA722958, AA780203, T25797, AI018410, AI024726, AI074321
841169	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 871 of SEQ ID NO:529, b is an integer of 15 to 885, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:529, and where b is greater than or equal to a + 14.	
841172	Preferably excluded from the present invention are	T47968, H14181, H26893, N40884,

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 728 of SEQ ID NO:530, b is an integer of 15 to 742, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:530, and where b is greater than or equal to a + 14.	Z42735
841174	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 511 of SEQ ID NO:531, b is an integer of 15 to 525, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:531, and where b is greater than or equal to a + 14.	
841179	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1911 of SEQ ID NO:532, b is an integer of 15 to 1925, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:532, and where b is greater than or equal to a + 14.	
841183	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 488 of SEQ ID NO:533, b is an integer of 15 to 502, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:533, and where b is greater than or equal to a + 14.	
841186	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1786 of SEQ ID NO:534, b is an integer of 15 to 1800, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:534, and where b is greater than or equal to a + 14.	
841204	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2483 of SEQ ID NO:535, b is an integer of 15 to 2497, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:535, and where b is greater than or equal to a + 14.	
841206	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4076 of SEQ ID NO:536, b is an integer of 15 to 4090, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:536, and where b is greater than or equal to a + 14.	
841207	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide	AA215286

	sequence described by the general formula of a-b, where a is any integer between 1 to 572 of SEQ ID NO:537, b is an integer of 15 to 586, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:537, and where b is greater than or equal to a + 14.	
841211	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1236 of SEQ ID NO:538, b is an integer of 15 to 1250, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:538, and where b is greater than or equal to a + 14.	
841225	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1336 of SEQ ID NO:539, b is an integer of 15 to 1350, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:539, and where b is greater than or equal to a + 14.	
841229	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2495 of SEQ ID NO:540, b is an integer of 15 to 2509, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:540, and where b is greater than or equal to a + 14.	
841237	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1729 of SEQ ID NO:541, b is an integer of 15 to 1743, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:541, and where b is greater than or equal to a + 14.	H39746, H38765, H53680, H84385, H84386, H95751, H96427, H96428, N22709, N24033, N27417, N27531, N31183, N34699, N35427, N40348, N46995, N47385, W47664, W52613, W58021, AA020909, AA032219, AA032277, AA036745, AA053732, AA055872, AA057318, AA062713, AA070398, AA134055, AA132315, AA132625, AA149601, AA149602, AA494458, AA516430, AA534386, AA582804, AA581987, AA588838, AA631158, AA635970, AA577392, AA577494, AA857008, AA894813, AA933084, AI000994, N47386, D11495, D11593, D12071, D11877, D11882, D11902, AA456436, AA683214, AA890528, AA983938, AI074406, AI084728
841241	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2196 of SEQ ID NO:542, b is an integer of 15 to 2210, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:542, and where b is greater than or equal to a + 14.	T64820, R18486, R48571, R48670, R51358, R51464, R70428, R71854, R77389, R77390, H18251, H18293, H18401, H18402, H19764, H19765, H21210, H21526, H24560, H25150, H26985, H28104, H30240, H30297, H30868, H30871, H40890, H41878, H41879, H43721, H43811, H43814,

		R84543, R85932, R87323, R93828, H49042, H49101, H51175, H51188, H68511, H75818, H80551, H80607, N41005, N45017, N56601, N70611, N74891, N93043, N93044, N94350, N98497, W04932, W21511, W21512, W24020, W31043, W47411, W47607, W47659, W47660, W48851, W48618, W52281, W56619, W56649, W68334, W68375, W70156, W70195, W84467, W84552, W90400, W94826, W96342, W96343, N91167, AA016293, AA017674, AA025151, AA025152, AA027955, AA031264, AA031395, AA031855, AA031854, AA035782, AA037318, AA040025, AA056359, AA069269, AA069418, AA069509, AA101608, AA114873, AA114837, AA115697, AA133516, AA220968, AA458530, AA460966, AA463596, AA419091, AA428836, AA507951, AA582836, AA640114, AA659114, AA836669, AA903136, AA903220, AA918099, AA928492, AA971856, AA973427, AA994099, AI016016, AI057267, AA069497, AA206877, AA218868, AA284783, AA284712, AA293434, AA293042, AA402851, AA454608, AA496283, AA609652, AA708123, AA757619, AA757695, AA774425, AA774630, AA775465, AA852435, AA852436, AA852604, AA852605, AA868271, AA884190, T03362, AI042345, AI042606, AI066399, AI086541, AI086967, AI091380, AI091725, AI092820, AI092945, T23722, F03416, F04814, F07127, F08608, F12341
841259	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1701 of SEQ ID NO:543, b is an integer of 15 to 1715, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:543, and where b is greater than or equal to a + 14.	
841260	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3095 of SEQ ID NO:544, b is an integer of 15 to 3109, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:544, and where b is greater than or equal to a + 14.	T93673, R01175, R01287, R72262, R72263, H53584, H53905, N57686, N59657, N63715, N98804, W86302, W86653, W87312, AA055614, AA058962, AA058961, AA149239, AA180323, AA460554, AA460555, AA492261, AA596073, AA604012, AA612811, AA617927, AA631804, AA767954, AA769298, AA804811, AA814647, AA833776, AA872768, AA873458, AA876551, AA886069,

		AA932445. AA976417. AA989268. AI055853. D80933. AI088938. AI096484. AA215901. AA393250, AA435612. AA449044. AA449758. AA653318. AA678103. AA678744. AA705036. AA854081. AA789188. AA813062. AA868902. AI023192. AI033456. AI090508. Z28555. T25877. D30980. D31048. D31377. F00724. AA682530. AA694353
841264	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1162 of SEQ ID NO:545. b is an integer of 15 to 1176, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:545, and where b is greater than or equal to a + 14.	
841275	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1721 of SEQ ID NO:546, b is an integer of 15 to 1735, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:546, and where b is greater than or equal to a + 14.	
841311	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1034 of SEQ ID NO:547, b is an integer of 15 to 1048, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:547, and where b is greater than or equal to a + 14.	
841313	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 722 of SEQ ID NO:548. b is an integer of 15 to 736, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:548, and where b is greater than or equal to a + 14.	
841317	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2217 of SEQ ID NO:549, b is an integer of 15 to 2231, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:549, and where b is greater than or equal to a + 14.	T78127, R31279. R31890, R38014, R68187, R68186, R68960. R81444, R81647, H03085, H42975. N22228, N35405. N40226, N52138, N66461, N66470, W48764, W49783. W58388, AA044222. AA044341, AA131687, AA131731. AA224224. AA224527, AA469092, AA580878, AA573581, AA863153. AA903745. AA971415, C03879, AA249392, AA448556, AA449703, F22605. AA723322. AA904943, Z18868, AA971554, AA991799. AI015846, AI037913, AI056007. AI082497, AI090170, AI095394

841322	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1802 of SEQ ID NO:550, b is an integer of 15 to 1816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:550, and where b is greater than or equal to a + 14.	R21970, R83459, H65911, W76286, AA182592, AA281797, AA281874, AA291943, H65824, AA580660, AA748474, AA829390, AA293389, AA401755, AA910004, AA994494, AI005165, AI081877
841331	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2596 of SEQ ID NO:551, b is an integer of 15 to 2610, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:551, and where b is greater than or equal to a + 14.	
841332	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 4007 of SEQ ID NO:552, b is an integer of 15 to 4021, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:552, and where b is greater than or equal to a + 14.	
841338	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1766 of SEQ ID NO:553, b is an integer of 15 to 1780, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:553, and where b is greater than or equal to a + 14.	
841345	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3699 of SEQ ID NO:554, b is an integer of 15 to 3713, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:554, and where b is greater than or equal to a + 14.	
841349	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1983 of SEQ ID NO:555, b is an integer of 15 to 1997, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:555, and where b is greater than or equal to a + 14.	
841355	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 892 of SEQ ID NO:556, b is an integer of 15 to 906, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:556, and where b is greater than or equal to a + 14.	
841417	Preferably excluded from the present invention are	

	one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3470 of SEQ ID NO:557, b is an integer of 15 to 3484, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:557, and where b is greater than or equal to a + 14.	
841548	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 776 of SEQ ID NO:558, b is an integer of 15 to 790, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:558, and where b is greater than or equal to a + 14.	AA223588
841632	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 544 of SEQ ID NO:559, b is an integer of 15 to 558, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:559, and where b is greater than or equal to a + 14.	
841662	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 520 of SEQ ID NO:560, b is an integer of 15 to 534, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:560, and where b is greater than or equal to a + 14.	H15850, H99706, N78646, W74702, W94916, AA809695
841771	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3029 of SEQ ID NO:561, b is an integer of 15 to 3043, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:561, and where b is greater than or equal to a + 14.	T50029, T67900, T74699, T74819, T88802, T81298, T84439, T95656, R06092, R06196, R14563, R14966, R14970, R16465, R38948, R40957, R40957, R63975, R64085, R66362, R66363, R67505, H17644, H17758, R92097, H48240, H48331, H49625, H49715, H61167, H62068, H69147, N25753, N36472, N69035, N71493, N92970, N98567, N99536, W00665, W24251, W40582, W45462, W45538, W45525, W45687, W44315, W57971, W57944, W70012, W70013, W86733, AA044684, AA071192, AA071199, AA190325, AA191520, AA533197, AA558210, AA581106, AA581161, AA577119, AA857551, AA878885, AA936839, AA975697, D78980, W28535, C02075, C17857
841827	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1372 of SEQ ID NO:562, b is an integer of 15 to 1386, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:562, and where b is	

	greater than or equal to a + 14.	
841835	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2624 of SEQ ID NO:563, b is an integer of 15 to 2638, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:563, and where b is greater than or equal to a + 14.	
842259	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 677 of SEQ ID NO:564, b is an integer of 15 to 691, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:564, and where b is greater than or equal to a + 14.	
842463	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1953 of SEQ ID NO:565, b is an integer of 15 to 1967, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:565, and where b is greater than or equal to a + 14.	
842595	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1320 of SEQ ID NO:566, b is an integer of 15 to 1334, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:566, and where b is greater than or equal to a + 14.	
842722	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1596 of SEQ ID NO:567, b is an integer of 15 to 1610, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:567, and where b is greater than or equal to a + 14.	
842815	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1398 of SEQ ID NO:568, b is an integer of 15 to 1412, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:568, and where b is greater than or equal to a + 14.	
842818	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1111 of SEQ ID NO:569, b is an integer of 15 to 1125, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:569, and where b is greater than or equal to a + 14.	

843251	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1902 of SEQ ID NO:570, b is an integer of 15 to 1916, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:570, and where b is greater than or equal to a + 14.	
843422	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1239 of SEQ ID NO:571, b is an integer of 15 to 1253, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:571, and where b is greater than or equal to a + 14.	
843784	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1999 of SEQ ID NO:572, b is an integer of 15 to 2013, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:572, and where b is greater than or equal to a + 14.	
844017	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 655 of SEQ ID NO:573, b is an integer of 15 to 669, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:573, and where b is greater than or equal to a + 14.	AA075932
844138	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2418 of SEQ ID NO:574, b is an integer of 15 to 2432, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:574, and where b is greater than or equal to a + 14.	T54096, T54187, T54360, T39143, T40432, T90493, T90589, T89428, T89794, T80000, R00221, R00327, R25952, R26450, R26761, R28459, R55293, R55390, R73233, H42630, H44454, H44498, R83525, R86282, H85785, N33586, N34419, N36244, N48653, N49430, W51915, AA055530, AA055939, AA069732, AA100817, AA122084, AA121407, AA126332, AA133329, AA134151, AA134152, AA134714, AA136470, AA136960, AA157850, AA157906, AA157976, AA159365, AA171854, AA187219, AA186342, AA250818, AA464565, AA464666, AA428826, AA429361, AA491863, AA505512, AA524490, AA558038, AA581979, AA588712, AA593885, AA601110, AA573930, AA577156, AA578735, AA689519, AA730155, AA768486, AA805061, AA826981, AA865985, AA931167, AA947324, AA953202, AA961105, AA962413, AA976440, AA977760, AI032134, AI053416, AI053575,

		AI054013, AI054146, AI054281, U46376, W22126, C00371, C05283, AA641416, AA643346, AA292261, AA421818, AA496452, AA496521, AA653437, AA664399, AA680123, AA431832, AA434143, AA678582, AA705952, AA679763, AA733019, AA781645, AA813232, AA833597, AA844624, AI024151, AI038232, AI042551, AI080152, AI086490, T24101, F03522, F07244
844166	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1358 of SEQ ID NO:575, b is an integer of 15 to 1372, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:575, and where b is greater than or equal to a + 14.	
844194	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2006 of SEQ ID NO:576, b is an integer of 15 to 2020, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:576, and where b is greater than or equal to a + 14.	
844394	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3147 of SEQ ID NO:577, b is an integer of 15 to 3161, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:577, and where b is greater than or equal to a + 14.	
844450	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2032 of SEQ ID NO:578, b is an integer of 15 to 2046, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:578, and where b is greater than or equal to a + 14.	
844534	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 288 of SEQ ID NO:579, b is an integer of 15 to 302, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:579, and where b is greater than or equal to a + 14.	
844535	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 3053 of SEQ ID NO:580, b is an integer of 15 to 3067, where both a and b correspond to the positions of nucleotide	

	residues shown in SEQ ID NO:580. and where b is greater than or equal to a + 14.	
844644	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 1560 of SEQ ID NO:581, b is an integer of 15 to 1574, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:581, and where b is greater than or equal to a + 14.	
844653	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 946 of SEQ ID NO:582, b is an integer of 15 to 960. where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:582, and where b is greater than or equal to a + 14.	
844659	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 527 of SEQ ID NO:583, b is an integer of 15 to 541, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:583, and where b is greater than or equal to a + 14.	
844796	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2954 of SEQ ID NO:584, b is an integer of 15 to 2968, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:584, and where b is greater than or equal to a + 14.	
844812	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2594 of SEQ ID NO:585, b is an integer of 15 to 2608, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:585, and where b is greater than or equal to a + 14.	
844894	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1879 of SEQ ID NO:586, b is an integer of 15 to 1893, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:586, and where b is greater than or equal to a + 14.	
845361	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b. where a is any integer between 1 to 2449 of SEQ ID NO:587, b is an integer of 15 to 2463, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:587, and where b is	T93072, T93161, T69748, T70732, R01200, R01312, R05457, R05477, R05584, R43190, R43190, R65942, R75719, R78234, H03875, H03876, H15845, H16155, H17787, H40269, H45881, R84787, R92493, R92931, H58301, H58912, H58913, H62257,

	greater than or equal to a + 14.	H67051, H68135, H81385, H83681, H91363, H96711, N20348, N22509, N27952, N28616, N31997, N32005, N36007, N39356, N40718, N70011, N70094, N92576, N99870, W00896, W00925, W04623, W25220, W31522, W37278, W37791, W38868, W52654, W51751, AA017158, AA019458, AA022914, AA022915, AA037370, AA037502, AA045696, AA045697, AA046013, AA054565, AA054625, AA069778, AA079736, AA081087, AA081144, AA100055, AA100504, AA100334, AA115581, AA115554, AA126149, AA126373, AA133101, AA130558, AA136439, AA151673, AA151821, AA151822, AA159031, AA165200, AA165201, AA176477, AA176498, AA176771, AA176830, AA182601, AA176736, AA187943, AA188578, AA188675, AA190342, AA190343, AA195091, AA213662, AA213715, AA232222, AA426516, AA424760, AA483564, AA490859, AA491042, AA505249, AA507988, AA508858, AA513433, AA514771, AA514785, AA514980, AA527545, AA534100, AA554008, AA557148, AA584946, AA586481, AA587849, AA588781, AA593916, AA605049, AA604893, AA617650, AA568567, AA621979, AA627588, AA578585, AA578744, AA661910, AA729355, AA729902, AA736994, AA738388, AA740375, AA741213, AA760943, AA830401, AA834201, AA834208, AA834250, AA864864, AA888527, AA906940, AA922073, AA927272, AA931625, AA933055, AA932772, AA936861, AA938504, AA975187, AA977857, AA975594, AI000724, AI014600, AI017381, AI066441, D82733, U47688, N83708, N83790, N85010, W22533, W23255, N86314, N87393, N88971, AA642249, AA642903, AA090403, AA091011, AA095990, AA205824, AA204931, AA643262, AA648446, AA216706, AA219615, AA249170, C75338, AA599187, AA668746, AA670340, AA405611, AA405150, AA708635, AA716044, AA722076, AA722829, AA725716, AA781064, AA844379, AI037987, AI039577, AI078722, AI077655, AI080306, AI084320, AI085219, AI093296, AI093479, AI095168, AI095267, D29018, F02782,

		F06502. F00762. F00966
845620	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1931 of SEQ ID NO:588, b is an integer of 15 to 1945, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:588, and where b is greater than or equal to a + 14.	
845639	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 802 of SEQ ID NO:589, b is an integer of 15 to 816, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:589, and where b is greater than or equal to a + 14.	
845660	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2293 of SEQ ID NO:590, b is an integer of 15 to 2307, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:590, and where b is greater than or equal to a + 14.	
845720	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1424 of SEQ ID NO:591, b is an integer of 15 to 1438, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:591, and where b is greater than or equal to a + 14.	
845785	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1064 of SEQ ID NO:592, b is an integer of 15 to 1078, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:592, and where b is greater than or equal to a + 14.	
845897	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2478 of SEQ ID NO:593, b is an integer of 15 to 2492, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:593, and where b is greater than or equal to a + 14.	
845922	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1890 of SEQ ID NO:594, b is an integer of 15 to 1904, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:594, and where b is greater than or equal to a + 14.	

846016	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 323 of SEQ ID NO:595, b is an integer of 15 to 337, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:595, and where b is greater than or equal to a + 14.	
846040	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1274 of SEQ ID NO:596, b is an integer of 15 to 1288, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:596, and where b is greater than or equal to a + 14.	
846073	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 1038 of SEQ ID NO:597, b is an integer of 15 to 1052, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:597, and where b is greater than or equal to a + 14.	T83567, T83771, R51147, N26938, N32715, N36666, W57781, W74108, AA082091, AA425613
846257	Preferably excluded from the present invention are one or more polynucleotides comprising a nucleotide sequence described by the general formula of a-b, where a is any integer between 1 to 2079 of SEQ ID NO:598, b is an integer of 15 to 2093, where both a and b correspond to the positions of nucleotide residues shown in SEQ ID NO:598, and where b is greater than or equal to a + 14.	

Polynucleotide and Polypeptide Variants

The present invention is directed to variants of the polynucleotide sequence disclosed in SEQ ID NO:X or the complementary strand thereto, and/or the cDNA sequence contained in a cDNA clone contained in the deposit.

The present invention also encompasses variants of the cancer polypeptide sequence disclosed in SEQ ID NO:Y, a polypeptide sequence encoded by the polynucleotide sequence in SEQ ID NO:X, and/or a polypeptide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

"Variant" refers to a polynucleotide or polypeptide differing from the polynucleotide or polypeptide of the present invention, but retaining essential properties thereof. Generally, variants are overall closely similar, and, in many regions, identical to the polynucleotide or polypeptide of the present invention.

The present invention is also directed to nucleic acid molecules which comprise, or alternatively consist of, a nucleotide sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100%, identical to, for example, the nucleotide coding sequence in SEQ ID NO:X or the complementary strand thereto, the nucleotide coding sequence of the related cDNA contained in a deposited library or the complementary strand thereto, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA in the related cDNA contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polypeptides encoded by these nucleic acid molecules are also encompassed by the invention. In another embodiment, the invention encompasses nucleic acid molecules which comprise or alternatively consist of, a polynucleotide which hybridizes under stringent hybridization conditions, or alternatively, under low stringency conditions, to the nucleotide coding sequence in SEQ ID NO:X, the nucleotide coding sequence of the related cDNA clone contained in a deposited library, a nucleotide sequence encoding the polypeptide of SEQ ID NO:Y, a nucleotide sequence encoding a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a nucleotide sequence encoding the polypeptide encoded by the cDNA in the related cDNA clone contained in a deposited library, and/or polynucleotide fragments of any of these nucleic acid molecules (e.g., those fragments described herein). Polynucleotides which

hybridize to the complement of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

The present invention is also directed to polypeptides which comprise, or alternatively consist of, an amino acid sequence which is at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to, for example, the polypeptide sequence shown in SEQ ID NO:Y, a polypeptide sequence encoded by the nucleotide sequence in SEQ ID NO:X, a polypeptide sequence encoded by the cDNA in the related cDNA clone contained in a deposited library, and/or polypeptide fragments of any of these polypeptides (e.g., those fragments described herein). Polynucleotides which hybridize to the complement of the nucleic acid molecules encoding these polypeptides under stringent hybridization conditions, or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides.

By a nucleic acid having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence of the present invention, it is intended that the nucleotide sequence of the nucleic acid is identical to the reference sequence except that the nucleotide sequence may include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence encoding the polypeptide. In other words, to obtain a nucleic acid having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence. The query sequence may be, for example, an entire sequence referred to in Table 1, an ORF (open reading frame), or any fragment specified as described herein.

As a practical matter, whether any particular nucleic acid molecule or polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to a nucleotide sequence of the present invention can be determined conventionally using known computer programs. A preferred method for determining the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci. 6:237-245 (1990)). In a sequence alignment the query and subject sequences are both DNA sequences. An RNA sequence can be

compared by converting U's to T's. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB alignment of DNA sequences to calculate percent identiy are: Matrix=Unitary, k-tuple=4, Mismatch Penalty=1, Joining Penalty=30, Randomization Group Length=0, Cutoff Score=1, Gap Penalty=5, Gap Size Penalty 0.05, Window Size=500 or the lenght of the subject nucleotide sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence because of 5' or 3' deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for 5' and 3' truncations of the subject sequence when calculating percent identity. For subject sequences truncated at the 5' or 3' ends, relative to the query sequence, the percent identity is corrected by calculating the number of bases of the query sequence that are 5' and 3' of the subject sequence, which are not matched/aligned, as a percent of the total bases of the query sequence. Whether a nucleotide is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This corrected score is what is used for the purposes of the present invention. Only bases outside the 5' and 3' bases of the subject sequence, as displayed by the FASTDB alignment, which are not matched/aligned with the query sequence, are calculated for the purposes of manually adjusting the percent identity score.

For example, a 90 base subject sequence is aligned to a 100 base query sequence to determine percent identity. The deletions occur at the 5' end of the subject sequence and therefore, the FASTDB alignment does not show a matched/alignment of the first 10 bases at 5' end. The 10 unpaired bases represent 10% of the sequence (number of bases at the 5' and 3' ends not matched/total number of bases in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 bases were perfectly matched the final percent identity would be 90%. In another example, a 90 base subject sequence is compared with a 100 base query sequence. This time the deletions are internal deletions so that there are no bases on the 5' or 3' of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only bases 5' and 3' of the subject sequence which are not matched/aligned with the query sequence are manually corrected for. No other

manual corrections are to made for the purposes of the present invention.

By a polypeptide having an amino acid sequence at least, for example, 95% "identical" to a query amino acid sequence of the present invention, it is intended that the amino acid sequence of the subject polypeptide is identical to the query sequence except that the subject polypeptide sequence may include up to five amino acid alterations per each 100 amino acids of the query amino acid sequence. In other words, to obtain a polypeptide having an amino acid sequence at least 95% identical to a query amino acid sequence, up to 5% of the amino acid residues in the subject sequence may be inserted, deleted, (indels) or substituted with another amino acid. These alterations of the reference sequence may occur at the amino or carboxy terminal positions of the reference amino acid sequence or anywhere between those terminal positions, interspersed either individually among residues in the reference sequence or in one or more contiguous groups within the reference sequence.

As a practical matter, whether any particular polypeptide is at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to, for instance, the amino acid sequence in SEQ ID NO:Y or a fragment thereof, the amino acid sequence encoded by the nucleotide sequence in SEQ ID NO:X or a fragment thereof, or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library, or a fragment thereof, can be determined conventionally using known computer programs. A preferred method for determing the best overall match between a query sequence (a sequence of the present invention) and a subject sequence, also referred to as a global sequence alignment, can be determined using the FASTDB computer program based on the algorithm of Brutlag et al. (Comp. App. Biosci.6:237- 245(1990)). In a sequence alignment the query and subject sequences are either both nucleotide sequences or both amino acid sequences. The result of said global sequence alignment is in percent identity. Preferred parameters used in a FASTDB amino acid alignment are: Matrix=PAM 0, k-tuple=2, Mismatch Penalty=1, Joining Penalty=20, Randomization Group Length=0, Cutoff Score=1, Window Size=sequence length, Gap Penalty=5, Gap Size Penalty=0.05, Window Size=500 or the length of the subject amino acid sequence, whichever is shorter.

If the subject sequence is shorter than the query sequence due to N- or C-terminal deletions, not because of internal deletions, a manual correction must be made to the results. This is because the FASTDB program does not account for N- and C-terminal truncations of the subject sequence when calculating global percent identity. For subject sequences

truncated at the N- and C-termini, relative to the query sequence, the percent identity is corrected by calculating the number of residues of the query sequence that are N- and C-terminal of the subject sequence, which are not matched/aligned with a corresponding subject residue, as a percent of the total bases of the query sequence. Whether a residue is matched/aligned is determined by results of the FASTDB sequence alignment. This percentage is then subtracted from the percent identity, calculated by the above FASTDB program using the specified parameters, to arrive at a final percent identity score. This final percent identity score is what is used for the purposes of the present invention. Only residues to the N- and C-termini of the subject sequence, which are not matched/aligned with the query sequence, are considered for the purposes of manually adjusting the percent identity score. That is, only query residue positions outside the farthest N- and C- terminal residues of the subject sequence.

For example, a 90 amino acid residue subject sequence is aligned with a 100 residue query sequence to determine percent identity. The deletion occurs at the N-terminus of the subject sequence and therefore, the FASTDB alignment does not show a matching/alignment of the first 10 residues at the N-terminus. The 10 unpaired residues represent 10% of the sequence (number of residues at the N- and C- termini not matched/total number of residues in the query sequence) so 10% is subtracted from the percent identity score calculated by the FASTDB program. If the remaining 90 residues were perfectly matched the final percent identity would be 90%. In another example, a 90 residue subject sequence is compared with a 100 residue query sequence. This time the deletions are internal deletions so there are no residues at the N- or C-termini of the subject sequence which are not matched/aligned with the query. In this case the percent identity calculated by FASTDB is not manually corrected. Once again, only residue positions outside the N- and C-terminal ends of the subject sequence, as displayed in the FASTDB alignment, which are not matched/aligned with the query sequence are manually corrected for. No other manual corrections are to made for the purposes of the present invention.

The variants may contain alterations in the coding regions, non-coding regions, or both. Especially preferred are polynucleotide variants containing alterations which produce silent substitutions, additions, or deletions, but do not alter the properties or activities of the encoded polypeptide. Nucleotide variants produced by silent substitutions due to the degeneracy of the genetic code are preferred. Moreover, variants in which less than 50, less

than 40, less than 30, less than 20, less than 10, or 5-50, 5-25, 5-10, 1-5, or 1-2 amino acids are substituted, deleted, or added in any combination are also preferred. Polynucleotide variants can be produced for a variety of reasons, e.g., to optimize codon expression for a particular host (change codons in the human mRNA to those preferred by a bacterial host such as E. coli).

Naturally occurring variants are called "allelic variants," and refer to one of several alternate forms of a gene occupying a given locus on a chromosome of an organism. (Genes II, Lewin, B., ed., John Wiley & Sons, New York (1985).) These allelic variants can vary at either the polynucleotide and/or polypeptide level and are included in the present invention. Alternatively, non-naturally occurring variants may be produced by mutagenesis techniques or by direct synthesis.

Using known methods of protein engineering and recombinant DNA technology, variants may be generated to improve or alter the characteristics of the polypeptides of the present invention. For instance, as discussed herein, one or more amino acids can be deleted from the N-terminus or C-terminus of the polypeptide of the present invention without substantial loss of biological function. The authors of Ron et al., J. Biol. Chem. 268: 2984-2988 (1993), reported variant KGF proteins having heparin binding activity even after deleting 3, 8, or 27 amino-terminal amino acid residues. Similarly, Interferon gamma exhibited up to ten times higher activity after deleting 8-10 amino acid residues from the carboxy terminus of this protein. (Dobeli et al., J. Biotechnology 7:199-216 (1988).)

Moreover, ample evidence demonstrates that variants often retain a biological activity similar to that of the naturally occurring protein. For example, Gayle and coworkers (J. Biol. Chem 268:22105-22111 (1993)) conducted extensive mutational analysis of human cytokine IL-1a. They used random mutagenesis to generate over 3,500 individual IL-1a mutants that averaged 2.5 amino acid changes per variant over the entire length of the molecule. Multiple mutations were examined at every possible amino acid position. The investigators found that "[m]ost of the molecule could be altered with little effect on either [binding or biological activity]." (See, Abstract.) In fact, only 23 unique amino acid sequences, out of more than 3,500 nucleotide sequences examined, produced a protein that significantly differed in activity from wild-type.

Furthermore, as discussed herein, even if deleting one or more amino acids from the N-terminus or C-terminus of a polypeptide results in modification or loss of one or more

biological functions, other biological activities may still be retained. For example, the ability of a deletion variant to induce and/or to bind antibodies which recognize the secreted form will likely be retained when less than the majority of the residues of the secreted form are removed from the N-terminus or C-terminus. Whether a particular polypeptide lacking N- or C-terminal residues of a protein retains such immunogenic activities can readily be determined by routine methods described herein and otherwise known in the art.

Thus, the invention further includes polypeptide variants which show a functional activity (e.g., biological activity) of the polypeptide of the invention of which they are a variant. Such variants include deletions, insertions, inversions, repeats, and substitutions selected according to general rules known in the art so as have little effect on activity.

The present application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein or fragments thereof, (e.g., including but not limited to fragments encoding a polypeptide having the amino acid sequence of an N and/or C terminal deletion), irrespective of whether they encode a polypeptide having functional activity. This is because even where a particular nucleic acid molecule does not encode a polypeptide having functional activity, one of skill in the art would still know how to use the nucleic acid molecule, for instance, as a hybridization probe or a polymerase chain reaction (PCR) primer. Uses of the nucleic acid molecules of the present invention that do not encode a polypeptide having functional activity include, inter alia, (1) isolating a gene or allelic or splice variants thereof in a cDNA library; (2) in situ hybridization (e.g., "FISH") to metaphase chromosomal spreads to provide precise chromosomal location of the gene, as described in Verma et al., Human Chromosomes: A Manual of Basic Techniques, Pergamon Press, New York (1988); and (3) Northern Blot analysis for detecting mRNA expression in specific tissues.

Preferred, however, are nucleic acid molecules having sequences at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99% or 100% identical to the nucleic acid sequences disclosed herein, which do, in fact, encode a polypeptide having a functional activity of a polypeptide of the invention.

Of course, due to the degeneracy of the genetic code, one of ordinary skill in the art will immediately recognize that a large number of the nucleic acid molecules having a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical to, for example, the nucleic acid sequence of the cDNA in the related cDNA clone contained in a

deposited library, the nucleic acid sequence referred to in Table 1 (SEQ ID NO:X), or fragments thereof, will encode polypeptides "having functional activity." In fact, since degenerate variants of any of these nucleotide sequences all encode the same polypeptide, in many instances, this will be clear to the skilled artisan even without performing the above described comparison assay. It will be further recognized in the art that, for such nucleic acid molecules that are not degenerate variants, a reasonable number will also encode a polypeptide having functional activity. This is because the skilled artisan is fully aware of amino acid substitutions that are either less likely or not likely to significantly effect protein function (e.g., replacing one aliphatic amino acid with a second aliphatic amino acid), as further described below.

For example, guidance concerning how to make phenotypically silent amino acid substitutions is provided in Bowie et al., "Deciphering the Message in Protein Sequences: Tolerance to Amino Acid Substitutions," Science 247:1306-1310 (1990), wherein the authors indicate that there are two main strategies for studying the tolerance of an amino acid sequence to change.

The first strategy exploits the tolerance of amino acid substitutions by natural selection during the process of evolution. By comparing amino acid sequences in different species, conserved amino acids can be identified. These conserved amino acids are likely important for protein function. In contrast, the amino acid positions where substitutions have been tolerated by natural selection indicates that these positions are not critical for protein function. Thus, positions tolerating amino acid substitution could be modified while still maintaining biological activity of the protein.

The second strategy uses genetic engineering to introduce amino acid changes at specific positions of a cloned gene to identify regions critical for protein function. For example, site directed mutagenesis or alanine-scanning mutagenesis (introduction of single alanine mutations at every residue in the molecule) can be used. (Cunningham and Wells, Science 244:1081-1085 (1989).) The resulting mutant molecules can then be tested for biological activity.

As the authors state, these two strategies have revealed that proteins are surprisingly tolerant of amino acid substitutions. The authors further indicate which amino acid changes are likely to be permissive at certain amino acid positions in the protein. For example, most buried (within the tertiary structure of the protein) amino acid residues require nonpolar side

chains, whereas few features of surface side chains are generally conserved. Moreover, tolerated conservative amino acid substitutions involve replacement of the aliphatic or hydrophobic amino acids Ala, Val, Leu and Ile; replacement of the hydroxyl residues Ser and Thr; replacement of the acidic residues Asp and Glu; replacement of the amide residues Asn and Gln, replacement of the basic residues Lys, Arg, and His; replacement of the aromatic residues Phe, Tyr, and Trp, and replacement of the small-sized amino acids Ala, Ser, Thr, Met, and Gly. Besides conservative amino acid substitution, variants of the present invention include (i) substitutions with one or more of the non-conserved amino acid residues, where the substituted amino acid residues may or may not be one encoded by the genetic code, or (ii) substitution with one or more of amino acid residues having a substituent group, or (iii) fusion of the mature polypeptide with another compound, such as a compound to increase the stability and/or solubility of the polypeptide (for example, polyethylene glycol), or (iv) fusion of the polypeptide with additional amino acids, such as, for example, an IgG Fc fusion region peptide, or leader or secretory sequence, or a sequence facilitating purification. Such variant polypeptides are deemed to be within the scope of those skilled in the art from the teachings herein.

For example, polypeptide variants containing amino acid substitutions of charged amino acids with other charged or neutral amino acids may produce proteins with improved characteristics, such as less aggregation. Aggregation of pharmaceutical formulations both reduces activity and increases clearance due to the aggregate's immunogenic activity. (Pinckard et al., Clin. Exp. Immunol. 2:331-340 (1967); Robbins et al., Diabetes 36: 838-845 (1987); Cleland et al., Crit. Rev. Therapeutic Drug Carrier Systems 10:307-377 (1993).)

A further embodiment of the invention relates to a polypeptide which comprises the amino acid sequence of a polypeptide having an amino acid sequence which contains at least one amino acid substitution, but not more than 50 amino acid substitutions, even more preferably, not more than 40 amino acid substitutions, still more preferably, not more than 30 amino acid substitutions, and still even more preferably, not more than 20 amino acid substitutions. Of course it is highly preferable for a polypeptide to have an amino acid sequence which comprises the amino acid sequence of a polypeptide of SEQ ID NO:Y, an amino acid sequence encoded by SEQ ID NO:X, and/or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library which contains, in order of ever-increasing preference, at least one, but not more than 10, 9, 8, 7, 6, 5, 4, 3, 2 or 1

amino acid substitutions. In specific embodiments, the number of additions, substitutions, and/or deletions in the amino acid sequence of SEQ ID NO:Y or fragments thereof (e.g., the mature form and/or other fragments described herein), an amino acid sequence encoded by SEQ ID NO:X or fragments thereof, and/or the amino acid sequence encoded by the cDNA in the related cDNA clone contained in a deposited library or fragments thereof, is 1-5, 5-10, 5-25, 5-50, 10-50 or 50-150, conservative amino acid substitutions are preferable.

Polynucleotide and Polypeptide Fragments

The present invention is also directed to polynucleotide fragments of the cancer polynucleotides (nucleic acids) of the invention. In the present invention, a "polynucleotide fragment" refers, for example, to a polynucleotide having a nucleic acid sequence which: is a portion of the cDNA contained in a depostied cDNA clone; or is a portion of a polynucleotide sequence encoding the polypeptide encoded by the cDNA contained in a deposited cDNA clone; or is a portion of the polynucleotide sequence in SEQ ID NO:X or the complementary strand thereto; or is a polynucleotide sequence encoding a portion of the polypeptide of SEQ ID NO:Y; or is a polynucleotide sequence encoding a portion of a polypeptide encoded by SEQ ID NO:X or the complementary strand thereto. The nucleotide fragments of the invention are preferably at least about 15 nt, and more preferably at least about 20 nt, still more preferably at least about 30 nt, and even more preferably, at least about 40 nt, at least about 50 nt, at least about 75 nt, at least about 100 nt, at least about 125 nt or at least about 150 nt in length. A fragment "at least 20 nt in length," for example, is intended to include 20 or more contiguous bases from, for example, the sequence contained in the cDNA in a related cDNA clone contained in a deposited library, the nucleotide sequence shown in SEQ ID NO:X or the complementary stand thereto. In this context "about" includes the particularly recited value or a value larger or smaller by several (5, 4, 3, 2, or 1) nucleotides. These nucleotide fragments have uses that include, but are not limited to, as diagnostic probes and primers as discussed herein. Of course, larger fragments (e.g., at least 150, 175, 200, 250, 500, 600, 1000, or 2000 nucleotides in length) are also encompassed by the invention.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700,701- 750, 751-800, 800-850, 851-900,

901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, and 3551 to the end of SEQ ID NO:X, or the complementary strand thereto. In this context "about" includes the particularly recited range or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity) of the polypeptide encoded by the polynucleotide of which the sequence is a portion. More preferably, these fragments can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these nucleic acid molecules under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides or fragments.

Moreover, representative examples of polynucleotide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, a sequence from about nucleotide number 1-50, 51-100, 101-150, 151-200, 201-250, 251-300, 301-350, 351-400, 401-450, 451-500, 501-550, 551-600, 651-700,701- 750, 751-800, 800-850, 851-900, 901-950, 951-1000, 1001-1050, 1051-1100, 1101-1150, 1151-1200, 1201-1250, 1251-1300, 1301-1350, 1351-1400, 1401-1450, 1451-1500, 1501-1550, 1551-1600, 1601-1650, 1651-1700, 1701-1750, 1751-1800, 1801-1850, 1851-1900, 1901-1950, 1951-2000, 2001-2050, 2051-2100, 2101-2150, 2151-2200, 2201-2250, 2251-2300, 2301-2350, 2351-2400, 2401-2450, 2451-2500, 2501-2550, 2551-2600, 2601-2650, 2651-2700, 2701-2750, 2751-2800, 2801-2850, 2851-2900, 2901-2950, 2951-3000, 3001-3050, 3051-3100, 3101-3150, 3151-3200, 3201-3250, 3251-3300, 3301-3350, 3351-3400, 3401-3450, 3451-3500, 3501-3550, and 3551 to the end of the cDNA nucleotide sequence contained in the deposited cDNA clone, or the complementary strand thereto. In this context "about" includes the particularly recited range, or a range larger or smaller by several (5, 4, 3, 2, or 1) nucleotides, at either terminus or at both termini. Preferably, these fragments encode a polypeptide which has a functional activity (e.g., biological activity) of the polypeptide encoded by the cDNA

nucleotide sequence contained in the deposited cDNA clone. More preferably, these fragments can be used as probes or primers as discussed herein. Polynucleotides which hybridize to one or more of these fragments under stringent hybridization conditions or alternatively, under lower stringency conditions, are also encompassed by the invention, as are polypeptides encoded by these polynucleotides or fragments.

In the present invention, a "polypeptide fragment" refers to an amino acid sequence which is a portion of that contained in SEQ ID NO:Y, a portion of an amino acid sequence encoded by the polynucleotide sequence of SEQ ID NO:X, and/or encoded by the cDNA contained in the related cDNA clone contained in a deposited library. Protein (polypeptide) fragments may be "free-standing," or comprised within a larger polypeptide of which the fragment forms a part or region, most preferably as a single continuous region. Representative examples of polypeptide fragments of the invention, include, for example, fragments comprising, or alternatively consisting of, an amino acid sequence from about amino acid number 1-20, 21-40, 41-60, 61-80, 81-100, 102-120, 121-140, 141-160, 161-180, 181-200, 201-220, 221-240, 241-260, 261-280, 281-300, 301-320, 321-340, 341-360, 361-380, 381-400, 401-420, 421-440, 441-460, 461-480, 481-500, 501-520, 521-540, 541-560, 561-580, 581-600, 601-620, 621-640, 641-660, 661-680, 681-700, 701-720, 721-740, 741-760, 761-780, 781-800, 801-820, 821-840, 841-860, 861-880, 881-900, 901-920, 921-940, 941-960, 961-980, 981-1000, 1001-1020, 1021-1040, 1041-1060, 1061-1080, 1081-1100, 1101-1120, 1121-1140, 1141-1160, 1161-1180, and 1181 to the end of SEQ ID NO:Y. Moreover, polypeptide fragments of the invention may be at least about 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 100, 110, 120, 130, 140, or 150 amino acids in length. In this context "about" includes the particularly recited ranges or values, or ranges or values larger or smaller by several (5, 4, 3, 2, or 1) amino acids, at either terminus or at both termini. Polynucleotides encoding these polypeptide fragments are also encompassed by the invention.

Even if deletion of one or more amino acids from the N-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example, the ability of shortened muteins to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptides generally will be retained when less than the majority of the residues of the complete or mature polypeptide are

removed from the N-terminus. Whether a particular polypeptide lacking N-terminal residues of a complete polypeptide retains such immunologic activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted N-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, polypeptide fragments of the invention include the secreted protein as well as the mature form. Further preferred polypeptide fragments include the secreted protein or the mature form having a continuous series of deleted residues from the amino or the carboxy terminus, or both. For example, any number of amino acids, ranging from 1-60, can be deleted from the amino terminus of either the secreted polypeptide or the mature form. Similarly, any number of amino acids, ranging from 1-30, can be deleted from the carboxy terminus of the secreted protein or mature form. Furthermore, any combination of the above amino and carboxy terminus deletions are preferred. Similarly, polynucleotides encoding these polypeptide fragments are also preferred.

The present invention further provides polypeptides having one or more residues deleted from the amino terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained in the related cDNA clone contained in a deposited library). In particular, N-terminal deletions may be described by the general formula m-q, where q is a whole integer representing the total number of amino acid residues in a polypeptide of the invention (e.g., the polypeptide disclosed in SEQ ID NO:Y), and m is defined as any integer ranging from 2 to q-6. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Also as mentioned above, even if deletion of one or more amino acids from the C-terminus of a protein results in modification of loss of one or more biological functions of the protein, other functional activities (e.g., biological activities, ability to multimerize, ability to bind a ligand) may still be retained. For example the ability of the shortened mutein to induce and/or bind to antibodies which recognize the complete or mature forms of the polypeptide generally will be retained when less than the majority of the residues of the complete or mature polypeptide are removed from the C-terminus. Whether a particular polypeptide lacking C-terminal residues of a complete polypeptide retains such immunologic

activities can readily be determined by routine methods described herein and otherwise known in the art. It is not unlikely that a mutein with a large number of deleted C-terminal amino acid residues may retain some biological or immunogenic activities. In fact, peptides composed of as few as six amino acid residues may often evoke an immune response.

Accordingly, the present invention further provides polypeptides having one or more residues from the carboxy terminus of the amino acid sequence of a polypeptide disclosed herein (e.g., a polypeptide of SEQ ID NO:Y, a polypeptide encoded by the polynucleotide sequence contained in SEQ ID NO:X, and/or a polypeptide encoded by the cDNA contained in deposited cDNA clone referenced in Table 1). In particular, C-terminal deletions may be described by the general formula 1-n, where n is any whole integer ranging from 6 to q-1, and where n corresponds to the position of an amino acid residue in a polypeptide of the invention. Polynucleotides encoding these polypeptides are also encompassed by the invention.

In addition, any of the above described N- or C-terminal deletions can be combined to produce a N- and C-terminal deleted polypeptide. The invention also provides polypeptides having one or more amino acids deleted from both the amino and the carboxyl termini, which may be described generally as having residues m-n of a polypeptide encoded by SEQ ID NO:X (e.g., including, but not limited to, the preferred polypeptide disclosed as SEQ ID NO:Y), and/or the cDNA in the related cDNA clone contained in a deposited library, where n and m are integers as described above. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Any polypeptide sequence contained in the polypeptide of SEQ ID NO:Y, encoded by the polynucleotide sequences set forth as SEQ ID NO:X, or encoded by the cDNA in the related cDNA clone contained in a deposited library may be analyzed to determine certain preferred regions of the polypeptide. For example, the amino acid sequence of a polypeptide encoded by a polynucleotide sequence of SEQ ID NO:X, or the cDNA in a deposited cDNA clone may be analyzed using the default parameters of the DNASTAR computer algorithm (DNASTAR, Inc., 1228 S. Park St., Madison, WI 53715 USA; http://www.dnastar.com/).

Polypeptide regions that may be routinely obtained using the DNASTAR computer algorithm include, but are not limited to, Garnier-Robson alpha-regions, beta-regions, turn-regions, and coil-regions, Chou-Fasman alpha-regions, beta-regions, and turn-regions, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Eisenberg alpha- and

beta-amphipathic regions, Karplus-Schulz flexible regions, Emini surface-forming regions and Jameson-Wolf regions of high antigenic index. Among highly preferred polynucleotides of the invention in this regard are those that encode polypeptides comprising regions that combine several structural features, such as several (e.g., 1, 2, 3 or 4) of the features set out above.

Additionally, Kyte-Doolittle hydrophilic regions and hydrophobic regions, Emini surface-forming regions, and Jameson-Wolf regions of high antigenic index (i.e., containing four or more contiguous amino acids having an antigenic index of greater than or equal to 1.5, as identified using the default parameters of the Jameson-Wolf program) can routinely be used to determine polypeptide regions that exhibit a high degree of potential for antigenicity. Regions of high antigenicity are determined from data by DNASTAR analysis by choosing values which represent regions of the polypeptide which are likely to be exposed on the surface of the polypeptide in an environment in which antigen recognition may occur in the process of initiation of an immune response.

Preferred polypeptide fragments of the invention are fragments comprising, or alternatively consisting of, an amino acid sequence that displays a functional activity of the polypeptide sequence of which the amino acid sequence is a fragment.

By a polypeptide demonstrating a "functional activity" is meant, a polypeptide capable of displaying one or more known functional activities associated with a full-length (complete) protein of the invention. Such functional activities include, but are not limited to, biological activity, antigenicity [ability to bind (or compete with a polypeptide for binding) to an anti-polypeptide antibody], immunogenicity (ability to generate antibody which binds to a specific polypeptide of the invention), ability to form multimers with polypeptides of the invention, and ability to bind to a receptor or ligand for a polypeptide.

Other preferred polypeptide fragments are biologically active fragments. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

In preferred embodiments, polypeptides of the invention comprise, or alternatively consist of, one, two, three, four, five or more of the antigenic fragments of the polypeptide of SEQ ID NO:Y, or portions thereof. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Table 4.

Sequence/ Contig ID	Epitope
507291	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 843 as residues: Pro-12 to Pro-20, Lys-27 to Gly-34. Pro-67 to Arg-72, Asp-102 to Thr-111, Asp-136 to Gly-142, Ser-153 to Pro-158.
508000	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 844 as residues: Ala-16 to Trp-35.
518325	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 845 as residues: Glu-60 to Asp-67.
523111	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 846 as residues: Ser-1 to Gln-10.
532211	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 848 as residues: Cys-17 to Arg-22.
532247	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 849 as residues: Val-4 to His-10.
537932	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 850 as residues: Ser-62 to Gly-68.
540117	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 851 as residues: Pro-24 to Arg-30, Met-101 to Phe-106. Thr-138 to Asn-153.
547710	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 852 as residues: Asp-1 to Arg-7, Glu-25 to His-31. Ile-51 to Lys-56, Pro-61 to Pro-67, Gly-113 to Thr-119, Lys-125 to Asp-130. His-335 to Gly-340, Arg-364 to Pro-371.
551747	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 853 as residues: Lys-79 to Ala-88, Ser-109 to Leu-125, Asp-155 to Lys-163, Tyr-211 to Thr-219. Pro-221 to Ala-226.
552799	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 854 as residues: Gln-81 to Thr-114. Gln-200 to Arg-206.
553243	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 855 as residues: Ala-43 to Asp-48, Asp-64 to Lys-69, His-88 to Thr-94, Ala-107 to Phe-113, Leu-117 to Ser-125. Thr-132 to Glu-138, Ser-169 to Trp-181. Ser-194 to Thr-200.
553368	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 856 as residues: Ser-52 to Arg-57, Leu-76 to Gly-82. Ser-91 to Glu-96, Tyr-132 to Ala-147.
554349	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 857 as residues: Ala-31 to Gly-36, Ala-68 to Tyr-75. Gln-121 to Asp-127.
558491	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 858 as residues: Pro-1 to Arg-10.
558983	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 859 as residues: Pro-37 to Gly-42, Val-67 to Lys-84, Gln-122 to Gly-127.
589390	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 862 as residues: Glu-14 to Asn-19, Arg-68 to Ser-74, Ser-79 to Ala-84, Lys-95 to Ile-101, Lys-125 to Glu-138.
596882	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 863 as residues: Lys-15 to Lys-23. Pro-29 to Gly-34.
616289	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 864 as residues: Leu-1 to Pro-13, Thr-64 to Gly-70. Lys-119 to Arg-130.
622140	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 865 as residues: Ser-1 to Lys-6, Pro-16 to Ser-23, Arg-49 to Glu-58.
647714	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 867 as residues: Arg-1 to Gly-9, Glu-27 to Gly-36. Pro-72 to Phe-86, Pro-104 to Cys-111. Gln-145 to Lys-162. Arg-226 to Trp-233.
652156	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 871 as residues: Asn-30 to Ile-43. Ile-76 to Lys-81.
653010	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 872 as

	residues: Ser-1 to Ala-10.
655904	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 873 as residues: Ala-21 to Cys-27, Ser-76 to Gly-87, Ser-112 to Trp-121, Trp-128 to Asn-133, Glu-225 to Cys-231, Tyr-238 to Cys-248, Lys-269 to Asp-279, Phe-292 to Thr-298, Cys-357 to Ala-362, Pro-383 to Pro-388, Lys-412 to Lys-420.
657852	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 874 as residues: Arg-10 to Lys-22, Gln-48 to Glu-53, Arg-73 to Asn-86.
666414	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 875 as residues: Asn-9 to Lys-19, Arg-27 to Gly-32, Ser-58 to Thr-70, Ala-81 to Pro-86.
670188	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 877 as residues: Asn-68 to Ser-75.
670279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 878 as residues: Lys-86 to Lys-91, Glu-101 to Val-120, Ala-130 to Glu-136.
670729	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 879 as residues: Ala-116 to Asp-134.
676496	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 881 as residues: Ile-1 to Arg-8.
678248	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 883 as residues: Ala-16 to Lys-22, Tyr-30 to Asn-35, Asp-61 to Val-70, Arg-129 to Asn-135, Thr-142 to Gly-148.
683668	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 884 as residues: Ser-3 to Gly-28, Gly-46 to Pro-56, Gly-70 to Ile-92, Gln-102 to Ser-117, Ala-123 to Pro-129, Pro-135 to Leu-140, Pro-150 to Asp-158, Pro-165 to Pro-177, Gln-188 to Asp-205, Ile-230 to Arg-245, His-251 to Trp-260, Asp-262 to Cys-267, Asn-296 to Arg-307, Glu-322 to Pro-330, Ile-351 to Asn-357, Asp-363 to Leu-369, Glu-386 to Phe-391, Lys-415 to Ser-420.
693172	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 885 as residues: Arg-11 to Arg-18, Pro-51 to Lys-58.
694303	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 886 as residues: Pro-12 to Ser-17, Leu-30 to Cys-39, Val-49 to Pro-54, Pro-67 to Leu-73, Pro-84 to Gln-90, His-99 to Leu-109.
695042	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 887 as residues: Ser-4 to Trp-28, Pro-51 to Leu-56, Asn-64 to His-70.
699799	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 888 as residues: Gln-17 to Phe-25, Glu-42 to Tyr-48, Val-52 to Gly-57, Pro-67 to Ser-73, Thr-97 to Gln-106, Gln-113 to Leu-123, Arg-171 to Asp-178, Arg-184 to Leu-191, Ile-195 to Phe-203, Lys-212 to Glu-217, Ala-236 to Asp-244, Arg-255 to Leu-260, Lys-266 to His-273, Glu-357 to Glu-363.
703015	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 890 as residues: Pro-27 to Asp-37, Gly-55 to Pro-61, His-96 to Ala-101, Glu-151 to Asn-156, Tyr-166 to Cys-178.
706391	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 891 as residues: Pro-22 to Ala-34, Pro-40 to Glu-52.
706924	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 893 as residues: Gly-1 to Gly-9, Gln-21 to Met-27.
707642	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 894 as residues: Glu-33 to Lys-40, Asn-55 to Lys-64, Tyr-104 to Cys-110, Ser-138 to Arg-148, Arg-157 to Gly-163, Lys-165 to Asn-172.
710369	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 895 as residues: Asn-1 to Thr-10.
718826	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 896 as residues: Ser-57 to Pro-63, Lys-93 to Ser-99.
719790	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 897 as residues: Phe-4 to Gln-23, Glu-47 to Ala-56, Asn-95 to Gln-102, Gln-109 to Glu-115, Arg-168 to Glu-175, Thr-196 to Arg-201, Lys-209 to Asp-215, Val-236 to Val-243.
720222	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 898 as

	residues: Glu-37 to Arg-43, Gly-62 to Pro-67, Gly-95 to Val-101, Gln-109 to Asp-114, Ala-137 to Phe-145, Asp-181 to Ser-188.
724033	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 899 as residues: Glu-55 to Glu-60, Asp-76 to Ser-85, Lys-106 to Asp-111, Gln-131 to Arg-137, Ala-172 to Gly-218.
724767	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 900 as residues: Leu-49 to Tyr-56, Tyr-114 to Glu-136, Arg-142 to Gly-148.
727065	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 901 as residues: Asn-41 to Gly-46, Lys-82 to His-88, Glu-107 to His-112, Leu-127 to Asp-132, Phe-163 to Phe-175, Thr-202 to Ile-209, Lys-229 to Gly-237, Ala-239 to Tyr-245.
727246	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 902 as residues: Pro-2 to Gly-10.
739448	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 908 as residues: His-2 to Leu-8, Gln-33 to Glu-40, Ala-44 to Glu-55, Gly-57 to Ser-67, Glu-70 to Ala-84, Glu-95 to Lys-111, Ile-186 to Asp-205, Leu-232 to Asp-238.
740060	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 910 as residues: Pro-44 to Thr-50, Arg-72 to Lys-80, Tyr-241 to Asn-251, Lys-273 to Gly-282, Ser-302 to Asn-312, Pro-337 to Ser-343, Ile-367 to Asp-376, Gly-395 to Tyr-417, Ser-442 to Gln-448.
741560	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 911 as residues: Gln-33 to Tyr-39, Pro-42 to Phe-47.
742543	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 912 as residues: Phe-10 to Tyr-15, Glu-139 to Asp-144, Glu-166 to Asn-171, Lys-175 to Glu-181.
742831	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 913 as residues: Val-64 to Glu-69.
745327	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 914 as residues: Arg-1 to Pro-13, Pro-54 to Ala-61.
745695	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 915 as residues: Trp-130 to Ser-135, Leu-199 to Thr-210, Ser-221 to Gln-229, Ala-249 to Tyr-255, Pro-257 to Pro-267, Ser-309 to Arg-314.
750316	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 916 as residues: Pro-18 to Asn-24, Thr-65 to Asp-70.
750522	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 917 as residues: Gln-10 to Lys-15.
750583	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 918 as residues: Lys-9 to Thr-15, Gln-32 to Gln-40.
751020	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 919 as residues: Arg-39 to Leu-47, Ser-107 to Ile-117, Pro-135 to Gln-144.
752196	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 920 as residues: Lys-20 to Lys-28.
753084	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 921 as residues: Lys-84 to Thr-98, Arg-128 to Ser-134, Arg-244 to Asn-252, Lys-365 to His-372.
754957	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 922 as residues: Pro-101 to Glu-106, Glu-116 to Asp-127, Ser-199 to Ile-210, Asp-217 to Asp-229, Ser-239 to Gly-244, Gln-262 to Asn-273, Pro-279 to Ser-284, Lys-318 to Arg-326, Lys-334 to Ile-341.
756557	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 923 as residues: Val-13 to Phe-21, Ile-55 to Pro-63, Ser-69 to Leu-74, Arg-82 to Leu-96, Asn-131 to Leu-139, Ile-156 to Thr-164, Thr-241 to Leu-249, Gly-273 to Ser-279, Thr-282 to Arg-289.
756712	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 924 as residues: Ile-4 to Thr-37, Gln-42 to Ser-48, Asn-56 to Lys-69, Ser-79 to Ser-85.
757414	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 925 as residues: Glu-14 to Thr-23, His-50 to Arg-62, Tyr-72 to Cys-78, Gly-121 to Pro-128.

757614	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 926 as residues: Gly-13 to Cys-19, Thr-32 to Glu-38, Val-44 to Gln-53, Lys-55 to Asp-60, Gln-65 to Glu-70, Lys-89 to Glu-105, Glu-112 to Asp-142, Glu-147 to Arg-152, Glu-211 to Leu-216, Leu-227 to Ser-232, Lys-245 to Lys-255, Glu-278 to Tyr-291, Gln-297 to Arg-303.
759878	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 928 as residues: Trp-16 to Glu-21, Trp-45 to Pro-54, Ile-154 to Phe-162, Gly-174 to Leu-181.
760227	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 929 as residues: Arg-99 to Asp-104.
766051	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 931 as residues: Asp-10 to Lys-19.
768053	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 933 as residues: Ile-1 to Tyr-7, Phe-52 to Cys-61, Val-118 to Ser-125.
768055	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 934 as residues: Asp-39 to Ser-46, Lys-92 to Lys-99, Val-165 to Phe-172, Lys-252 to Ala-261, Asn-268 to Ala-273.
769685	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 935 as residues: Pro-129 to Arg-135.
771920	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 936 as residues: Pro-47 to Val-53, Asp-85 to Phe-97, Val-136 to Gly-144, Pro-166 to Glu-172, Leu-190 to Ser-197.
772790	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 937 as residues: Leu-5 to Trp-13, Met-20 to Leu-39, Ile-50 to Pro-63, Glu-66 to Ser-72, Leu-112 to Gln-120, Ala-141 to Lys-146, Tyr-165 to Asp-173.
772916	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 938 as residues: Lys-16 to Arg-25.
773632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 940 as residues: Arg-1 to His-33.
774364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 941 as residues: Ser-97 to Asn-103.
775355	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 942 as residues: Ser-40 to Ala-46.
775844	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 943 as residues: Leu-20 to Ser-31, Thr-38 to Val-47.
777760	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 944 as residues: Thr-22 to Ser-28, Thr-35 to Glu-42, Met-47 to Thr-55.
779837	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 945 as residues: Thr-26 to Arg-31, Leu-75 to Lys-100.
780769	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 946 as residues: Gly-1 to Asp-7, Lys-25 to Lys-31, Tyr-65 to Gly-70, Thr-100 to Arg-106, Pro-118 to Glu-124, Lys-162 to Ser-172, Leu-176 to Leu-182.
781445	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 947 as residues: Asn-33 to Lys-38, Leu-67 to Met-73, Ser-111 to Lys-121, Lys-127 to Leu-134, Pro-153 to Trp-158, Lys-237 to Met-249, Pro-280 to Tyr-292.
781531	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 948 as residues: Ala-8 to Pro-23, Gln-56 to Cys-61, Asn-66 to Pro-72.
783018	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 949 as residues: Asn-4 to Leu-17, Gly-19 to Phe-26, Pro-37 to Glu-43, Val-58 to Ser-64, Gln-80 to Gly-85.
783097	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 950 as residues: Pro-1 to Asp-9, Pro-24 to Gly-40, Pro-47 to Thr-55, Gln-62 to Ser-76.
784198	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 951 as residues: Met-1 to Arg-15, Leu-43 to Glu-48, Asp-55 to Asp-62, Ser-111 to Lys-160.
784868	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 952 as residues: Trp-8 to Gly-17, Glu-20 to Arg-35, Gly-40 to Cys-45, Ser-59 to Ser-64, Ala-73 to Leu-78, Val-85 to Leu-91, Arg-130 to Lys-135, Leu-138 to Glu-146, Pro-188 to

	Pro-194. Ser-206 to Cys-212. Ser-232 to Ala-246. Asp-293 to Ser-298.
785428	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 953 as residues: Arg-9 to Met-20, Glu-28 to Gly-33. Asn-49 to Lys-57, Thr-67 to Arg-75. Ser-81 to Leu-87, Glu-103 to Thr-109, Pro-115 to Ile-120, Asn-146 to Ser-174, Ser-177 to His-195, Met-197 to Ile-221, Asp-232 to Glu-240, Glu-289 to Phe-302, Cys-306 to Arg-314. Ser-357 to Ser-366, Lys-385 to Glu-401. Val-419 to Asp-427.
785845	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 954 as residues: Arg-41 to Asp-52, Pro-82 to Arg-94, Pro-102 to Gln-107, Gln-170 to Tyr-181, Glu-248 to Lys-254, Asp-277 to Gly-287, Ala-302 to Arg-308, Thr-367 to Gly-374.
785854	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 955 as residues: Asp-1 to Asp-17, Cys-59 to Asp-65.
787279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 958 as residues: Lys-13 to Lys-20.
789002	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 959 as residues: Met-20 to Glu-29.
789008	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 960 as residues: Ser-24 to Arg-33, Ile-44 to Gly-57, Arg-63 to Asn-72, Ile-76 to Pro-82.
789555	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 961 as residues: Trp-106 to Thr-117, Trp-156 to Gln-163, Gln-173 to Asp-178, Gln-227 to Glu-233, Gln-255 to Glu-261, Glu-297 to Tyr-306, Thr-339 to Val-345, Leu-378 to Ile-385, Asp-414 to Lys-420, Cys-437 to Ile-444, Thr-491 to Gln-497, Glu-509 to Ser-515, Lys-526 to Glu-538.
789631	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 962 as residues: Thr-10 to Gly-18.
789779	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 963 as residues: Glu-1 to Ala-13, Leu-103 to Ser-109.
790387	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 964 as residues: His-1 to Ala-12.
790461	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 965 as residues: Glu-14 to Gly-23, Asp-47 to Met-53, Ala-55 to Thr-60, Pro-67 to Thr-73, Pro-78 to Gly-86, Tyr-91 to Pro-101, Ala-133 to Asn-139, Glu-169 to Gln-182, Glu-189 to Thr-195, Asn-197 to Arg-203, Gln-265 to Asp-271.
790931	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 966 as residues: Val-3 to Glu-13, Pro-29 to Pro-35, Glu-116 to Arg-125.
791176	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 967 as residues: Pro-1 to Pro-10, Pro-17 to Phe-28, Ser-61 to Pro-67.
792539	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 969 as residues: Ser-12 to Trp-17, Gln-20 to Lys-29, Asp-45 to Glu-51, Tyr-75 to Lys-83, Arg-103 to Gly-119, Gln-145 to Lys-155, Lys-166 to Leu-180, Thr-195 to Gly-203, Gln-209 to Val-219, Ser-222 to Ala-244, Leu-251 to Leu-260, Lys-277 to Lys-285.
792749	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 970 as residues: Ala-22 to Asp-41, Thr-61 to Met-66, Asp-191 to Lys-198, Arg-280 to Phe-287, Thr-289 to Lys-299, Pro-325 to Asp-332, Ser-351 to Arg-357.
793206	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 972 as residues: Gly-1 to Arg-6, Gln-11 to Arg-22, Glu-86 to Asp-91.
793626	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 974 as residues: Ser-1 to Gly-13, Gly-17 to Asn-26.
794417	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 975 as residues: Ser-7 to Trp-16.
795197	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 976 as residues: Ser-67 to Glu-73, Arg-129 to Gly-136, Phe-154 to Ala-161, Tyr-198 to Tyr-203, Pro-206 to Asp-212, Glu-222 to Cys-231.
795251	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 977 as residues: Phe-44 to Ser-50, Asp-57 to Pro-62, Asn-80 to His-90, Ser-110 to Ala-115, Ile-141 to Val-148, Glu-155 to Thr-173, Val-202 to Pro-217, Ile-221 to Val-229, Thr-

	233 to Ser-243. Val-253 to Thr-259. Ala-290 to Asn-320. Pro-322 to Ile-330, Ala-333 to Met-344. Val-362 to Leu-367, Asp-397 to Val-402, Glu-422 to Gly-448, Met-453 to Gly-460.
795752	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 978 as residues: Pro-52 to Asn-63. Pro-70 to Ile-79. Arg-93 to Gln-111.
796261	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 979 as residues: His-1 to Val-6, Cys-10 to Ser-15, Gly-26 to Ser-34, Trp-36 to Pro-58, Pro-96 to Thr-102, Pro-111 to Tyr-116. Phe-131 to Gly-138, Pro-184 to Leu-190, Glu-237 to Gly-244, Pro-255 to Lys-267. Lys-271 to Leu-280.
796933	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 980 as residues: Arg-1 to Pro-14, Gln-47 to Cys-52, Asn-57 to Pro-63. Ser-277 to Lys-282.
799424	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 981 as residues: Tyr-18 to Leu-27, Met-50 to Met-60, Leu-169 to His-178, Ser-233 to Ser-241.
799698	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 982 as residues: Pro-16 to Pro-21, Ala-54 to Glu-61, Ala-96 to Gly-105.
800351	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 983 as residues: Gly-21 to Gln-34, His-39 to Lys-53, Ser-63 to Tyr-71.
800573	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 984 as residues: Asp-33 to Arg-39, Ala-43 to Leu-48, Glu-256 to Gln-266, Gly-305 to Ile-311, Pro-314 to Ala-320, Gln-388 to Asn-394.
805815	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 985 as residues: Arg-1 to Lys-22, Ser-34 to Arg-48, Thr-64 to Arg-70. Pro-81 to Phe-89, Arg-148 to Asn-154, Tyr-172 to Asp-185, Ser-205 to Asp-216, Tyr-278 to His-285, His-294 to Pro-299, Glu-326 to Gly-333, Gly-336 to Ser-345.
806445	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 986 as residues: Arg-15 to Gly-24, Lys-26 to Trp-32.
810309	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 987 as residues: Pro-33 to Phe-50, Ile-57 to Gly-62, Gln-72 to Asn-85, Ala-87 to Thr-172.
811022	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 988 as residues: Ala-1 to Met-11, Gln-62 to Trp-68, Ala-89 to Val-99.
811023	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 989 as residues: Tyr-54 to Lys-61, Met-64 to Thr-70.
811143	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 990 as residues: Ala-1 to Ser-7, Ser-19 to Gly-36, Arg-53 to Pro-58, Thr-87 to Glu-102, Arg-115 to Tyr-120, Thr-159 to Thr-164, Ala-171 to Ser-179, Ala-206 to Pro-217, Pro-224 to Ala-233, Arg-253 to Ser-259.
813000	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 993 as residues: Tyr-25 to Lys-30, Lys-36 to Ile-43, Lys-52 to Gln-69, Glu-76 to Asp-81, Arg-92 to Trp-104, Leu-120 to Lys-126, Ser-129 to Ser-135, Ser-139 to Thr-156, Pro-165 to Glu-178, Ser-181 to Thr-186, Tyr-196 to Lys-201, Cys-225 to Lys-230, Glu-234 to Ser-242.
813431	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 995 as residues: Leu-23 to His-29, Pro-38 to Leu-46, Ser-59 to Gly-68, Pro-85 to Lys-108, Arg-119 to Phe-124. Ser-139 to Lys-156.
813450	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 996 as residues: Asn-1 to Trp-10.
813478	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 997 as residues: Ala-8 to Arg-14, Ile-64 to Thr-69, Val-94 to Asp-101. His-112 to Gln-117, Tyr-139 to Glu-145, Tyr-195 to Cys-208. Gly-216 to Gly-223, Asp-297 to Ser-307, Gly-378 to Leu-383. Ile-391 to Pro-404, Asn-451 to Ser-466.
813505	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 998 as residues: Thr-1 to Ala-20, Pro-22 to Lys-27, His-44 to Thr-51, Pro-53 to Thr-60, Arg-62 to Lys-79, Lys-97 to Asn-103, Pro-139 to Lys-144.
815552	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 999 as residues: Pro-1 to Ser-6, Pro-25 to Cys-31, Arg-142 to Lys-150.

815606	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1000 as residues: Arg-1 to Ala-11.
816048	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1001 as residues: Ala-13 to Thr-24, Glu-30 to Gln-39, Arg-69 to Gly-77, Gln-119 to Gly-126, Tyr-156 to Asn-162, Ser-184 to Gly-191.
823981	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1004 as residues: Lys-1 to Cys-7, Ala-11 to Lys-17, Glu-90 to Ile-95, Asn-141 to Arg-148, Leu-158 to Ala-163, Ala-171 to Thr-177.
824364	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1005 as residues: Gln-43 to Gly-54.
824423	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1006 as residues: Cys-33 to Arg-42, Val-53 to Met-63, Lys-71 to Lys-78, Gly-107 to Pro-118, Ala-159 to Leu-165, Val-272 to Arg-284, Pro-422 to Pro-427, Arg-437 to Gln-443, Ala-474 to Asp-482, His-519 to Cys-525, Ala-529 to Gln-535, Arg-540 to Gln-548.
825279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1007 as residues: Ser-8 to Arg-14, Asp-23 to Gly-28, Ser-30 to Pro-37, His-52 to Ala-57, Pro-65 to Ser-74, Pro-112 to Ser-118, Ala-181 to Pro-189.
825548	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1009 as residues: Pro-2 to Ser-9.
825725	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1010 as residues: Pro-1 to Gly-8, Leu-95 to Lys-100, Glu-118 to Thr-125, Ser-162 to Lys-167, Arg-201 to Tyr-206.
827079	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1012 as residues: Arg-9 to Ser-17.
827153	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1013 as residues: Val-32 to Ala-44, Pro-49 to Ser-57, Gln-77 to Gly-82, Asp-116 to Gly-127, Arg-165 to Asn-172.
827351	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1014 as residues: Gly-5 to Lys-11, Ser-59 to Lys-67, Glu-130 to Arg-136, Asn-176 to Leu-183.
827503	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1015 as residues: Asp-61 to Val-67, Arg-113 to Asp-119, Ser-180 to Gly-191, Pro-199 to Ser-211, Ser-228 to Asn-238, Gly-276 to Ser-286, His-343 to Gly-351, Gln-354 to Arg-366, Leu-368 to Gln-382, Pro-393 to Ser-400, Asp-412 to Cys-418, Gly-430 to Leu-435, Gln-445 to Asp-450, Lys-484 to Val-491, Leu-513 to Gly-520.
827563	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1016 as residues: Pro-69 to Ala-81, Pro-84 to Gly-91, Ala-106 to Leu-112, Arg-216 to Lys-224, Trp-239 to Gly-250.
827565	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1017 as residues: Ala-1 to Ser-8, Ser-88 to Gly-96, Asn-121 to Asp-128, Cys-191 to Gly-196, Met-242 to Thr-248.
827893	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1018 as residues: Ser-41 to Ala-50, Glu-72 to His-77, Ala-120 to Glu-125, Thr-144 to Ile-153.
828072	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1019 as residues: Lys-30 to Leu-35.
828241	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1021 as residues: Gly-35 to Phe-45, Pro-47 to Arg-55, Glu-62 to Leu-70, Arg-102 to Tyr-111, Phe-128 to Gln-134, Val-139 to Met-144, Ser-180 to Gly-188, Lys-214 to Leu-219, Ser-241 to Glu-246, Phe-292 to Thr-298.
828287	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1022 as residues: Ala-12 to Thr-21, Ala-23 to Gly-31, Leu-43 to Gly-51, Lys-127 to Val-134.
828371	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1024 as residues: Gln-1 to Ala-6, Lys-50 to Pro-71, Pro-98 to Ser-111, Asp-148 to His-164, Asp-185 to Arg-191, Asp-238 to Gly-244, Pro-262 to Cys-274.
828403	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1025 as residues: Gly-1 to Trp-15, Arg-73 to Leu-82.
828501	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1026 as

	residues: Arg-99 to Arg-105. Pro-171 to Ser-176, Lys-189 to Val-195, Lys-291 to Ala-296.
828527	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1028 as residues: Glu-58 to Cys-63.
828538	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1029 as residues: Pro-9 to Thr-24. Thr-46 to Gly-52. Ser-70 to Thr-76. Ser-142 to Thr-149, Pro-154 to Ser-171. Glu-189 to Ser-196.
828541	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1030 as residues: Arg-9 to Pro-23, Gln-64 to Leu-69, Asp-76 to Asn-83, Lys-88 to Gln-93, Pro-129 to Thr-135, Gly-194 to Gly-203, Asp-223 to Gly-231. Thr-265 to Ile-281, Leu-287 to Lys-297.
828549	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1031 as residues: Pro-22 to Asn-28.
828562	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1032 as residues: Arg-26 to Asp-33, Asp-42 to Pro-58, Thr-63 to Lys-70, Thr-103 to Asp-114.
828576	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1033 as residues: Arg-11 to Gly-17. Pro-26 to Gly-31, Ala-48 to His-58.
828602	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1034 as residues: Tyr-1 to Met-8. Leu-10 to Lys-26. Pro-47 to Pro-54, Lys-128 to Ser-133.
828628	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1035 as residues: Thr-124 to Thr-129, Gly-136 to Phe-142. Asp-164 to His-171, Asp-180 to Tyr-194.
828684	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1037 as residues: Ser-16 to Thr-22, Arg-39 to Ala-51, Arg-60 to Gly-65, Thr-67 to Arg-90, Lys-109 to Gln-125, Ser-146 to Arg-159, Gln-166 to Thr-176. Glu-192 to Tyr-197, Val-267 to His-279, Ala-351 to Gly-356, Phe-363 to Gly-368, Gly-387 to Arg-392, Asp-488 to Ala-498.
828727	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1038 as residues: Gly-14 to Val-21, Asp-40 to Gln-57, Gln-86 to Tyr-93, Gln-98 to Asp-104, Lys-124 to Asp-130, Gln-138 to Cys-156, Tyr-170 to Gln-175, Gln-196 to Ala-201.
828734	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1039 as residues: Asp-5 to Trp-19, Ile-37 to Pro-42, Asp-52 to Asp-72, Glu-85 to Ser-92, Ser-107 to Leu-117, Asp-128 to His-147.
828842	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1041 as residues: Ala-25 to Phe-32. Glu-54 to Ser-61, Thr-74 to Glu-79, Glu-99 to Lys-105, Glu-112 to Glu-121.
828843	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1042 as residues: Pro-3 to Asn-11, Gln-46 to Ala-51, Asn-62 to Lys-74, Val-108 to Gln-113, Arg-119 to Gly-163, Ala-223 to Lys-237.
828851	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1043 as residues: Thr-3 to Lys-8, Leu-63 to Val-70, Lys-141 to Val-149, Ile-326 to Thr-333.
828856	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1044 as residues: Leu-1 to Gly-10.
828862	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1045 as residues: Pro-1 to Pro-9. Arg-81 to Glu-87, Gln-114 to Glu-119.
828870	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1046 as residues: Ser-1 to Gly-18, Trp-25 to Gly-31, Arg-46 to Ser-52, Ala-103 to Ala-108, Ser-154 to Gly-165, Gln-228 to Pro-236, Ser-284 to Gly-291, Ala-321 to Asp-327. Lys-377 to Asn-394, Asp-406 to Ser-416.
828873	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1047 as residues: Tyr-15 to Gly-20, Asn-72 to Asp-80, Pro-105 to Pro-110, Gln-149 to Arg-154, Glu-161 to Gly-167. Ile-312 to Asp-318, Lys-353 to Leu-361, Arg-379 to Thr-385. Pro-423 to Trp-435, Pro-437 to Cys-444, Asn-450 to Met-466.
828892	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1048 as residues: Asp-19 to Asn-25, Gly-67 to Glu-79.
828893	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1049 as

	residues: Ser-55 to Thr-60, Glu-97 to Ser-103, Thr-164 to Glu-170, Gly-192 to Gly-197, Leu-204 to Ser-218, Ala-238 to Ser-250, Asp-265 to Tyr-292, Gly-298 to Gly-307, Gly-351 to Met-359, Phe-389 to Glu-400.
828897	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1050 as residues: Phe-28 to Arg-33.
828910	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1051 as residues: His-1 to Ile-13, Arg-20 to Glu-64, Arg-83 to Gln-89, Tyr-145 to Asp-152.
828927	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1052 as residues: Glu-10 to Pro-21, Thr-54 to Gly-60, Cys-79 to Glu-90, Lys-154 to Lys-159.
828932	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1053 as residues: Arg-1 to Arg-9, Phe-54 to Pro-60, Gln-74 to Gly-90, Asn-114 to Gly-119, Cys-124 to Ser-132, Thr-139 to Leu-151, Asp-171 to Lys-182, Ala-188 to Leu-193, Val-203 to Trp-222, Lys-230 to Glu-236, Glu-244 to Asp-250, Leu-258 to Gly-268, Gly-283 to Asp-288, Ser-291 to Trp-297, Gly-300 to Ala-308.
828933	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1054 as residues: Glu-21 to Ser-34, Thr-130 to Tyr-138.
828941	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1055 as residues: Gly-1 to Ala-6, Pro-15 to Gly-22, Asn-160 to Gln-177, Asn-193 to Asp-199, Glu-205 to Leu-211.
828963	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1057 as residues: Pro-48 to Gly-54, Ser-56 to Ser-76, Lys-102 to Pro-107, Ser-146 to Gly-153, Ser-208 to Arg-213, Tyr-285 to Leu-299, Pro-314 to Phe-319, Asn-322 to Asn-327.
828964	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1058 as residues: Thr-36 to Cys-47.
828966	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1059 as residues: Gly-1 to Ser-16, Met-26 to Pro-31, Lys-128 to Glu-134, His-165 to Gln-170, Asp-207 to Asn-216, Pro-348 to Arg-359, Lys-433 to Ala-439, Gly-448 to Tyr-457.
828967	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1060 as residues: Met-135 to Arg-141, Gly-149 to Lys-166, Ile-188 to Ser-196, Gly-203 to Tyr-213, Gln-267 to Asp-278, Arg-298 to Trp-317, Leu-319 to Leu-326, Gln-344 to Thr-349, Pro-410 to Ser-419, Ala-500 to Ala-510.
828977	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1061 as residues: Gly-32 to Tyr-42, Asn-52 to Glu-58, Ser-78 to Gly-87, Lys-97 to Gly-109, Glu-116 to Arg-127, Pro-147 to Pro-152, Pro-162 to Asn-171, Leu-179 to Glu-185, Ile-203 to Glu-208, Val-222 to Gln-228.
828978	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1062 as residues: Asp-24 to Lys-30, Arg-49 to Lys-62, Arg-121 to Thr-149, Gly-163 to Leu-171, Ala-186 to Glu-195, Glu-216 to Ser-221, Ile-229 to Ser-236, Lys-258 to Lys-264, Lys-305 to Arg-313.
829001	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1064 as residues: Thr-11 to Cys-24, Arg-48 to His-55, Arg-62 to Gly-70.
829003	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1065 as residues: Lys-14 to Gly-22, Ser-61 to Asp-66, Cys-80 to Lys-91, Lys-97 to Arg-107, Gly-135 to Asn-146, Lys-198 to Lys-208, Met-221 to Thr-227, Phe-244 to Gly-256, Asp-292 to Gln-300.
829016	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1066 as residues: Arg-1 to Asp-11, Ala-17 to Gln-25, Glu-30 to His-37, Cys-39 to Thr-44, Asn-86 to Phe-93.
829027	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1067 as residues: Pro-1 to Ser-7, Thr-45 to Leu-63, Arg-113 to Thr-118, Pro-172 to Gly-182.
829028	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1068 as residues: Ser-1 to Gln-19, Gly-32 to Phe-39, Ala-95 to Arg-116, Lys-122 to Glu-142, Ile-148 to Asn-156, Ser-168 to Asn-191, Ala-196 to Thr-204, Ser-289 to Lys-304, Leu-308 to Ser-314, Thr-332 to Ile-341.
829034	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1070 as residues: Ser-32 to Ala-43, Thr-62 to Glu-69, Phe-128 to Thr-156, Thr-179 to His-188,

	Gly-196 to Glu-203, Pro-205 to Ala-219, Gln-221 to Ile-230, Pro-246 to Thr-255, Thr-271 to His-276, Asn-324 to Thr-344, Pro-364 to Ala-370, Tyr-427 to Arg-434, Gly-440 to Pro-445.
829036	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1071 as residues: Leu-16 to Phe-21, Thr-69 to Lys-74, Asn-87 to His-92, Thr-126 to Leu-137, Phe-154 to Lys-164, Ala-171 to Asp-178, Ile-192 to Thr-203, Glu-261 to Ser-273.
829049	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1072 as residues: Gly-50 to Tyr-59.
829073	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1073 as residues: Asn-1 to Met-6, Asn-26 to Ser-35, Pro-43 to Ile-54.
829075	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1074 as residues: Gly-14 to Pro-30, Ser-64 to Ser-69, Asn-97 to Arg-109.
829076	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1075 as residues: Lys-84 to Gly-94, Asn-142 to Ile-147.
829080	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1076 as residues: Gly-13 to Trp-23, Pro-39 to Gly-44.
829087	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1077 as residues: Pro-13 to Arg-24.
829095	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1079 as residues: Pro-8 to Pro-13.
829118	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1081 as residues: Arg-7 to Val-12, Ile-52 to Thr-70, Ser-86 to Asp-91, Thr-126 to Ser-138.
829152	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1082 as residues: Asp-12 to Ser-19.
829160	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1083 as residues: Ala-7 to Arg-20.
829163	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1084 as residues: Ser-23 to Asp-32, Val-36 to Glu-59, Ser-65 to Asn-76, Cys-91 to Ser-102, Pro-108 to Leu-115, Thr-151 to Gln-164, Glu-167 to Lys-176.
829176	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1085 as residues: His-1 to Asn-8, Cys-22 to Arg-27, Gly-34 to Ser-44, Tyr-60 to Ser-65, Ser-118 to Gln-123, Ser-149 to Trp-154, Pro-159 to Gly-168, Gln-207 to Leu-220.
829204	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1086 as residues: Ala-11 to Ser-19, Thr-104 to Lys-133.
829207	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1087 as residues: Lys-5 to Ser-11, Pro-31 to Ser-37, Pro-87 to Asp-92, Asp-115 to Lys-123, Ser-149 to Arg-155, Thr-243 to Pro-253.
829228	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1088 as residues: Pro-1 to Trp-6, Leu-73 to Tyr-79, Glu-108 to Thr-117, Asp-136 to Asp-142, Ser-201 to Pro-207, Leu-224 to Pro-233, Val-242 to Ala-248, Ser-312 to Leu-319, Val-349 to Ser-359, Ala-362 to His-368, Thr-370 to Gly-376, Lys-403 to Tyr-409, Glu-426 to Arg-431, Lys-455 to Asp-460, Arg-499 to Thr-505, Asp-561 to Ser-570, Ser-665 to Ser-673.
829252	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1089 as residues: Thr-9 to Val-16.
829269	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1091 as residues: Ser-1 to Glu-7, Lys-76 to Gln-83.
829277	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1092 as residues: Lys-88 to Phe-97, Thr-106 to Leu-120, Thr-147 to Pro-152, Pro-173 to Met-179.
829290	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1093 as residues: Pro-1 to Pro-19, Pro-25 to Lys-30.
829308	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1096 as residues: Met-26 to Asn-37, Glu-42 to Gln-51, Thr-68 to Ser-95, Ala-97 to Lys-113, Asp-156 to Val-161, Val-208 to Asp-215, Pro-217 to Ala-228.
829349	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1097 as

	residues: Asn-18 to Lys-24, Asp-87 to Asn-94, Glu-116 to Gly-125.
829354	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1098 as residues: Ala-1 to Asn-16, Pro-36 to Arg-43.
829388	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1099 as residues: Glu-91 to Pro-100, Tyr-122 to Thr-127, Thr-168 to Val-173, Thr-210 to Asp-215, Leu-219 to Gly-224, Gly-232 to Val-237.
829626	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1101 as residues: Gly-145 to Ala-151.
829730	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1102 as residues: Pro-22 to His-27, Pro-87 to Asp-93, Arg-109 to Lys-115, Arg-172 to Glu-177, Glu-219 to Asp-226.
829892	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1103 as residues: Tyr-36 to Ala-46, Val-58 to Asn-63, Glu-73 to Asn-78, Asn-90 to Asn-95, Ser-125 to Leu-133, Glu-143 to Pro-150, Phe-186 to Leu-191, Leu-274 to Glu-281, Lys-303 to Phe-308, Thr-323 to Gly-330.
829938	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1105 as residues: Thr-1 to Pro-14, Ser-36 to Thr-57, Ser-81 to Thr-91, Glu-103 to Leu-110, Glu-124 to Tyr-130, Ala-135 to Lys-140, Leu-146 to Glu-162, Lys-167 to Glu-172, Glu-199 to Val-213.
829969	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1106 as residues: Arg-12 to His-21, Arg-77 to Ser-88.
829982	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1107 as residues: Arg-6 to His-14, Ser-40 to Met-47, Thr-68 to Cys-74, Ile-97 to His-115, Gly-118 to Pro-124.
830007	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1108 as residues: Ala-7 to Ala-16.
830019	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1109 as residues: Leu-21 to Pro-27.
830073	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1110 as residues: Gly-16 to Val-22, Pro-45 to Lys-50, Phe-58 to Arg-65, Ser-135 to Gly-141, Gly-153 to Ser-158, Pro-160 to Tyr-168.
830148	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1114 as residues: Asp-63 to Lys-81, Gly-101 to Gly-108, Pro-182 to Ala-200, Pro-210 to Met-216, Pro-235 to Gly-243.
830183	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1117 as residues: Pro-29 to Lys-37, Pro-40 to Val-47, Tyr-62 to His-67.
830194	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1118 as residues: Ala-43 to Lys-51, Glu-66 to Leu-74, His-81 to Glu-88, Arg-98 to Ser-105, Gly-111 to Gln-116, Leu-166 to Lys-182, Leu-261 to Ala-273, Glu-294 to Arg-302, Glu-335 to Asp-347.
830207	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1119 as residues: Pro-14 to Pro-48, Asp-55 to Gly-61, Lys-94 to Asn-99, Ala-107 to Ser-115, Ile-117 to Asn-124, Thr-133 to Cys-139, Thr-142 to Ile-147, Gly-163 to Ser-169.
830242	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1120 as residues: Glu-29 to Lys-34, Leu-151 to Gln-157, Arg-160 to Ser-171, Gln-177 to Pro-190.
830328	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1121 as residues: Pro-18 to Met-24, Glu-66 to Gln-78, Ala-85 to Arg-93, Glu-99 to His-108, Leu-114 to Asp-137, Pro-171 to Gln-176, Gly-205 to Leu-213.
830340	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1122 as residues: Gly-12 to Lys-18, Arg-46 to Glu-56, Leu-67 to Gly-73, Ala-91 to Tyr-112.
830341	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1123 as residues: Leu-14 to Gln-20, Asn-34 to Glu-41, Lys-193 to Asn-198.
830351	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1124 as residues: Pro-1 to Leu-13, Gly-42 to Pro-51, Arg-64 to Ala-69, Met-104 to Asp-109, Cys-125 to Trp-132, Asp-161 to Trp-175, Glu-206 to Glu-218.

830358	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1125 as residues: Cys-75 to Thr-81.
830400	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1127 as residues: Pro-1 to Gly-6, Arg-17 to Arg-33, Glu-151 to Trp-157, Ile-187 to Tyr-193, Lys-249 to Glu-258, Asn-289 to Ser-294, Pro-340 to Lys-353.
830437	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1128 as residues: Ala-87 to Ser-94, Asp-104 to Arg-112, Leu-114 to Asp-119, Ser-186 to Thr-202.
830466	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1130 as residues: Pro-14 to Ile-24, Thr-35 to Phe-42, Ser-45 to Asn-57, Pro-65 to Trp-89.
830497	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1131 as residues: Thr-1 to Leu-9, Ser-46 to Leu-56, Glu-117 to Lys-124, Pro-129 to Asp-135, Ala-144 to Gln-150, Gly-156 to Lys-162, Phe-182 to Pro-187, Pro-196 to Gln-201, Lys-217 to Asp-227.
830511	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1132 as residues: Lys-13 to Cys-44, Lys-101 to Arg-109, Gln-120 to Gly-129.
830540	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1135 as residues: Leu-31 to Lys-37, Arg-48 to Asn-54.
830550	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1136 as residues: Pro-8 to Cys-15, Val-80 to Cys-85.
830567	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1137 as residues: Lys-28 to Leu-33, Pro-60 to Ser-66.
830586	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1138 as residues: Pro-1 to Gln-15, Arg-33 to Leu-40, Arg-72 to Ser-78, Leu-98 to Asp-103, Phe-116 to Gly-124, Pro-152 to Arg-158, Thr-193 to Pro-200, Leu-213 to Phe-219, Asp-229 to Lys-237, Lys-246 to Lys-258, Arg-275 to Thr-280, Thr-306 to Lys-312, Leu-320 to Arg-328, Ala-335 to Asn-340, Gly-342 to Trp-349, Cys-364 to Pro-372.
830632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1139 as residues: Ala-6 to Thr-14, Arg-143 to Lys-148.
830659	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1142 as residues: Thr-32 to Tyr-40, Ala-67 to Gln-82, Arg-128 to Thr-133, Leu-137 to Thr-146, Pro-187 to Ser-193.
830696	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1143 as residues: Glu-83 to Lys-91.
830743	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1145 as residues: Pro-11 to Phe-16, Thr-48 to Ser-60.
830770	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1146 as residues: Thr-36 to Thr-44.
830830	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1147 as residues: Lys-73 to Thr-78, Pro-84 to Pro-96, Lys-107 to Glu-124, Ile-142 to Cys-153, Asp-179 to Asn-184.
830838	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1148 as residues: Ser-17 to Arg-22, Gly-48 to Val-56, Asn-217 to Asp-223, Thr-238 to Asn-243.
830851	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1149 as residues: Arg-1 to Val-7, Ala-156 to Phe-162, Arg-216 to Lys-239.
830856	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1151 as residues: Trp-29 to Gly-35, Thr-41 to His-47, Val-95 to Lys-111.
830862	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1152 as residues: Arg-14 to Val-22, Ala-24 to Gly-35, Arg-37 to Lys-58, Ala-88 to Ala-94, Lys-164 to Ser-172.
830879	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1153 as residues: Cys-34 to Leu-44, Ser-60 to Gly-69, Asp-118 to Gly-123, Cys-148 to Gln-154.
830919	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1154 as residues: Pro-1 to Ser-41, Arg-53 to Pro-61, Arg-66 to Gln-132.

830969	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1155 as residues: His-17 to Pro-27, Phe-31 to Val-38, Gly-53 to Thr-62.
830991	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1156 as residues: Arg-1 to Pro-14, Ala-44 to Ser-56, His-69 to Lys-75, Gly-89 to Lys-98, Tyr-101 to Tyr-121, Pro-123 to Thr-131, Pro-149 to Gly-171, Tyr-186 to Glu-192.
831002	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1157 as residues: Glu-63 to Asn-73, Pro-114 to Tyr-122, Ser-194 to Glu-201, Ile-263 to Ser-269.
831003	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1158 as residues: Ile-9 to Leu-17, Asp-63 to Gly-70, Leu-112 to Ala-128.
831021	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1159 as residues: Asn-6 to Asp-12.
831036	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1160 as residues: Ser-6 to Ser-25, Tyr-37 to Lys-42, Arg-49 to Tyr-54, Pro-56 to Glu-61, Gln-72 to Cys-77, Lys-104 to Glu-110, Lys-134 to Met-142, Asp-147 to Arg-158, Arg-189 to Asn-194.
831071	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1161 as residues: Thr-41 to Arg-49, Glu-137 to Asp-142, Tyr-158 to Glu-163, Arg-184 to Thr-199, Arg-239 to Gly-253, Pro-297 to Gly-304, Pro-319 to Ile-327, Leu-347 to Val-356, Asn-435 to Leu-441, Asp-443 to Ser-452, Ala-457 to Thr-462, Asp-479 to Arg-484, Gly-510 to His-516, Glu-555 to Thr-565, Asp-597 to Ser-602, Thr-615 to Asp-622, Val-653 to Leu-661, Ala-684 to Arg-697, Ser-704 to Glu-712, Ala-731 to Ala-737, Lys-800 to Met-805.
831099	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1163 as residues: Leu-12 to Gly-18, Leu-93 to Ile-98, Lys-165 to Ser-183, Thr-198 to Lys-211, Glu-232 to Gly-237, Pro-239 to Gly-249, Arg-257 to Asp-278, Cys-292 to Glu-297, Arg-306 to Ser-316, Asp-323 to Asn-331, Glu-347 to Gly-354, Thr-365 to Asn-370, Pro-390 to Thr-396, Asn-420 to Ser-433, Val-440 to Gln-451, His-457 to Asp-465, Phe-533 to Met-538, Ala-540 to Tyr-550, Pro-560 to Lys-565.
831113	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1164 as residues: Ser-26 to Arg-33, Pro-51 to Thr-56, Cys-82 to Asp-94, Pro-104 to Gly-128.
831120	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1165 as residues: Ala-39 to Leu-47, Val-49 to Lys-55, Thr-66 to Asp-75, Thr-85 to Gly-104, Ala-114 to Gly-147, Pro-176 to Thr-199, Ser-205 to Ser-221, Glu-233 to Lys-240, Lys-246 to Asp-251, Glu-256 to Ser-267, Ser-291 to Leu-302, Thr-305 to Asp-324, Cys-336 to Val-345, Phe-367 to Cys-375.
831172	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1166 as residues: Pro-1 to Gly-7, His-119 to Gly-125, His-145 to Asp-151, Leu-173 to Leu-178.
831178	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1167 as residues: Glu-37 to Asn-42, Ser-48 to Thr-54, Pro-101 to Glu-106.
831184	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1168 as residues: Gln-1 to Pro-29.
831203	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1169 as residues: Thr-1 to Ser-6, Leu-10 to Asn-23, Gln-31 to Arg-36, Arg-43 to His-49, Ala-58 to Leu-63, Gln-81 to Asp-105, Glu-113 to Ile-122, Pro-132 to Lys-137, Ser-175 to Gln-181.
831257	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1173 as residues: Arg-87 to Leu-96, His-104 to Lys-112, Asp-144 to Pro-150.
831277	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1174 as residues: Arg-1 to Gly-13.
831317	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1175 as residues: Ser-97 to Lys-102, Thr-108 to Gly-119, Lys-151 to Gly-157, Pro-204 to Glu-210, Gln-224 to Gly-230, Val-238 to Cys-245, Met-279 to Asn-284, Gly-332 to Glu-349.
831339	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1176 as

	residues: Met-1 to His-19, Pro-21 to Pro-27, Ala-49 to Gly-59, Pro-82 to Ala-104.
831363	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1177 as residues: Thr-1 to Ser-14, Thr-82 to Pro-89, Met-102 to Ala-109, Phe-117 to Ile-124, Asp-142 to Arg-148, Thr-196 to Trp-205, Gln-304 to Leu-310, Gln-325 to Ser-331, Gly-387 to Thr-393, Ala-415 to Lys-430, Pro-469 to Pro-477, Gly-500 to Ile-506, Arg-521 to Gly-529, Pro-534 to Gly-541, Gln-553 to Lys-558, Ala-571 to Glu-579.
831385	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1180 as residues: Ser-1 to Thr-9, Ala-32 to Asn-37, Thr-40 to Tyr-49, Gln-71 to Thr-80.
831390	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1181 as residues: Trp-50 to Gly-55, Leu-109 to Val-119, Phe-146 to Asp-158, Ser-165 to Trp-172, Phe-192 to Ile-197, Leu-241 to Asp-252, Lys-268 to Pro-273, Ser-310 to Lys-315, Asp-334 to Ala-342, Pro-348 to Tyr-353.
831391	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1182 as residues: Ser-28 to Pro-38, Pro-45 to Cys-55, Leu-70 to Ser-77, Glu-98 to Phe-104, Asp-112 to Ser-122, Thr-152 to Lys-158.
831405	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1183 as residues: Asp-47 to Ser-55, Glu-86 to Cys-95, Glu-105 to Gly-113, Gln-133 to Asn-138, Arg-144 to Asp-156.
831476	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1185 as residues: Gln-28 to Gly-33, Asp-41 to Trp-47, Asn-51 to Ser-56, Ser-73 to Asn-83, Trp-111 to Asn-117, Leu-133 to Gln-138, Arg-143 to Tyr-150, Thr-156 to Glu-165.
831488	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1186 as residues: Glu-53 to Asn-59, Lys-97 to Phe-104, Lys-133 to Ala-138.
831519	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1188 as residues: Ser-17 to Gly-25, Thr-47 to Leu-59, His-71 to Arg-77, Pro-83 to Gln-90, Tyr-133 to Ser-143, Arg-160 to Gly-169, Pro-188 to Val-193, Glu-202 to Glu-208, Leu-283 to Arg-288, Glu-295 to Leu-301, Ala-327 to Leu-333, Ala-426 to Pro-433, Leu-444 to Leu-456, Asn-492 to Ala-498.
831550	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1190 as residues: Arg-1 to Gly-15, Ser-42 to Trp-51, Pro-59 to Arg-64.
831560	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1191 as residues: Arg-58 to Asp-64.
831570	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1193 as residues: Thr-61 to Cys-74, Gly-92 to Cys-104, Cys-128 to Ser-133, Asn-179 to Gly-186, Ser-198 to Cys-226, Asn-265 to Ser-274, Ser-280 to Ile-285, Ser-291 to Asp-297, Leu-305 to Gly-315, Phe-317 to Gly-333, Asp-336 to Leu-344, Phe-354 to Cys-361.
831596	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1195 as residues: Gln-80 to Gly-85.
831627	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1196 as residues: Arg-1 to Ser-12, Gly-94 to Thr-106, Ser-161 to Leu-169, Ser-183 to Val-188, Glu-199 to Cys-205, Ser-246 to Ile-251, Leu-271 to Thr-276.
831649	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1197 as residues: Tyr-32 to Lys-39.
831664	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1198 as residues: Lys-1 to Asp-42, Arg-71 to Ala-76, Gln-138 to Phe-145, Lys-170 to Thr-178, Cys-186 to Asp-192.
831684	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1200 as residues: Ile-135 to Ala-140, Tyr-151 to Asn-157, Ser-183 to Ile-190, Gly-196 to Lys-201, Lys-226 to Lys-232, Asn-246 to Thr-252, Asp-293 to Gly-300.
831687	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1201 as residues: Ala-56 to Tyr-63.
831726	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1202 as residues: Arg-3 to Arg-15, Lys-34 to Thr-39, Asn-41 to Lys-59, Ala-104 to Glu-110.
831762	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1204 as residues: Pro-83 to Leu-91, His-116 to Ala-122, Pro-141 to Ser-155.
831848	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1206 as

	residues: Gln-16 to Thr-23.
831861	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1207 as residues: Ala-20 to Lys-26. Pro-59 to Pro-67. Ser-104 to Thr-121. Gln-130 to Gln-136.
831866	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1208 as residues: Arg-11 to Ala-24, Ile-39 to Lys-45, Arg-76 to Pro-85. Lys-124 to Lys-130, Pro-139 to Ser-153. Ala-156 to Glu-170, Ser-179 to Thr-184. Asp-234 to Gly-244. Gly-321 to Lys-329.
831899	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1210 as residues: Asp-11 to Trp-16. Pro-37 to Thr-44, Pro-74 to Pro-82. Arg-112 to Gln-119, Cys-126 to Arg-138. Arg-199 to Thr-204.
831913	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1211 as residues: Pro-22 to Cys-27, Glu-54 to Glu-60, Asp-112 to Phe-117. Lys-183 to Asp-189. Gln-277 to Tyr-282. Pro-325 to Arg-331. Gly-336 to Tyr-346.
831985	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1213 as residues: Cys-7 to Asp-12. Pro-21 to Gly-26.
831986	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1214 as residues: Cys-1 to Ser-7. Ala-62 to Gly-72. Pro-83 to Ala-101.
832010	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1215 as residues: Leu-1 to Lys-21, Glu-39 to Cys-47, Lys-49 to Gln-61, His-64 to Gly-76, Thr-83 to Lys-90. His-92 to Ile-99.
832016	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1216 as residues: Phe-28 to Asn-33. Leu-55 to Tyr-80, Pro-126 to Gly-132. Pro-162 to Gly-169, Pro-194 to Arg-201.
832041	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1217 as residues: Lys-55 to Met-63, Arg-120 to Asp-132, Gly-266 to Glu-281, Val-313 to Thr-319, Leu-361 to Ser-370. Tyr-406 to Met-412. Leu-465 to Trp-470.
832049	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1219 as residues: Leu-80 to Lys-87, Lys-102 to Thr-109, Glu-195 to Thr-200. Thr-203 to Asp-209.
832122	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1220 as residues: Asn-29 to Phe-36, Asp-41 to Ser-50.
832197	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1222 as residues: Glu-61 to Leu-70.
832237	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1223 as residues: Lys-28 to Val-35. Arg-41 to Arg-55. Pro-76 to Thr-87.
832246	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1224 as residues: Arg-17 to Asn-23, Arg-90 to Gly-95, Leu-114 to Glu-121, Pro-153 to Asp-158.
832256	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1225 as residues: Gly-15 to Asn-22.
832280	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1226 as residues: Glu-1 to Trp-16, Ala-32 to Glu-38, Ala-49 to Gln-55, Pro-61 to Gln-66, Ala-78 to Asp-100, Leu-107 to Thr-127, Pro-133 to Phe-157, Pro-160 to Thr-171, Leu-179 to Asp-196, Asp-201 to Lys-222, Pro-249 to Ile-254, Val-258 to Val-263, Thr-268 to Ser-277, Thr-279 to Ala-295, Gly-299 to Phe-327, Val-335 to Asp-346, Lys-366 to Asp-378.
832285	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1227 as residues: Phe-18 to Leu-23.
832294	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1228 as residues: Pro-21 to Gln-28, Pro-56 to Leu-64, Glu-79 to Pro-95. Met-125 to Gly-138.
832326	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1229 as residues: Ser-30 to Trp-45. Gln-64 to Cys-72. Pro-74 to Pro-80, Ala-92 to Arg-98, Trp-104 to Ser-112, Ser-129 to Asp-135, Pro-145 to Gln-152, Arg-168 to Gly-173, Gln-176 to Pro-183.
832370	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1232 as residues: Ala-5 to Ala-11, Pro-23 to Pro-36. Glu-72 to Gly-82, Pro-85 to Pro-91, Asp-

	98 to Gly-119, Pro-121 to Glu-127.
832381	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1233 as residues: Arg-1 to Glu-6, Arg-52 to Ala-58, Phe-72 to Leu-79, Gly-88 to Glu-93, Tyr-124 to Arg-134.
832454	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1235 as residues: Ala-23 to Asp-41.
832465	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1236 as residues: Ala-1 to Gly-7, Ala-32 to Val-45, Ile-65 to Ser-75, Ser-93 to Ser-108.
832475	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1237 as residues: Arg-1 to Val-10, Thr-65 to Ser-71, Arg-83 to Tyr-96, Trp-104 to Trp-111.
832495	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1238 as residues: Arg-9 to Arg-14.
832498	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1239 as residues: Pro-26 to Asp-31, Thr-113 to Gly-125, Asn-158 to Glu-163, Asn-288 to Val-293.
832501	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1240 as residues: Ser-8 to Glu-13.
832505	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1241 as residues: Ala-27 to Arg-46, Pro-54 to Arg-76, Arg-134 to Lys-140, Asn-148 to Ser-154, Lys-166 to Thr-172, Pro-175 to Gln-182, Asp-185 to Asp-192.
832554	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1243 as residues: Arg-26 to Val-31, Asn-122 to Thr-128.
832569	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1244 as residues: Gln-6 to Met-16.
832578	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1245 as residues: Arg-15 to Leu-27, Ser-62 to Gly-72, Pro-107 to His-112, Pro-122 to Gln-142, Glu-147 to Arg-158, Lys-177 to Lys-191, Leu-195 to Val-202, Leu-206 to Pro-218, Glu-228 to Gln-233, Asp-239 to Asp-244, Glu-258 to Gln-278.
832615	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1246 as residues: Gln-41 to Ala-48.
832632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1248 as residues: Asn-60 to Val-70, Glu-93 to Trp-107, Arg-116 to Gln-125, Leu-133 to Lys-141, Lys-162 to Glu-167.
832633	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1249 as residues: Gly-8 to Trp-13, Pro-36 to Gly-41, Pro-91 to Ala-96.
834859	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1252 as residues: Tyr-16 to Leu-22, Asp-24 to Asp-34, Gly-43 to Ala-48, Gly-57 to Thr-68, Gly-118 to Ser-127, Ile-129 to Tyr-134, Pro-139 to Asp-162.
834861	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1253 as residues: Glu-14 to Glu-50, Glu-67 to Asp-74, Leu-89 to Asn-95.
834890	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1254 as residues: Arg-8 to Lys-13, Gly-35 to Lys-42, Ala-48 to Lys-54, Ala-105 to Leu-110, Gly-150 to Val-157, Phe-164 to Asn-173.
835079	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1255 as residues: Ser-53 to Pro-60.
835554	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1256 as residues: Ile-31 to Ile-38, Asp-116 to Arg-121, Phe-246 to Leu-251, Lys-280 to Tyr-291, Met-363 to Arg-373, Gly-381 to Trp-386.
835723	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1258 as residues: Glu-20 to Thr-26, Trp-47 to Ser-57, Pro-98 to Asn-105, Pro-124 to Phe-129, Ala-173 to Val-183, Lys-190 to Ser-196, Asn-277 to Asn-284, Glu-297 to Phe-306, Thr-322 to Lys-327, Gln-372 to Val-383, Pro-387 to Gly-395, Ser-406 to Thr-415, Arg-432 to Thr-442.
835791	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1259 as residues: Ala-4 to Gly-10.
835817	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1260 as

	residues: Glu-37 to Leu-43.
835840	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1261 as residues: Gln-1 to Asn-6, Pro-18 to Ile-31.
836048	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1262 as residues: Lys-1 to Lys-11, Tyr-27 to Glu-35, Glu-61 to Gly-68.
836898	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1263 as residues: Gln-94 to Lys-102, Gly-140 to Thr-154, Arg-173 to Asp-196, Thr-201 to Asp-206, Glu-241 to Gly-248.
836927	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1264 as residues: His-1 to Arg-12.
837344	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1265 as residues: Pro-15 to Ile-24.
837789	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1266 as residues: Ser-1 to Trp-7, Asp-47 to Ile-52, Pro-70 to Ser-80, Cys-89 to Thr-98, Ala-131 to Ser-142, Phe-169 to Cys-176, Gly-183 to Ser-193, Phe-202 to Pro-209, Arg-243 to Ala-249, Ser-256 to Lys-265, Arg-277 to Asp-284.
838754	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1268 as residues: Phe-27 to Ser-37, Tyr-91 to Arg-96, Pro-156 to Gln-164, Cys-207 to Val-216, Met-242 to Tyr-251.
839561	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1271 as residues: Arg-2 to Gly-7, Arg-16 to Gln-22, Phe-41 to Gly-49, Ala-60 to Asn-74, Leu-125 to Gln-131, Asp-170 to Pro-175, Ala-209 to Arg-218, Glu-222 to Glu-258, Ala-265 to Ser-300.
839816	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1272 as residues: His-32 to Arg-37, Ser-42 to Ser-48, Glu-77 to Glu-88.
840068	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1273 as residues: Ala-1 to Gln-14.
840279	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1274 as residues: Ala-1 to Asp-15.
840538	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1276 as residues: Ala-8 to Pro-13, Pro-18 to Gln-26, Lys-107 to Pro-114, Ala-149 to Arg-157, Ile-294 to Leu-299, Ser-356 to Pro-363, Pro-384 to Phe-392, Ala-474 to Gly-481, Ala-489 to Tyr-494, Pro-512 to Lys-517, Arg-623 to Thr-630, Lys-673 to Ser-678, Thr-703 to His-709, Arg-714 to Arg-720, Gly-755 to Glu-766.
840549	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1278 as residues: Ala-5 to Lys-15, Pro-28 to Gln-34, Tyr-105 to His-111, Gln-150 to Cys-157.
840557	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1280 as residues: Gly-34 to Leu-40, Thr-125 to Gly-134, Ala-148 to Arg-156, Lys-196 to Lys-215.
840561	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1281 as residues: Ser-21 to Phe-30.
840562	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1282 as residues: Gln-33 to Arg-41, Tyr-66 to Glu-71, Thr-112 to Gly-118, Thr-141 to Gly-148, Thr-160 to Cys-168, Arg-171 to Gly-177, Thr-180 to Pro-191, Glu-217 to Asp-225, Asp-236 to Lys-243.
840564	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1283 as residues: Val-13 to Pro-19, Gln-34 to Gly-39.
840600	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1285 as residues: Leu-26 to Ile-39.
840620	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1288 as residues: Ser-17 to Ser-26, His-32 to Gly-42, Thr-78 to Gln-83, Asp-130 to Leu-136, Arg-158 to Pro-164.
840626	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1290 as residues: Phe-7 to Tyr-13, Pro-19 to Ala-35, Asp-87 to Leu-96, Lys-98 to Glu-105, Glu-120 to Leu-133.
840638	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1291 as

	residues: Gly-8 to Leu-13, Gly-21 to Ser-31, Arg-45 to Arg-54.
840649	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1292 as residues: Asn-30 to Thr-37, Asp-44 to Lys-52, Ser-71 to Asp-80, Glu-127 to Glu-133, Arg-162 to Ala-173, Glu-191 to Leu-199.
840651	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1293 as residues: Gly-14 to Glu-38, Asn-90 to Lys-100, Lys-150 to Val-158, Ser-166 to Gly-175.
840681	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1295 as residues: Thr-25 to Gly-31, Pro-86 to Trp-97, Ser-132 to Phe-138.
840682	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1296 as residues: Arg-12 to Lys-19, Asn-30 to Gly-36, Asp-50 to Gly-57, Glu-64 to Thr-69, Thr-79 to Lys-91, Gln-110 to Thr-115, Arg-223 to Gln-229, Asp-255 to Asp-260, Arg-278 to Gly-287, Glu-294 to Gln-300, Glu-433 to Glu-451, Leu-474 to Glu-479, Asp-490 to Leu-498, Gln-519 to Asp-527, Tyr-566 to Asp-575.
840684	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1297 as residues: Pro-1 to Ala-9, Val-56 to Val-63, Gly-86 to Glu-91.
840697	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1298 as residues: Pro-9 to Arg-15, Pro-36 to Ser-42, Ser-65 to Phe-72, Gly-99 to Ser-105, Ala-122 to Phe-129.
840698	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1299 as residues: Thr-75 to Pro-84, His-94 to Met-99, Asp-149 to Ile-168, Asn-370 to Asn-375, Ser-384 to Lys-392, His-427 to Tyr-438.
840708	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1300 as residues: Ala-27 to Ser-36.
840714	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1301 as residues: Gly-1 to Gly-20, Arg-54 to His-59, Asn-89 to Leu-95, Ser-119 to Lys-125, Trp-127 to Cys-133, Gln-175 to Gln-185, Asp-213 to Lys-222, Pro-267 to Gln-275, Asp-306 to Asp-313, Thr-321 to Cys-331.
840716	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1302 as residues: Asn-40 to Thr-45, His-210 to Pro-215, Glu-369 to Thr-375, Lys-383 to Leu-397, Pro-438 to Ile-447, Pro-510 to Tyr-520, Arg-528 to Arg-533, Thr-549 to Thr-555.
840721	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1303 as residues: Arg-1 to Arg-7, Pro-29 to Lys-56, Asp-103 to Arg-108, Tyr-122 to Ser-127, Gly-219 to Glu-227, Asp-250 to Glu-255, Glu-294 to Pro-301, Ala-321 to Tyr-327, Arg-367 to Pro-373, Glu-396 to Asn-405, Gly-411 to Arg-418, Asn-433 to Lys-441.
840735	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1304 as residues: Glu-1 to Gly-11, Thr-20 to Asp-40, Gly-51 to Glu-61, Ala-64 to Leu-78, Leu-82 to Arg-94.
840738	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1305 as residues: Gln-26 to Asn-34.
840745	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1306 as residues: Gln-7 to Gly-12, Leu-60 to Pro-65, Arg-85 to Lys-99, Ser-132 to Pro-145, Pro-150 to Asp-155, Pro-183 to Asn-193, Arg-200 to Tyr-206.
840747	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1307 as residues: Gln-1 to Asp-15, Ile-35 to Glu-41, Leu-66 to Asn-71, Leu-73 to Pro-79, Gln-87 to Lys-94, Val-117 to Arg-123, Pro-144 to Tyr-150.
840756	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1308 as residues: Arg-8 to Gln-19, Arg-25 to Lys-38.
840776	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1309 as residues: Val-2 to Pro-10, Ser-28 to Ala-33, Pro-39 to Tyr-44, Thr-46 to Trp-55, Ser-64 to Ser-72, Ala-103 to Pro-109, Pro-111 to Gln-118.
840784	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1310 as residues: Pro-9 to Gly-20, Asn-32 to Leu-42, Asn-60 to Lys-70, Pro-76 to Gln-81, Glu-86 to Val-93, Arg-106 to Arg-111, Lys-176 to Asn-183.
840788	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1311 as residues: Ser-1 to Gln-8, Val-40 to Ser-49, Arg-105 to Lys-110.

840794	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1312 as residues: Arg-1 to Gln-14. Arg-43 to Glu-54.
840797	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1313 as residues: Gly-1 to Arg-9. Asn-31 to Asp-37. Arg-44 to Asn-53. Gly-62 to Lys-77, Thr-123 to Ile-137. Gly-389 to Thr-394, Lys-486 to Asn-493. Glu-512 to Phe-520. Met-555 to Lys-560. Leu-618 to Ser-623. Ile-698 to Glu-706, Gly-723 to Leu-730, Ala-773 to Gln-790.
840818	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1315 as residues: Pro-1 to Ile-12. Asp-30 to Tyr-35. Leu-38 to Pro-45. Lys-54 to Thr-60. Thr-75 to Leu-80, Asp-92 to Tyr-100, Ile-133 to Thr-138, Thr-194 to Glu-199, Asp-233 to Leu-239. Met-243 to Ala-251. Asp-254 to Glu-261.
840822	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1316 as residues: Val-100 to Tyr-106, Ala-127 to His-135, Gln-153 to Lys-158, Gly-214 to Glu-219. Gln-236 to His-244. Lys-253 to Tyr-258.
840846	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1318 as residues: Ala-20 to Thr-27, Glu-47 to Tyr-57, Tyr-87 to Lys-95, Pro-121 to Ala-127, Pro-208 to Ala-224.
840848	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1319 as residues: Arg-77 to Asn-82, Glu-119 to Arg-124, Gln-156 to Thr-162. Lys-209 to Lys-215.
840860	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1320 as residues: Ile-27 to Asp-41. Glu-43 to Ala-58, Glu-149 to Glu-154, Lys-158 to Ile-165, Glu-167 to Gly-189. Glu-242 to Phe-247, Arg-259 to Phe-268, Ile-283 to Val-291, Thr-295 to Thr-307, Glu-328 to Asp-338. Asp-372 to Gly-387.
840871	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1322 as residues: Gly-31 to Tyr-38. Leu-40 to Leu-45. Pro-203 to Trp-208.
840874	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1323 as residues: Ala-23 to Gly-28.
840878	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1324 as residues: Thr-40 to Glu-46, Pro-69 to Arg-76. Glu-108 to Asp-150.
840880	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1325 as residues: Ser-5 to Lys-14, Phe-32 to Gln-37.
840884	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1326 as residues: Leu-4 to Ser-10.
840926	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1328 as residues: Met-6 to Thr-15, Ser-17 to Phe-37, Ser-148 to Lys-154, Lys-260 to Phe-276, Glu-285 to Ile-292. Lys-410 to Asp-424.
840932	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1329 as residues: Tyr-75 to Pro-83, Ile-181 to Gln-191, Glu-267 to Leu-275, Met-301 to Ala-307, Phe-322 to Gln-328, Met-371 to Gly-381, Gln-458 to Leu-463, Glu-474 to Lys-480. Lys-551 to Ser-558.
840940	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1330 as residues: Ser-26 to Thr-34, Thr-80 to Lys-88.
840947	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1331 as residues: Ile-1 to Arg-11, Pro-19 to Gln-46, Ala-55 to Pro-62, Cys-65 to Cys-82, Lys-93 to Pro-108.
840964	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1333 as residues: Ser-41 to Cys-46.
840979	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1334 as residues: Tyr-10 to His-27, Tyr-31 to Arg-41, Thr-44 to Leu-61, Cys-68 to Phe-73, Lys-98 to Glu-106, Gln-132 to Val-142, Glu-184 to Leu-191.
840984	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1335 as residues: Arg-38 to Gln-48, Met-137 to Asn-144, Gln-167 to Gln-172, Lys-182 to Gln-189. Gln-196 to Glu-206, Ile-210 to Glu-223. Gln-225 to Arg-246, Glu-250 to Thr-269. Gln-296 to Ile-318. Arg-323 to Glu-328, Tyr-337 to Lys-343, Glu-349 to Thr-357. Ser-393 to Glu-403. Arg-405 to Ile-427, Arg-431 to Glu-442. Leu-446 to Lys-473. Glu-475

	to Leu-486, Ile-488 to Asp-503, Ser-505 to Arg-623, Ala-625 to Asn-631, His-634 to Trp-792, Gly-799 to Gly-870, Arg-872 to Glu-929, Ser-931 to Pro-954, Ala-957 to Ala-977, Glu-982 to Trp-1000.
840986	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1336 as residues: Asp-41 to Tyr-51.
840988	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1337 as residues: Pro-17 to Leu-31, Ser-95 to Val-100, Lys-123 to Gly-129.
840990	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1338 as residues: Met-9 to Glu-16, Glu-41 to Trp-47, Arg-55 to Glu-62, Asp-135 to Ile-146, Gly-154 to Gly-160, Met-207 to Phe-214, Ser-245 to Lys-252, Gln-282 to Gln-288.
841009	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1340 as residues: Glu-12 to Thr-27, Met-45 to Asn-52, Tyr-79 to Thr-87, Asp-97 to Gly-102, Met-112 to Asp-120, Pro-141 to Tyr-155.
841012	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1341 as residues: Lys-36 to Ile-44, Arg-49 to Lys-69.
841016	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1342 as residues: Cys-75 to His-82, Asp-126 to Tyr-135, Pro-144 to Tyr-155, Gly-179 to Trp-198, Tyr-201 to Met-208, Pro-226 to Lys-234, Gln-249 to Asp-267.
841017	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1343 as residues: Gln-1 to Trp-19.
841021	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1344 as residues: Glu-58 to Gly-63, Leu-75 to Leu-82.
841032	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1345 as residues: Pro-1 to Gly-13, Pro-30 to Ser-57, Gln-61 to Thr-77, Arg-82 to Thr-88, Pro-100 to Lys-105, Gly-119 to Gly-126.
841051	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1346 as residues: Asn-1 to Lys-6, Thr-16 to Glu-21, Asn-45 to Ser-58, Asp-68 to Ser-75.
841064	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1347 as residues: Asp-53 to Pro-58, Glu-78 to Lys-85, Pro-95 to Arg-102, Ser-142 to Arg-148, Lys-209 to Arg-214, Lys-241 to Gly-246, Ser-287 to Leu-292, Lys-307 to Val-313, Arg-389 to Gln-394.
841069	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1348 as residues: Thr-1 to Trp-14, Lys-27 to Leu-44, Glu-59 to Arg-73, Lys-87 to Phe-95, Pro-160 to Asn-166, Leu-212 to Ile-220, Arg-236 to Asp-243.
841072	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1349 as residues: Pro-7 to Arg-12, Phe-71 to Gln-76, Arg-82 to Asp-98, Ala-108 to Glu-128.
841078	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1350 as residues: Arg-32 to Ala-39.
841080	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1351 as residues: Glu-1 to Gly-7, Glu-25 to Gly-33, Ala-54 to Phe-60, Gly-64 to Gln-108, Glu-116 to Ser-122, Pro-130 to Asn-138, Gln-141 to Lys-153, Arg-164 to Ser-172, Leu-186 to Met-194, Pro-197 to Tyr-205, Asp-218 to Lys-229, Thr-236 to Ser-246, Ala-259 to Trp-266, Pro-281 to Pro-287, Cys-291 to Gln-298.
841092	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1353 as residues: Glu-45 to Lys-50.
841095	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1354 as residues: Lys-1 to Ser-19, Gly-33 to Gly-63, Gly-77 to Pro-89, Ser-164 to Ser-180, Ser-233 to Lys-238, Lys-267 to Leu-286.
841096	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1355 as residues: Gly-5 to Leu-12, Tyr-18 to Asp-25, Ile-88 to Ala-125, Ser-129 to Tyr-141, Gln-191 to Gln-196, Thr-290 to Asn-296, Thr-301 to Thr-309, Leu-360 to Ala-365, Leu-367 to Gly-378, Pro-398 to Gly-418, Pro-443 to Gly-454.
841102	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1356 as residues: Ser-61 to Leu-71.
841108	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1358 as residues: Ala-8 to Leu-20, Lys-27 to Arg-33, Arg-40 to Ala-50, Asp-77 to Glu-84,

	Asn-99 to Gly-109.
841119	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1360 as residues: Lys-6 to Ala-14, Ile-68 to Asn-73, Val-84 to Leu-90, Glu-110 to Val-116, Leu-182 to Gly-190, Tyr-264 to Phe-270, Ile-300 to Lys-306, Pro-354 to Glu-367.
841124	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1361 as residues: Ser-21 to Thr-26.
841143	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1363 as residues: Thr-1 to Lys-9, Pro-20 to Gly-27, Gly-29 to Gly-52, Arg-54 to Gly-61, Gly-69 to Gly-75, Ser-79 to Gly-96, Val-130 to Arg-135, His-207 to Asp-212, Val-296 to Leu-310, Arg-327 to Asn-334.
841148	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1364 as residues: Pro-1 to Met-43, Pro-55 to Ala-66, Pro-118 to Glu-128, Arg-181 to Lys-192, Tyr-197 to Thr-207, Trp-278 to Cys-284, Arg-334 to Asp-349.
841155	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1367 as residues: Gly-9 to Arg-24, Glu-69 to Met-74, Leu-86 to Leu-92, Asp-95 to Arg-115.
841163	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1370 as residues: Gly-29 to Gly-35, Ala-37 to Ala-48, Arg-97 to Thr-102, Arg-114 to Leu-119, Lys-144 to Lys-155.
841169	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1371 as residues: Ala-31 to Thr-69, Pro-90 to Pro-95, Pro-117 to Trp-126, Pro-128 to Arg-136.
841172	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1372 as residues: Gly-17 to Arg-35, His-76 to Pro-90, Pro-92 to Cys-103.
841174	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1373 as residues: Arg-1 to Arg-8, Arg-14 to Phe-19.
841179	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1374 as residues: Leu-4 to Met-10, Leu-17 to Tyr-36, Arg-38 to Asp-63, Tyr-82 to Glu-90, Pro-97 to Gly-134, Arg-137 to Pro-148, Thr-160 to Lys-171, Tyr-183 to Asn-228, Gln-249 to Asn-258, Arg-263 to Glu-271, Arg-277 to Gln-296, Phe-298 to Asp-320, Glu-322 to Lys-329, Thr-337 to Thr-343, Glu-356 to Arg-363, Gly-371 to Asp-384.
841183	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1375 as residues: His-1 to Ser-27, Arg-60 to Arg-73, Arg-96 to Asp-124, Asp-131 to Gly-143, Lys-145 to Glu-150.
841186	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1376 as residues: Leu-7 to Val-18, Ser-27 to Pro-57, Arg-124 to Thr-135, Pro-212 to Ser-230, Gly-282 to Lys-287, Lys-441 to Lys-448.
841204	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1377 as residues: Lys-29 to Arg-35, Glu-81 to Arg-87, Ala-251 to Glu-261, Thr-266 to Gly-271, Thr-289 to Glu-295, Gly-328 to Tyr-334, Phe-432 to Lys-438, Asn-440 to Trp-458.
841206	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1378 as residues: Val-17 to Pro-25, Thr-55 to Asp-70, Lys-75 to Leu-81.
841207	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1379 as residues: Pro-9 to Glu-15, Arg-22 to Trp-32, Ser-54 to Glu-62, Asn-92 to Gly-103.
841211	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1380 as residues: Arg-7 to Gly-12, Met-42 to Ser-58, Gln-65 to Asn-73, Glu-91 to Ala-99, Pro-103 to Tyr-109, Arg-174 to Ala-179, His-189 to Gln-196, Asn-208 to Pro-219.
841225	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1381 as residues: Ala-32 to Ala-40, Glu-93 to Phe-103, Lys-173 to Thr-189.
841237	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1383 as residues: Arg-2 to Gln-12, Lys-76 to Ala-86, Tyr-155 to Lys-163, Glu-228 to Leu-234, Lys-263 to Lys-273, Ile-286 to Lys-296.
841241	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1384 as residues: Asp-41 to Ile-52, Thr-59 to Lys-64, Glu-75 to Asn-89, Thr-99 to Thr-105.
841259	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1385 as residues: His-1 to Cys-22, Pro-24 to Pro-30, Tyr-84 to Ser-90, Ser-108 to Glu-118, Val-126 to Arg-143, Asp-175 to Gln-181, Ser-217 to Gly-224, Cys-262 to Cys-270.

	Tyr-296 to Glu-302, Thr-317 to Thr-324, Gln-341 to Gln-348. Trp-394 to Pro-399.
841260	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1386 as residues: Ala-25 to Glu-32, Ala-48 to Phe-53, Ser-69 to Ser-76, Asp-80 to Glu-86, Ser-125 to Ser-132. Ser-168 to Glu-179, Asn-201 to Ala-206, Lys-216 to Ile-246, Met-259 to Asn-272, Tyr-277 to Gln-287.
841264	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1387 as residues: Met-34 to Gly-50, Asp-69 to Trp-90, Asp-99 to Lys-107, Val-164 to Thr-170.
841311	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1389 as residues: Arg-4 to Val-15.
841313	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1390 as residues: His-6 to Gly-16, Gly-60 to Pro-95, Pro-125 to Gly-131, Gly-138 to Ala-147, Gln-173 to Glu-178.
841322	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1392 as residues: Lys-6 to Arg-23, Ser-74 to Arg-86, Lys-116 to Lys-122, Ser-127 to His-133, Ser-269 to Pro-275, Glu-344 to Phe-350, Gly-356 to His-362.
841331	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1393 as residues: Ser-45 to Lys-67, Asp-155 to Asp-172, Gln-193 to Ile-199, Gln-271 to Glu-285.
841332	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1394 as residues: Glu-8 to Ser-13, Lys-20 to Glu-27, Arg-81 to Ser-94, Thr-147 to Ile-154, Asn-200 to Glu-212, Asn-235 to Gly-244, Leu-433 to Thr-439, Pro-444 to Asn-455, Ser-470 to Asp-476, Ser-492 to Met-499, Glu-535 to Pro-547, Glu-703 to Thr-709, Glu-719 to Thr-726, Asn-802 to Leu-807, Asn-820 to Arg-825, Lys-830 to Tyr-836, Thr-838 to Thr-850, Ser-882 to Ser-894, Lys-944 to Gly-952, Gly-969 to Val-977, Glu-984 to Asn-990, Arg-996 to Lys-1001, Pro-1032 to Leu-1039, Thr-1050 to Gly-1058, Val-1103 to Arg-1108, Pro-1160 to His-1169, Tyr-1180 to Ser-1187, Glu-1211 to Ser-1217, Pro-1277 to Leu-1282.
841338	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1395 as residues: Ser-13 to Ser-18, Phe-48 to Ser-54.
841345	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1396 as residues: Trp-83 to Thr-89, Ser-135 to Asn-140, Ser-185 to Cys-190, Tyr-209 to Glu-220, Val-224 to Glu-232, Leu-258 to Asn-263, Ser-306 to Asn-312, Thr-319 to Glu-327, Thr-365 to Ile-373, Gly-417 to Cys-429, Lys-439 to Val-445, Lys-464 to Leu-469, Leu-477 to Asn-485, Arg-546 to Val-554, Glu-598 to Gly-607, Pro-634 to Ser-639, Asn-730 to Ala-746, Lys-812 to Gln-817, Glu-819 to Lys-835, Leu-867 to Asn-875, Leu-902 to Arg-910.
841349	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1397 as residues: Asp-13 to Arg-18, Pro-36 to Arg-43, Gly-66 to Ser-74, Gly-87 to Lys-92, Asp-110 to Glu-115.
841417	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1399 as residues: Leu-102 to Ile-111, Pro-131 to Ile-337, Thr-339 to Asp-376.
841632	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1401 as residues: Arg-13 to Gly-40, Arg-46 to Glu-52, Gln-55 to Lys-69.
841771	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1403 as residues: Pro-22 to Gly-30, Asp-45 to Gln-56, Ser-67 to Ser-73.
841827	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1404 as residues: Thr-1 to Ser-20.
841835	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1405 as residues: Tyr-5 to Lys-13, Cys-52 to Arg-61, Cys-85 to Ala-91, Gly-122 to Asn-127.
842259	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1406 as residues: Pro-16 to Gly-23, Glu-37 to Pro-45, Gly-52 to Ser-57.
842463	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1407 as residues: Cys-74 to Tyr-79.
842595	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1408 as residues: Pro-93 to Ala-105, Ser-133 to Ser-142, Arg-150 to Glu-155, Lys-220 to Trp-

	226, Glu-257 to Lys-271, Gln-280 to Leu-289.
842722	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1409 as residues: Glu-9 to Arg-20, Ser-48 to Lys-56, Ile-69 to Glu-81, Pro-83 to Lys-89, Lys-94 to Ile-99, Pro-104 to Gly-110, Glu-116 to Asp-133, Ile-140 to Ser-154, Gln-206 to His-217, Pro-219 to Leu-231, Arg-237 to Lys-243, Gln-247 to Pro-256, Leu-271 to Thr-283, Lys-289 to Lys-294, Ser-338 to Lys-355, Gly-375 to Thr-381, Ser-428 to Pro-454, Gly-460 to Gln-467, Lys-480 to Lys-488.
842818	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1411 as residues: Ala-25 to Ala-30, Lys-32 to Ala-51, Gln-61 to Ala-68, Glu-83 to Lys-91, Phe-99 to Glu-105, Glu-123 to Gly-129.
843251	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1412 as residues: Pro-30 to Ser-40, Lys-47 to Thr-52, Val-59 to Pro-64, Lys-129 to Arg-134, Leu-169 to Asp-177.
843422	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1413 as residues: Thr-9 to Lys-20, Lys-25 to Cys-31, Pro-33 to Tyr-42, Asn-76 to Lys-84, Leu-102 to Trp-112.
843784	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1414 as residues: Leu-16 to Thr-24, Glu-41 to Gln-47, Lys-64 to Cys-72, Thr-87 to Ser-100, Pro-130 to Asn-143, Thr-163 to Asp-170.
844017	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1415 as residues: Leu-11 to Ile-17, Leu-30 to Met-45.
844138	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1416 as residues: Lys-19 to Thr-28, Arg-47 to Gln-52, Leu-73 to Leu-81, Asp-122 to Phe-131, Ala-135 to Ser-148, Pro-155 to Asp-163, Ser-184 to His-191, Leu-219 to Asn-225, Asp-238 to Thr-248, Pro-253 to Cys-259, Cys-356 to His-368, Ser-426 to Gly-435, Pro-467 to Cys-478, Glu-504 to Cys-509, His-553 to Gly-568, Ala-581 to Cys-586, Ala-595 to Cys-600, Arg-602 to Trp-608.
844194	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1418 as residues: Pro-23 to Arg-31, Gln-79 to Gln-85, Cys-93 to Cys-107, Pro-216 to Leu-222.
844394	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1419 as residues: Arg-1 to Phe-11.
844450	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1420 as residues: Ser-37 to Trp-43, Pro-47 to Thr-55, Arg-60 to Lys-69, Tyr-125 to His-131, Pro-187 to Lys-195, Gly-346 to Lys-351.
844535	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1422 as residues: Asp-8 to Ala-18, Ser-47 to Ala-52, Thr-62 to Arg-69, Pro-119 to Asp-126, Trp-164 to Thr-170, Ala-206 to Ala-213, Pro-230 to Gly-235, Lys-304 to Lys-314, Lys-341 to Val-347, Tyr-387 to Thr-398.
844644	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1423 as residues: Ala-9 to Asp-16, Asn-78 to Tyr-86.
844653	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1424 as residues: Arg-1 to Gly-8, Ala-30 to Gln-36.
844796	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1426 as residues: His-12 to His-22.
844812	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1427 as residues: Gly-281 to Arg-290, Ala-349 to Ser-355, Glu-378 to Asp-388.
844894	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1428 as residues: Pro-2 to Phe-8, Ser-13 to Ala-34, Pro-37 to Phe-43, Lys-63 to Gly-73, Cys-88 to Asp-93, Gly-98 to Trp-103, Cys-273 to Ile-287, Ile-290 to Ser-296.
845361	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1429 as residues: Met-10 to Ile-21, Glu-108 to Lys-122, Lys-272 to Gly-280, Gly-298 to Lys-304, Trp-364 to Lys-369.
845620	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1430 as residues: Thr-62 to Ala-67, Leu-96 to Glu-101, Cys-184 to Trp-190.
845639	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1431 as residues: Arg-41 to Arg-48, Met-72 to Val-79, Gln-81 to Trp-89, Ala-96 to Asp-101,

	Arg-110 to Gly-118, Asn-126 to Arg-135, Ala-144 to Asp-149, Leu-199 to Lys-213, Gln-245 to Glu-256, Arg-261 to Thr-267.
845660	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1432 as residues: Gly-5 to Leu-17, Arg-19 to Arg-29, Pro-36 to Arg-50, Arg-60 to Pro-67, Gln-133 to Leu-150, Gln-168 to Phe-187, Pro-189 to Gln-194, Asp-240 to Gly-251, Thr-308 to Cys-317, Val-325 to Glu-331, Leu-354 to Pro-369, Lys-381 to Cys-388, Arg-410 to Phe-417.
845720	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1433 as residues: Thr-1 to Glu-11, Arg-21 to Pro-27, Pro-44 to His-49, Glu-56 to Leu-69, Ala-74 to Gly-80, Phe-82 to Pro-87.
845897	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1435 as residues: Gly-1 to Ser-9, Gly-31 to Ser-38, Arg-52 to Val-68, Leu-71 to Glu-84.
845922	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1436 as residues: Asn-1 to Pro-6, Pro-29 to Gln-36, Glu-95 to Arg-100, Pro-150 to Met-157, Ser-272 to Tyr-278, Gly-289 to Arg-294, Lys-397 to Ser-403.
846040	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1438 as residues: Cys-6 to Ser-16, Glu-52 to Tyr-58, Asn-144 to Lys-153.
846073	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1439 as residues: Arg-6 to Thr-16, Ile-43 to Gln-48, Leu-131 to Gly-139, Gly-147 to Asp-155, Asp-191 to Asp-198, Gly-204 to Thr-214.
846257	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1440 as residues: Lys-24 to Phe-44, Arg-58 to Gly-64, Ser-69 to Val-75, Lys-83 to Leu-90, Lys-93 to Glu-106.
HTXPN06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1441 as residues: Gly-1 to His-8.
HWAFU16R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1443 as residues: Ile-29 to Lys-34.
HOEMT44R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1445 as residues: Asp-73 to Lys-79.
HE2OW04R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1446 as residues: Cys-1 to Asn-6, Met-41 to Thr-51, Lys-77 to Thr-82.
HFCFG25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1447 as residues: Lys-29 to Ile-37, Arg-42 to Lys-47.
HAPQP94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1448 as residues: Pro-18 to Arg-23, Ala-43 to Ser-48.
H2CBI37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1449 as residues: Gly-5 to Lys-19, Phe-26 to Trp-31.
HCRNC25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1451 as residues: Leu-2 to Asn-8.
H2LAY26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1453 as residues: Pro-20 to His-36.
HAPQA06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1454 as residues: Tyr-15 to Ala-22, Ser-68 to Gly-74.
HBGOK18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1456 as residues: Gly-1 to Tyr-6, Asp-40 to Thr-47, Lys-91 to Glu-97.
HTWKF26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1458 as residues: Gly-31 to Gly-39.
HTAHR89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1459 as residues: Asp-73 to Gly-78.
HOELC27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1461 as residues: Asn-19 to Gln-25, Arg-33 to Ala-42, Pro-92 to Lys-99.
HWLVW62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1463 as residues: Lys-6 to Phe-13, His-25 to Ser-30, Glu-35 to Ala-41, Pro-57 to Gly-62.
HFKHD94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1465 as residues: Leu-1 to Gly-6, Pro-29 to Gly-42, Lys-52 to Gly-62.
HOFOA89R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1467 as

	residues: Ala-20 to Lys-29, Arg-48 to Ile-56.
HCROL58R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1470 as residues: Lys-1 to Ser-16.
HCHMV24R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1473 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41.
HCHPT49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1474 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-70.
HCHPF59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1477 as residues: Arg-10 to Lys-22.
HS2IA81R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1478 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76.
HCRNC17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1479 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76, Lys-107 to Pro-112.
HISDJ39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1480 as residues: Gly-4 to Lys-10, Gln-36 to Glu-41, Arg-61 to Arg-76.
HASCG71R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1482 as residues: Lys-6 to Ile-13.
HOEMO43R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1483 as residues: Lys-31 to Gln-43.
HSYDG18R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1486 as residues: Pro-1 to Glu-7, Asp-42 to Gly-47, Leu-61 to Glu-69, Lys-97 to Ile-107, Asp-115 to Gly-120.
HACAC47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1490 as residues: Ala-18 to Asp-26.
HLQFY41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1491 as residues: Val-11 to Asp-16, Glu-46 to Arg-51, Pro-55 to Lys-61, Lys-82 to Val-87.
HOFMO83R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1492 as residues: Thr-31 to Asp-39, Thr-52 to Gly-60.
HFTDR22R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1493 as residues: Glu-1 to Trp-13.
HOEKC39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1495 as residues: Tyr-25 to Phe-32.
HOSNR06R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1498 as residues: Thr-1 to Tyr-7.
HCQDL20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1499 as residues: Ser-12 to His-21.
HFKHD49R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1503 as residues: Ala-42 to Glu-68.
H6EAQ15R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1506 as residues: Ala-1 to Leu-9.
HCFLM34R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1507 as residues: Lys-7 to Thr-13, Asp-24 to Thr-30, Gly-39 to Glu-52, Leu-70 to Ile-78.
HKIXL19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1510 as residues: Thr-2 to Asn-12, Gly-14 to Arg-24.
HAJRB09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1512 as residues: Pro-1 to Glu-8, Ala-10 to Gly-26.
HAPNI86R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1513 as residues: Glu-53 to Ser-59, His-121 to Gln-130.
HAPRJ22R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1515 as residues: Gly-49 to Glu-64, Phe-76 to Thr-81.
HADGE45R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1518 as residues: Arg-1 to Gln-26, Phe-59 to Lys-68.
HTXPN11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1519 as residues: Asp-1 to Lys-8, Asp-35 to Glu-41.
HCDBN37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1520 as residues: Cys-1 to Leu-15.

HABGF46R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1527 as residues: Arg-11 to Arg-20, Asn-42 to Pro-57, Arg-64 to Ser-81.
HOELC15R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1528 as residues: His-8 to Gly-18, Gln-56 to Arg-61.
H2LAR26R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1529 as residues: Glu-11 to Asn-16, Lys-38 to Glu-43, Ala-62 to Asp-67, Asp-80 to Ser-101.
H2LAV85R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1530 as residues: Pro-14 to Thr-25, Asp-89 to Gln-102, Ile-121 to Thr-131.
HBSDC92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1531 as residues: Arg-1 to Leu-11.
HUTHN01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1532 as residues: Pro-34 to Ser-42, Cys-82 to Lys-89.
H2LAW03R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1533 as residues: Arg-120 to Arg-127.
HOEMO60R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1534 as residues: Pro-6 to Arg-11, Phe-18 to Asn-23, Leu-36 to Thr-41.
HOELF72R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1537 as residues: Arg-1 to Pro-14, Gln-47 to Cys-52.
HAPNX59R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1538 as residues: Cys-19 to Ser-25, Asp-28 to Trp-34, Lys-71 to Trp-76, Glu-112 to Lys-120.
HBJJS17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1539 as residues: His-14 to Glu-26.
H2CBN02R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1542 as residues: Ala-1 to Pro-9, Arg-20 to Val-25.
H2CBV68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1543 as residues: Pro-41 to Asp-46, Leu-56 to Lys-61, Ala-72 to Thr-83, Lys-100 to Asn-106, Leu-125 to Thr-133.
H6EDK07R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1544 as residues: Glu-32 to Glu-40, Val-45 to Thr-51, Pro-61 to Arg-67.
H2CBN54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1547 as residues: Cys-36 to Tyr-44, Glu-55 to Asp-61, Arg-79 to Pro-84, Asp-89 to Pro-105, Cys-108 to Ala-118, Lys-126 to Gly-142.
HWHPX50R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1549 as residues: Pro-35 to Tyr-41.
HAPQD84R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1550 as residues: Lys-32 to Glu-39.
HAMGQ78 R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1554 as residues: Arg-46 to Arg-60, Glu-69 to Gly-78.
HODEV64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1555 as residues: Glu-1 to Gly-27, Asn-34 to Phe-48, Gly-63 to Gly-68.
HOEMK78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1558 as residues: Asp-27 to Gly-34, Ser-41 to Glu-49, Val-55 to Gln-62.
H2CBD13R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1559 as residues: Ile-17 to His-22, Ser-24 to Arg-29.
HCFMU61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1560 as residues: Ser-10 to Asp-20, Leu-22 to Pro-36, Ser-42 to Lys-57, Gln-102 to Glu-110.
HOSNE94R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1561 as residues: Arg-1 to Glu-6, Asp-74 to Ser-79, Asp-122 to Thr-127.
HHBEF47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1563 as residues: Arg-25 to His-31, Ala-50 to Ala-55.
HOSNR67R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1566 as residues: Val-56 to Cys-61, Thr-108 to Gln-122, Gln-125 to Lys-131, Glu-140 to Leu-146.
H2LAV92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1567 as residues: Leu-3 to Ala-10, Pro-12 to Gly-21, Pro-32 to Pro-38, Ala-58 to Lys-64, Lys-67 to Val-75, Asp-92 to Leu-103.

HCLBZ27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1570 as residues: Asp-12 to Glu-18, Ala-22 to Ile-28, Ala-48 to Gly-60.
H2LAV11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1571 as residues: Thr-5 to Thr-14, Arg-20 to His-25, Arg-35 to Gly-40, Lys-58 to Arg-66, His-101 to Ser-107, Arg-111 to Lys-125.
HOEMJ56R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1573 as residues: Lys-27 to Tyr-48.
HDPLP40R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1576 as residues: Gly-1 to Cys-24, Cys-27 to Gly-43, Ala-46 to Trp-54, Ala-56 to Arg-68, Phe-83 to Arg-93.
HABAD57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1578 as residues: Gly-3 to Gln-16, Pro-36 to Ala-41.
H2CBL68R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1581 as residues: Pro-19 to Val-24, Thr-31 to Gln-38, His-103 to Lys-114, Arg-129 to Leu-137, Pro-139 to Ser-146.
HNTNE17R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1582 as residues: Val-8 to Lys-15, Tyr-25 to Asn-35, Lys-48 to Lys-53, Leu-77 to Asn-87, Asp-103 to Glu-108.
HBJLR37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1583 as residues: Asn-1 to His-11, Pro-82 to Glu-89, Pro-91 to Asp-96, Arg-103 to Met-109.
HOSNG20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1584 as residues: Thr-50 to Lys-55.
HBGNY11R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1586 as residues: Thr-10 to Trp-15, Leu-24 to Ala-30, Leu-32 to Glu-38, Asn-41 to Ala-59, Arg-81 to Asp-89, Lys-104 to Lys-111.
HOEKC80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1587 as residues: Pro-49 to Phe-55, Gly-82 to Gly-88.
HFCES53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1589 as residues: Thr-12 to Leu-18.
HWAFE36R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1592 as residues: Glu-2 to Ile-9, Glu-34 to Lys-42.
HTXPF20R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1594 as residues: Gly-4 to Thr-13.
HCRMD09R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1595 as residues: Thr-2 to Asn-10, Glu-22 to Gln-30, Ser-58 to Gln-80, Gln-88 to Phe-96, Thr-99 to Tyr-104, Lys-110 to Asp-115.
HAJRB47R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1596 as residues: Trp-18 to Ser-26, Asp-91 to Trp-99.
HAHCR61R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1603 as residues: Ser-17 to Cys-25.
HAPQK19R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1609 as residues: Arg-1 to Lys-10, Ser-15 to Tyr-22, Gly-25 to Leu-31.
HBGOK25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1615 as residues: Thr-38 to Trp-45, Pro-63 to Gln-70, Pro-78 to Gln-85.
HBJKI05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1619 as residues: Pro-43 to Trp-50.
HBLGD42R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1621 as residues: Pro-17 to Pro-27, Pro-32 to Tyr-38, Ala-44 to Pro-49.
HCHAK80R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1627 as residues: Gln-3 to His-13, Gly-48 to Gly-55.
HCHMW79R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1628 as residues: Ser-16 to His-21, Ala-29 to Thr-35.
HCHOB92R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1629 as residues: Lys-20 to Lys-28, Ser-53 to Leu-60.
HCLBO01R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1630 as residues: Leu-1 to Leu-18.

HCRPC63R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1633 as residues: Glu-1 to Arg-28.
HCUDC51R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1634 as residues: Pro-22 to Gly-32. Trp-67 to Lys-81.
HDPFI40R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1635 as residues: Tyr-1 to Phe-6. Pro-9 to Asn-22. Arg-30 to Ala-38. Pro-47 to Lys-69.
HDPRZ54R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1637 as residues: Gly-1 to Ala-8.
HFAUO64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1640 as residues: Asn-7 to Lys-29.
HJMAU64R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1645 as residues: Leu-58 to Tyr-69.
HKBAC48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1647 as residues: Ser-16 to His-46. Arg-49 to Thr-58.
HKBAD57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1648 as residues: Thr-23 to Ser-30.
HODAY16R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1653 as residues: Pro-15 to Thr-20.
HOEMO27R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1655 as residues: Ala-7 to Ser-12.
HOEMO62R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1656 as residues: Ile-3 to Lys-11.
HOENU53R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1658 as residues: Lys-37 to Asn-44.
HOGAP33R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1659 as residues: Gln-29 to Asp-35. Gln-43 to Thr-49.
HOSNF25R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1661 as residues: Pro-29 to Arg-36.
HPIAC23R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1663 as residues: Thr-62 to Thr-69.
HRAAD31R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1664 as residues: Val-1 to Thr-6, Arg-64 to Arg-69.
HRADJ57R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1666 as residues: Val-11 to Gln-16.
HROAX48R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1667 as residues: Gly-7 to Thr-20.
HTWDH05R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1670 as residues: Ala-5 to Lys-11. Arg-29 to Ser-36.
HUTHF75R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1673 as residues: Lys-40 to Gly-47.
HWAFW07 R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1674 as residues: Phe-44 to Arg-49.
HWLLX91R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1676 as residues: Gly-29 to Asp-34.
HMIAI78R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1678 as residues: Lys-24 to Arg-29, Cys-34 to Ala-41.
HBGFJ39R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1679 as residues: Leu-21 to Asp-38.
HAMHH32 R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1680 as residues: Ala-1 to Cys-10. Glu-15 to Gln-21.
HOSNE37R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1683 as residues: Lys-17 to Thr-23.
HWAFE41R	Preferred epitopes include those comprising a sequence shown in SEQ ID NO. 1684 as residues: Ser-3 to Lys-8. Trp-92 to Leu-97.

The present invention encompasses polypeptides comprising, or alternatively consisting of, an epitope of the polypeptide sequence shown in SEQ ID NO:Y, or an epitope of the polypeptide sequence encoded by the cDNA in the related cDNA clone contained in a deposited library or encoded by a polynucleotide that hybridizes to the complement of an epitope encoding sequence of SEQ ID NO:X, or an epitope encoding sequence contained in the deposited cDNA clone under stringent hybridization conditions, or alternatively, under lower stringency hybridization conditions, as defined supra. The present invention further encompasses polynucleotide sequences encoding an epitope of a polypeptide sequence of the invention (such as, for example, the sequence disclosed in SEQ ID NO:X), polynucleotide sequences of the complementary strand of a polynucleotide sequence encoding an epitope of the invention, and polynucleotide sequences which hybridize to this complementary strand under stringent hybridization conditions or alternatively, under lower stringency hybridization conditions, as defined supra.

The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in an animal, preferably a mammal, and most preferably in a human. In a preferred embodiment, the present invention encompasses a polypeptide comprising an epitope, as well as the polynucleotide encoding this polypeptide. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an antibody response in an animal, as determined by any method known in the art, for example, by the methods for generating antibodies described infra. (See, for example, Geysen et al., Proc. Natl. Acad. Sci. USA 81:3998- 4002 (1983)). The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody can immunospecifically bind its antigen as determined by any method well known in the art, for example, by the immunoassays described herein. Immunospecific binding excludes non-specific binding but does not necessarily exclude cross- reactivity with other antigens. Antigenic epitopes need not necessarily be immunogenic.

Fragments which function as epitopes may be produced by any conventional means. (See, e.g., Houghten, R. A., Proc. Natl. Acad. Sci. USA 82:5131-5135 (1985) further described in U.S. Patent No. 4,631,211.)

In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, more preferably at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 20, at least 25, at least 30, at least 40, at least 50, and, most preferably, between about 15 to about 30 amino acids. Preferred polypeptides comprising immunogenic or antigenic epitopes are at least 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Additional non-exclusive preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as portions thereof. Antigenic epitopes are useful, for example, to raise antibodies, including monoclonal antibodies, that specifically bind the epitope. Preferred antigenic epitopes include the antigenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these antigenic epitopes. Antigenic epitopes can be used as the target molecules in immunoassays. (See, for instance, Wilson et al., Cell 37:767-778 (1984); Sutcliffe et al., Science 219:660-666 (1983)).

Similarly, immunogenic epitopes can be used, for example, to induce antibodies according to methods well known in the art. (See, for instance, Sutcliffe et al., supra; Wilson et al., supra; Chow et al., Proc. Natl. Acad. Sci. USA 82:910-914; and Bittle et al., J. Gen. Virol. 66:2347-2354 (1985). Preferred immunogenic epitopes include the immunogenic epitopes disclosed herein, as well as any combination of two, three, four, five or more of these immunogenic epitopes. The polypeptides comprising one or more immunogenic epitopes may be presented for eliciting an antibody response together with a carrier protein, such as an albumin, to an animal system (such as rabbit or mouse), or, if the polypeptide is of sufficient length (at least about 25 amino acids), the polypeptide may be presented without a carrier. However, immunogenic epitopes comprising as few as 8 to 10 amino acids have been shown to be sufficient to raise antibodies capable of binding to, at the very least, linear epitopes in a denatured polypeptide (e.g., in Western blotting).

Epitope-bearing polypeptides of the present invention may be used to induce antibodies according to methods well known in the art including, but not limited to, in vivo immunization, in vitro immunization, and phage display methods. See, e.g., Sutcliffe et al., supra; Wilson et al., supra, and Bittle et al., J. Gen. Virol., 66:2347-2354 (1985). If in vivo immunization is used, animals may be immunized with free peptide; however, anti-peptide antibody titer may be boosted by coupling the peptide to a macromolecular carrier, such as keyhole limpet hemacyanin (KLH) or tetanus toxoid. For instance, peptides containing cysteine residues may be coupled to a carrier using a linker such as maleimidobenzoyl- N-hydroxysuccinimide ester (MBS), while other peptides may be coupled to carriers using a more general linking agent such as glutaraldehyde. Animals such as rabbits, rats and mice are immunized with either free or carrier- coupled peptides, for instance, by intraperitoneal and/or intradermal injection of emulsions containing about 100 μg of peptide or carrier protein and Freund's adjuvant or any other adjuvant known for stimulating an immune response. Several booster injections may be needed, for instance, at intervals of about two weeks, to provide a useful titer of anti-peptide antibody which can be detected, for example, by ELISA assay using free peptide adsorbed to a solid surface. The titer of anti-peptide antibodies in serum from an immunized animal may be increased by selection of anti-peptide antibodies, for instance, by adsorption to the peptide on a solid support and elution of the selected antibodies according to methods well known in the art.

As one of skill in the art will appreciate, and as discussed above, the polypeptides of the present invention , and immunogenic and/or antigenic epitope fragments thereof can be fused to other polypeptide sequences. For example, the polypeptides of the present invention may be fused with the constant domain of immunoglobulins (IgA, IgE, IgG, IgM), or portions thereof (CH1, CH2, CH3, or any combination thereof and portions thereof) resulting in chimeric polypeptides. Such fusion proteins may facilitate purification and may increase half-life in vivo. This has been shown for chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light

chains of mammalian immunoglobulins. See, e.g., EP 394,827; Traunecker et al., Nature, 331:84-86 (1988). Enhanced delivery of an antigen across the epithelial barrier to the immune system has been demonstrated for antigens (e.g., insulin) conjugated to an FcRn binding partner such as IgG or Fc fragments (see, e.g., PCT Publications WO 96/22024 and WO 99/04813). IgG Fusion proteins that have a disulfide-linked dimeric structure due to the IgG portion desulfide bonds have also been found to be more efficient in binding and neutralizing other molecules than monomeric polypeptides or fragments thereof alone. See, e.g., Fountoulakis et al., J. Biochem., 270:3958-3964 (1995).

Similarly, EP-A-O 464 533 (Canadian counterpart 2045869) discloses fusion proteins comprising various portions of constant region of immunoglobulin molecules together with another human protein or part thereof. In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP-A 0232 262.) Alternatively, deleting the Fc part after the fusion protein has been expressed, detected, and purified, may be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, D. Bennett et al., J. Molecular Recognition 8:52-58 (1995); K. Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).)

Moreover, the polypeptides of the present invention can be fused to marker sequences, such as a peptide which facilitates purification of the fused polypeptide. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Another peptide tag useful for purification, the "HA" tag, corresponds to an epitope

derived from the influenza hemagglutinin protein. (Wilson et al., Cell 37:767 (1984).)

Thus, any of these above fusions can be engineered using the polynucleotides or the polypeptides of the present invention.

Nucleic acids encoding the above epitopes can also be recombined with a gene of interest as an epitope tag (e.g., the hemagglutinin ("HA") tag or flag tag) to aid in detection and purification of the expressed polypeptide. For example, a system described by Janknecht et al. allows for the ready purification of non-denatured fusion proteins expressed in human cell lines (Janknecht et al., Proc. Natl. Acad. Sci. USA 88:8972- 897 (1991)). In this system, the gene of interest is subcloned into a vaccinia recombination plasmid such that the open reading frame of the gene is translationally fused to an amino-terminal tag consisting of six histidine residues. The tag serves as a matrix binding domain for the fusion protein. Extracts from cells infected with the recombinant vaccinia virus are loaded onto Ni2+ nitriloacetic acid-agarose column and histidine-tagged proteins can be selectively eluted with imidazole-containing buffers.

Additional fusion proteins of the invention may be generated through the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling"). DNA shuffling may be employed to modulate the activities of polypeptides of the invention, such methods can be used to generate polypeptides with altered activity, as well as agonists and antagonists of the polypeptides. See, generally, U.S. Patent Nos. 5,605,793; 5,811,238; 5,830,721; 5,834,252; and 5,837,458, and Patten et al., Curr. Opinion Biotechnol. 8:724-33 (1997); Harayama, Trends Biotechnol. 16(2):76-82 (1998); Hansson, et al., J. Mol. Biol. 287:265-76 (1999); and Lorenzo and Blasco, Biotechniques 24(2):308- 13 (1998) (each of these patents and publications are hereby incorporated by reference in its entirety). In one embodiment, alteration of polynucleotides corresponding to SEQ ID NO:X and the polypeptides encoded by these polynucleotides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments by homologous or site-specific recombination to generate variation in the

polynucleotide sequence. In another embodiment, polynucleotides of the invention, or the encoded polypeptides, may be altered by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of a polynucleotide encoding a polypeptide of the invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules.

As discussed herein, any polypeptide of the present invention can be used to generate fusion proteins. For example, the polypeptide of the present invention, when fused to a second protein, can be used as an antigenic tag. Antibodies raised against the polypeptide of the present invention can be used to indirectly detect the second protein by binding to the polypeptide. Moreover, because secreted proteins target cellular locations based on trafficking signals, polypeptides of the present invention which are shown to be secreted can be used as targeting molecules once fused to other proteins.

Examples of domains that can be fused to polypeptides of the present invention include not only heterologous signal sequences, but also other heterologous functional regions. The fusion does not necessarily need to be direct, but may occur through linker sequences.

In certain preferred embodiments, proteins of the invention comprise fusion proteins wherein the polypeptides are N and/or C- terminal deletion mutants. In preferred embodiments, the application is directed to nucleic acid molecules at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% identical to the nucleic acid sequences encoding polypeptides having the amino acid sequence of the specific N- and C-terminal deletions mutants. Polynucleotides encoding these polypeptides are also encompassed by the invention.

Moreover, fusion proteins may also be engineered to improve characteristics of the polypeptide of the present invention. For instance, a region of additional amino acids, particularly charged amino acids, may be added to the N-terminus of the polypeptide to improve stability and persistence during purification from the host cell

or subsequent handling and storage. Also, peptide moieties may be added to the polypeptide to facilitate purification. Such regions may be removed prior to final preparation of the polypeptide. The addition of peptide moieties to facilitate handling of polypeptides are familiar and routine techniques in the art.

Vectors, Host Cells, and Protein Production

The present invention also relates to vectors containing the polynucleotide of the present invention, host cells, and the production of polypeptides by recombinant techniques. The vector may be, for example, a phage, plasmid, viral, or retroviral vector. Retroviral vectors may be replication competent or replication defective. In the latter case, viral propagation generally will occur only in complementing host cells.

The polynucleotides of the invention may be joined to a vector containing a selectable marker for propagation in a host. Generally, a plasmid vector is introduced in a precipitate, such as a calcium phosphate precipitate, or in a complex with a charged lipid. If the vector is a virus, it may be packaged in vitro using an appropriate packaging cell line and then transduced into host cells.

The polynucleotide insert should be operatively linked to an appropriate promoter, such as the phage lambda PL promoter, the E. coli lac, trp, phoA and tac promoters, the SV40 early and late promoters and promoters of retroviral LTRs, to name a few. Other suitable promoters will be known to the skilled artisan. The expression constructs will further contain sites for transcription initiation, termination, and, in the transcribed region, a ribosome binding site for translation. The coding portion of the transcripts expressed by the constructs will preferably include a translation initiating codon at the beginning and a termination codon (UAA, UGA or UAG) appropriately positioned at the end of the polypeptide to be translated.

As indicated, the expression vectors will preferably include at least one selectable marker. Such markers include dihydrofolate reductase, G418 or neomycin resistance for eukaryotic cell culture and tetracycline, kanamycin or ampicillin resistance genes for culturing in E. coli and other bacteria. Representative examples

of appropriate hosts include, but are not limited to, bacterial cells, such as E. coli, Streptomyces and Salmonella typhimurium cells; fungal cells, such as yeast cells (e.g., Saccharomyces cerevisiae or Pichia pastoris (ATCC Accession No. 201178)); insect cells such as Drosophila S2 and Spodoptera Sf9 cells; animal cells such as CHO, COS, 293, and Bowes melanoma cells; and plant cells. Appropriate culture mediums and conditions for the above-described host cells are known in the art.

Among vectors preferred for use in bacteria include pQE70, pQE60 and pQE-9, available from QIAGEN, Inc.; pBluescript vectors, Phagescript vectors, pNH8A, pNH16a, pNH18A, pNH46A, available from Stratagene Cloning Systems, Inc.; and ptrc99a, pKK223-3, pKK233-3, pDR540, pRIT5 available from Pharmacia Biotech, Inc. Among preferred eukaryotic vectors are pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; and pSVK3, pBPV, pMSG and pSVL available from Pharmacia. Preferred expression vectors for use in yeast systems include, but are not limited to pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalph, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, and PAO815 (all available from Invitrogen, Carlbad, CA). Other suitable vectors will be readily apparent to the skilled artisan.

Introduction of the construct into the host cell can be effected by calcium phosphate transfection, DEAE-dextran mediated transfection, cationic lipid-mediated transfection, electroporation, transduction, infection, or other methods. Such methods are described in many standard laboratory manuals, such as Davis et al., Basic Methods In Molecular Biology (1986). It is specifically contemplated that the polypeptides of the present invention may in fact be expressed by a host cell lacking a recombinant vector.

A polypeptide of this invention can be recovered and purified from recombinant cell cultures by well-known methods including ammonium sulfate or ethanol precipitation, acid extraction, anion or cation exchange chromatography, phosphocellulose chromatography, hydrophobic interaction chromatography, affinity chromatography, hydroxylapatite chromatography and lectin chromatography. Most

preferably, high performance liquid chromatography ("HPLC") is employed for purification.

Polypeptides of the present invention can also be recovered from: products purified from natural sources, including bodily fluids, tissues and cells, whether directly isolated or cultured; products of chemical synthetic procedures; and products produced by recombinant techniques from a prokaryotic or eukaryotic host, including, for example, bacterial, yeast, higher plant, insect, and mammalian cells. Depending upon the host employed in a recombinant production procedure, the polypeptides of the present invention may be glycosylated or may be non-glycosylated. In addition, polypeptides of the invention may also include an initial modified methionine residue, in some cases as a result of host-mediated processes. Thus, it is well known in the art that the N-terminal methionine encoded by the translation initiation codon generally is removed with high efficiency from any protein after translation in all eukaryotic cells. While the N-terminal methionine on most proteins also is efficiently removed in most prokaryotes, for some proteins, this prokaryotic removal process is inefficient, depending on the nature of the amino acid to which the N-terminal methionine is covalently linked.

In one embodiment, the yeast *Pichia pastoris* is used to express polypeptides of the invention in a eukaryotic system. *Pichia pastoris* is a methylotrophic yeast which can metabolize methanol as its sole carbon source. A main step in the methanol metabolization pathway is the oxidation of methanol to formaldehyde using O_2. This reaction is catalyzed by the enzyme alcohol oxidase. In order to metabolize methanol as its sole carbon source, *Pichia pastoris* must generate high levels of alcohol oxidase due, in part, to the relatively low affinity of alcohol oxidase for O_2. Consequently, in a growth medium depending on methanol as a main carbon source, the promoter region of one of the two alcohol oxidase genes (*AOX1*) is highly active. In the presence of methanol, alcohol oxidase produced from the *AOX1* gene comprises up to approximately 30% of the total soluble protein in *Pichia pastoris*. *See*, Ellis, S.B., *et al.*, *Mol. Cell. Biol.* 5:1111-21 (1985); Koutz, P.J, *et al.*, *Yeast*

5:167-77 (1989); Tschopp, J.F., *et al.*, *Nucl. Acids Res.* 15:3859-76 (1987). Thus, a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, under the transcriptional regulation of all or part of the *AOX1* regulatory sequence is expressed at exceptionally high levels in *Pichia* yeast grown in the presence of methanol.

In one example, the plasmid vector pPIC9K is used to express DNA encoding a polypeptide of the invention, as set forth herein, in a *Pichea* yeast system essentially as described in "*Pichia* Protocols: Methods in Molecular Biology," D.R. Higgins and J. Cregg, eds. The Humana Press, Totowa, NJ, 1998. This expression vector allows expression and secretion of a polypeptide of the invention by virtue of the strong *AOX1* promoter linked to the *Pichia pastoris* alkaline phosphatase (PHO) secretory signal peptide (i.e., leader) located upstream of a multiple cloning site.

Many other yeast vectors could be used in place of pPIC9K, such as, pYES2, pYD1, pTEF1/Zeo, pYES2/GS, pPICZ, pGAPZ, pGAPZalpha, pPIC9, pPIC3.5, pHIL-D2, pHIL-S1, pPIC3.5K, and PAO815, as one skilled in the art would readily appreciate, as long as the proposed expression construct provides appropriately located signals for transcription, translation, secretion (if desired), and the like, including an in-frame AUG as required.

In another embodiment, high-level expression of a heterologous coding sequence, such as, for example, a polynucleotide of the present invention, may be achieved by cloning the heterologous polynucleotide of the invention into an expression vector such as, for example, pGAPZ or pGAPZalpha, and growing the yeast culture in the absence of methanol.

In addition to encompassing host cells containing the vector constructs discussed herein, the invention also encompasses primary, secondary, and immortalized host cells of vertebrate origin, particularly mammalian origin, that have been engineered to delete or replace endogenous genetic material (e.g., coding sequence), and/or to include genetic material (e.g., heterologous polynucleotide sequences) that is operably associated with polynucleotides of the invention, and

which activates, alters, and/or amplifies endogenous polynucleotides. For example, techniques known in the art may be used to operably associate heterologous control regions (e.g., promoter and/or enhancer) and endogenous polynucleotide sequences via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989), the disclosures of each of which are incorporated by reference in their entireties).

In addition, polypeptides of the invention can be chemically synthesized using techniques known in the art (e.g., see Creighton, 1983, Proteins: Structures and Molecular Principles, W.H. Freeman & Co., N.Y., and Hunkapiller et al., *Nature*, 310:105-111 (1984)). For example, a polypeptide corresponding to a fragment of a polypeptide can be synthesized by use of a peptide synthesizer. Furthermore, if desired, nonclassical amino acids or chemical amino acid analogs can be introduced as a substitution or addition into the polypeptide sequence. Non-classical amino acids include, but are not limited to, to the D-isomers of the common amino acids, 2,4-diaminobutyric acid, a-amino isobutyric acid, 4-aminobutyric acid, Abu, 2-amino butyric acid, g-Abu, e-Ahx, 6-amino hexanoic acid, Aib, 2-amino isobutyric acid, 3-amino propionic acid, ornithine, norleucine, norvaline, hydroxyproline, sarcosine, citrulline, homocitrulline, cysteic acid, t-butylglycine, t-butylalanine, phenylglycine, cyclohexylalanine, b-alanine, fluoro-amino acids, designer amino acids such as b-methyl amino acids, Ca-methyl amino acids, Na-methyl amino acids, and amino acid analogs in general. Furthermore, the amino acid can be D (dextrorotary) or L (levorotary).

Non-naturally occurring variants may be produced using art-known mutagenesis techniques, which include, but are not limited to oligonucleotide mediated mutagenesis, alanine scanning, PCR mutagenesis, site directed mutagenesis (*see, e.g.*, Carter *et al., Nucl. Acids Res. 13*:4331 (1986); and Zoller *et al., Nucl. Acids Res. 10*:6487 (1982)), cassette mutagenesis (*see, e.g.*, Wells *et al., Gene 34*:315

(1985)), restriction selection mutagenesis (*see, e.g.*, Wells *et al., Philos. Trans. R. Soc. London SerA 317*:415 (1986)).

The invention additionally, encompasses polypeptides of the present invention which are differentially modified during or after translation, e.g., by glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, linkage to an antibody molecule or other cellular ligand, etc. Any of numerous chemical modifications may be carried out by known techniques, including but not limited, to specific chemical cleavage by cyanogen bromide, trypsin, chymotrypsin, papain, V8 protease, $NaBH_4$; acetylation, formylation, oxidation, reduction; metabolic synthesis in the presence of tunicamycin; etc.

Additional post-translational modifications encompassed by the invention include, for example, e.g., N-linked or O-linked carbohydrate chains, processing of N-terminal or C-terminal ends), attachment of chemical moieties to the amino acid backbone, chemical modifications of N-linked or O-linked carbohydrate chains, and addition or deletion of an N-terminal methionine residue as a result of procaryotic host cell expression. The polypeptides may also be modified with a detectable label, such as an enzymatic, fluorescent, isotopic or affinity label to allow for detection and isolation of the protein.

Also provided by the invention are chemically modified derivatives of the polypeptides of the invention which may provide additional advantages such as increased solubility, stability and circulating time of the polypeptide, or decreased immunogenicity (see U.S. Patent No. 4,179,337). The chemical moieties for derivitization may be selected from water soluble polymers such as polyethylene glycol, ethylene glycol/propylene glycol copolymers, carboxymethylcellulose, dextran, polyvinyl alcohol and the like. The polypeptides may be modified at random positions within the molecule, or at predetermined positions within the molecule and may include one, two, three or more attached chemical moieties.

The polymer may be of any molecular weight, and may be branched or unbranched. For polyethylene glycol, the preferred molecular weight is between

about 1 kDa and about 100 kDa (the term "about" indicating that in preparations of polyethylene glycol, some molecules will weigh more, some less, than the stated molecular weight) for ease in handling and manufacturing. Other sizes may be used, depending on the desired therapeutic profile (e.g., the duration of sustained release desired, the effects, if any on biological activity, the ease in handling, the degree or lack of antigenicity and other known effects of the polyethylene glycol to a therapeutic protein or analog). For example, the polyethylene glycol may have an average molecular weight of about 200; 500; 1000; 1500; 2000; 2500; 3000; 3500; 4000; 4500; 5000; 5500; 6000; 6500; 7000; 7500; 8000; 8500; 9000; 9500; 10,000; 10,500; 11,000; 11,500; 12,000; 12,500; 13,000; 13,500; 14,000; 14,500; 15,000; 15,500; 16,000; 16,500; 17,000; 17,500; 18,000; 18,500; 19,000; 19,500; 20,000; 25,000; 30,000; 35,000; 40,000; 50,000; 55,000; 60,000; 65,000; 70,000; 75,000; 80,000; 85,000; 90,000; 95,000; or 100,000 kDa.

As noted above, the polyethylene glycol may have a branched structure. Branched polyethylene glycols are described, for example, in U.S. Patent No. 5,643,575; Morpurgo *et al., Appl. Biochem. Biotechnol. 56*:59-72 (1996); Vorobjev *et al., Nucleosides Nucleotides 18*:2745-2750 (1999); and Caliceti *et al., Bioconjug. Chem. 10*:638-646 (1999), the disclosures of each of which are incorporated herein by reference.

The polyethylene glycol molecules (or other chemical moieties) should be attached to the protein with consideration of effects on functional or antigenic domains of the protein. There are a number of attachment methods available to those skilled in the art, e.g., EP 0 401 384, herein incorporated by reference (coupling PEG to G-CSF), see also Malik et al., Exp. Hematol. 20:1028-1035 (1992) (reporting pegylation of GM-CSF using tresyl chloride). For example, polyethylene glycol may be covalently bound through amino acid residues via a reactive group, such as, a free amino or carboxyl group. Reactive groups are those to which an activated polyethylene glycol molecule may be bound. The amino acid residues having a free amino group may include lysine residues and the N-terminal amino acid residues; those having a free carboxyl group may include aspartic acid residues glutamic acid

residues and the C-terminal amino acid residue. Sulfhydryl groups may also be used as a reactive group for attaching the polyethylene glycol molecules. Preferred for therapeutic purposes is attachment at an amino group, such as attachment at the N-terminus or lysine group.

As suggested above, polyethylene glycol may be attached to proteins via linkage to any of a number of amino acid residues. For example, polyethylene glycol can be linked to a proteins via covalent bonds to lysine, histidine, aspartic acid, glutamic acid, or cysteine residues. One or more reaction chemistries may be employed to attach polyethylene glycol to specific amino acid residues (e.g., lysine, histidine, aspartic acid, glutamic acid, or cysteine) of the protein or to more than one type of amino acid residue (e.g., lysine, histidine, aspartic acid, glutamic acid, cysteine and combinations thereof) of the protein.

One may specifically desire proteins chemically modified at the N-terminus. Using polyethylene glycol as an illustration of the present composition, one may select from a variety of polyethylene glycol molecules (by molecular weight, branching, etc.), the proportion of polyethylene glycol molecules to protein (polypeptide) molecules in the reaction mix, the type of pegylation reaction to be performed, and the method of obtaining the selected N-terminally pegylated protein. The method of obtaining the N-terminally pegylated preparation (i.e., separating this moiety from other monopegylated moieties if necessary) may be by purification of the N-terminally pegylated material from a population of pegylated protein molecules. Selective proteins chemically modified at the N-terminus modification may be accomplished by reductive alkylation which exploits differential reactivity of different types of primary amino groups (lysine versus the N-terminal) available for derivatization in a particular protein. Under the appropriate reaction conditions, substantially selective derivatization of the protein at the N-terminus with a carbonyl group containing polymer is achieved.

As indicated above, pegylation of the proteins of the invention may be accomplished by any number of means. For example, polyethylene glycol may be attached to the protein either directly or by an intervening linker. Linkerless systems

for attaching polyethylene glycol to proteins are described in Delgado *et al., Crit. Rev. Thera. Drug Carrier Sys.* *9*:249-304 (1992); Francis *et al., Intern. J. of Hematol.* *68*:1-18 (1998); U.S. Patent No. 4,002,531; U.S. Patent No. 5,349,052; WO 95/06058; and WO 98/32466, the disclosures of each of which are incorporated herein by reference.

One system for attaching polyethylene glycol directly to amino acid residues of proteins without an intervening linker employs tresylated MPEG, which is produced by the modification of monmethoxy polyethylene glycol (MPEG) using tresylchloride ($ClSO_2CH_2CF_3$). Upon reaction of protein with tresylated MPEG, polyethylene glycol is directly attached to amine groups of the protein. Thus, the invention includes protein-polyethylene glycol conjugates produced by reacting proteins of the invention with a polyethylene glycol molecule having a 2,2,2-trifluoreothane sulphonyl group.

Polyethylene glycol can also be attached to proteins using a number of different intervening linkers. For example, U.S. Patent No. 5,612,460, the entire disclosure of which is incorporated herein by reference, discloses urethane linkers for connecting polyethylene glycol to proteins. Protein-polyethylene glycol conjugates wherein the polyethylene glycol is attached to the protein by a linker can also be produced by reaction of proteins with compounds such as MPEG-succinimidylsuccinate, MPEG activated with 1,1'-carbonyldiimidazole, MPEG-2,4,5-trichloropenylcarbonate, MPEG-p-nitrophenolcarbonate, and various MPEG-succinate derivatives. A number additional polyethylene glycol derivatives and reaction chemistries for attaching polyethylene glycol to proteins are described in WO 98/32466, the entire disclosure of which is incorporated herein by reference. Pegylated protein products produced using the reaction chemistries set out herein are included within the scope of the invention.

The number of polyethylene glycol moieties attached to each protein of the invention (*i.e.*, the degree of substitution) may also vary. For example, the pegylated proteins of the invention may be linked, on average, to 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 15, 17, 20, or more polyethylene glycol molecules. Similarly, the average degree of

substitution within ranges such as 1-3, 2-4, 3-5, 4-6, 5-7, 6-8, 7-9, 8-10, 9-11, 10-12, 11-13, 12-14, 13-15, 14-16, 15-17, 16-18, 17-19, or 18-20 polyethylene glycol moieties per protein molecule. Methods for determining the degree of substitution are discussed, for example, in Delgado *et al., Crit. Rev. Thera. Drug Carrier Sys. 9*:249-304 (1992).

The cancer antigen polypeptides of the invention may be in monomers or multimers (i.e., dimers, trimers, tetramers and higher multimers). Accordingly, the present invention relates to monomers and multimers of the polypeptides of the invention, their preparation, and compositions (preferably, Therapeutics) containing them. In specific embodiments, the polypeptides of the invention are monomers, dimers, trimers or tetramers. In additional embodiments, the multimers of the invention are at least dimers, at least trimers, or at least tetramers.

Multimers encompassed by the invention may be homomers or heteromers. As used herein, the term homomer, refers to a multimer containing only polypeptides corresponding to the amino acid sequence of SEQ ID NO:Y or an amino acid sequence encoded by SEQ ID NO:X, and/or an amino acid sequence encoded by the cDNA in a related cDNA clone contained in a deposited library (including fragments, variants, splice variants, and fusion proteins, corresponding to any one of these as described herein). These homomers may contain polypeptides having identical or different amino acid sequences. In a specific embodiment, a homomer of the invention is a multimer containing only polypeptides having an identical amino acid sequence. In another specific embodiment, a homomer of the invention is a multimer containing polypeptides having different amino acid sequences. In specific embodiments, the multimer of the invention is a homodimer (e.g., containing polypeptides having identical or different amino acid sequences) or a homotrimer (e.g., containing polypeptides having identical and/or different amino acid sequences). In additional embodiments, the homomeric multimer of the invention is at least a homodimer, at least a homotrimer, or at least a homotetramer.

As used herein, the term heteromer refers to a multimer containing one or more heterologous polypeptides (i.e., polypeptides of different proteins) in addition to

the polypeptides of the invention. In a specific embodiment, the multimer of the invention is a heterodimer, a heterotrimer, or a heterotetramer. In additional embodiments, the heteromeric multimer of the invention is at least a heterodimer, at least a heterotrimer, or at least a heterotetramer.

Multimers of the invention may be the result of hydrophobic, hydrophilic, ionic and/or covalent associations and/or may be indirectly linked, by for example, liposome formation. Thus, in one embodiment, multimers of the invention, such as, for example, homodimers or homotrimers, are formed when polypeptides of the invention contact one another in solution. In another embodiment, heteromultimers of the invention, such as, for example, heterotrimers or heterotetramers, are formed when polypeptides of the invention contact antibodies to the polypeptides of the invention (including antibodies to the heterologous polypeptide sequence in a fusion protein of the invention) in solution. In other embodiments, multimers of the invention are formed by covalent associations with and/or between the polypeptides of the invention. Such covalent associations may involve one or more amino acid residues contained in the polypeptide sequence (e.g., that recited in SEQ ID NO:Y, or contained in a polypeptide encoded by SEQ ID NO:X, and/or by the cDNA in the related cDNA clone contained in a deposited library). In one instance, the covalent associations are cross-linking between cysteine residues located within the polypeptide sequences which interact in the native (i.e., naturally occurring) polypeptide. In another instance, the covalent associations are the consequence of chemical or recombinant manipulation. Alternatively, such covalent associations may involve one or more amino acid residues contained in the heterologous polypeptide sequence in a fusion protein. In one example, covalent associations are between the heterologous sequence contained in a fusion protein of the invention (see, e.g., US Patent Number 5,478,925). In a specific example, the covalent associations are between the heterologous sequence contained in a Fc fusion protein of the invention (as described herein). In another specific example, covalent associations of fusion proteins of the invention are between heterologous polypeptide sequence from another protein that is capable of forming covalently associated multimers, such as for

example, oseteoprotegerin (see, e.g., International Publication NO: WO 98/49305, the contents of which are herein incorporated by reference in its entirety). In another embodiment, two or more polypeptides of the invention are joined through peptide linkers. Examples include those peptide linkers described in U.S. Pat. No. 5,073,627 (hereby incorporated by reference). Proteins comprising multiple polypeptides of the invention separated by peptide linkers may be produced using conventional recombinant DNA technology.

Another method for preparing multimer polypeptides of the invention involves use of polypeptides of the invention fused to a leucine zipper or isoleucine zipper polypeptide sequence. Leucine zipper and isoleucine zipper domains are polypeptides that promote multimerization of the proteins in which they are found. Leucine zippers were originally identified in several DNA-binding proteins (Landschulz et al., Science 240:1759, (1988)), and have since been found in a variety of different proteins. Among the known leucine zippers are naturally occurring peptides and derivatives thereof that dimerize or trimerize. Examples of leucine zipper domains suitable for producing soluble multimeric proteins of the invention are those described in PCT application WO 94/10308, hereby incorporated by reference. Recombinant fusion proteins comprising a polypeptide of the invention fused to a polypeptide sequence that dimerizes or trimerizes in solution are expressed in suitable host cells, and the resulting soluble multimeric fusion protein is recovered from the culture supernatant using techniques known in the art.

Trimeric polypeptides of the invention may offer the advantage of enhanced biological activity. Preferred leucine zipper moieties and isoleucine moieties are those that preferentially form trimers. One example is a leucine zipper derived from lung surfactant protein D (SPD), as described in Hoppe et al. (FEBS Letters 344:191, (1994)) and in U.S. patent application Ser. No. 08/446,922, hereby incorporated by reference. Other peptides derived from naturally occurring trimeric proteins may be employed in preparing trimeric polypeptides of the invention.

In another example, proteins of the invention are associated by interactions between Flag® polypeptide sequence contained in fusion proteins of the invention

containing Flag® polypeptide seuqence. In a further embodiment, associations proteins of the invention are associated by interactions between heterologous polypeptide sequence contained in Flag® fusion proteins of the invention and anti-Flag® antibody.

The multimers of the invention may be generated using chemical techniques known in the art. For example, polypeptides desired to be contained in the multimers of the invention may be chemically cross-linked using linker molecules and linker molecule length optimization techniques known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, multimers of the invention may be generated using techniques known in the art to form one or more inter-molecule cross-links between the cysteine residues located within the sequence of the polypeptides desired to be contained in the multimer (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Further, polypeptides of the invention may be routinely modified by the addition of cysteine or biotin to the C-terminus or N-terminus of the polypeptide and techniques known in the art may be applied to generate multimers containing one or more of these modified polypeptides (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). Additionally, techniques known in the art may be applied to generate liposomes containing the polypeptide components desired to be contained in the multimer of the invention (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

Alternatively, multimers of the invention may be generated using genetic engineering techniques known in the art. In one embodiment, polypeptides contained in multimers of the invention are produced recombinantly using fusion protein technology described herein or otherwise known in the art (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In a specific embodiment, polynucleotides coding for a homodimer of the invention are generated by ligating a polynucleotide sequence encoding a polypeptide of the invention to a sequence encoding a linker polypeptide and then further to a synthetic

polynucleotide encoding the translated product of the polypeptide in the reverse orientation from the original C-terminus to the N-terminus (lacking the leader sequence) (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety). In another embodiment, recombinant techniques described herein or otherwise known in the art are applied to generate recombinant polypeptides of the invention which contain a transmembrane domain (or hyrophobic or signal peptide) and which can be incorporated by membrane reconstitution techniques into liposomes (see, e.g., US Patent Number 5,478,925, which is herein incorporated by reference in its entirety).

Antibodies

Further polypeptides of the invention relate to antibodies and T-cell antigen receptors (TCR) which immunospecifically bind a polypeptide, polypeptide fragment, or variant of SEQ ID NO:Y, and/or an epitope, of the present invention (as determined by immunoassays well known in the art for assaying specific antibody-antigen binding). Antibodies of the invention include, but are not limited to, polyclonal, monoclonal, multispecific, human, humanized or chimeric antibodies, single chain antibodies, Fab fragments, F(ab') fragments, fragments produced by a Fab expression library, anti-idiotypic (anti-Id) antibodies (including, e.g., anti-Id antibodies to antibodies of the invention), and epitope-binding fragments of any of the above. The term "antibody," as used herein, refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that immunospecifically binds an antigen. The immunoglobulin molecules of the invention can be of any type (e.g., IgG, IgE, IgM, IgD, IgA and IgY), class (e.g., IgG1, IgG2, IgG3, IgG4, IgA1 and IgA2) or subclass of immunoglobulin molecule.

Most preferably the antibodies are human antigen-binding antibody fragments of the present invention and include, but are not limited to, Fab, Fab' and F(ab')2, Fd, single-chain Fvs (scFv), single-chain antibodies, disulfide-linked Fvs (sdFv) and fragments comprising either a VL or VH domain. Antigen-binding antibody

fragments, including single-chain antibodies, may comprise the variable region(s) alone or in combination with the entirety or a portion of the following: hinge region, CH1, CH2, and CH3 domains. Also included in the invention are antigen-binding fragments also comprising any combination of variable region(s) with a hinge region, CH1, CH2, and CH3 domains. The antibodies of the invention may be from any animal origin including birds and mammals. Preferably, the antibodies are human, murine (e.g., mouse and rat), donkey, ship rabbit, goat, guinea pig, camel, horse, or chicken. As used herein, "human" antibodies include antibodies having the amino acid sequence of a human immunoglobulin and include antibodies isolated from human immunoglobulin libraries or from animals transgenic for one or more human immunoglobulin and that do not express endogenous immunoglobulins, as described infra and, for example in, U.S. Patent No. 5,939,598 by Kucherlapati et al.

The antibodies of the present invention may be monospecific, bispecific, trispecific or of greater multispecificity. Multispecific antibodies may be specific for different epitopes of a polypeptide of the present invention or may be specific for both a polypeptide of the present invention as well as for a heterologous epitope, such as a heterologous polypeptide or solid support material. See, e.g., PCT publications WO 93/17715; WO 92/08802; WO 91/00360; WO 92/05793; Tutt, et al., J. Immunol. 147:60-69 (1991); U.S. Patent Nos. 4,474,893; 4,714,681; 4,925,648; 5,573,920; 5,601,819; Kostelny et al., J. Immunol. 148:1547-1553 (1992).

Antibodies of the present invention may be described or specified in terms of the epitope(s) or portion(s) of a polypeptide of the present invention which they recognize or specifically bind. The epitope(s) or polypeptide portion(s) may be specified as described herein, e.g., by N-terminal and C-terminal positions, or by size in contiguous amino acid residues. Antibodies which specifically bind any epitope or polypeptide of the present invention may also be excluded. Therefore, the present invention includes antibodies that specifically bind polypeptides of the present invention, and allows for the exclusion of the same.

Antibodies of the present invention may also be described or specified in terms of their cross-reactivity. Antibodies that do not bind any other analog, ortholog,

or homolog of a polypeptide of the present invention are included. Antibodies that bind polypeptides with at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 65%, at least 60%, at least 55%, and at least 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In specific embodiments, antibodies of the present invention cross-react with murine, rat and/or rabbit homologs of human proteins and the corresponding epitopes thereof. Antibodies that do not bind polypeptides with less than 95%, less than 90%, less than 85%, less than 80%, less than 75%, less than 70%, less than 65%, less than 60%, less than 55%, and less than 50% identity (as calculated using methods known in the art and described herein) to a polypeptide of the present invention are also included in the present invention. In a specific embodiment, the above-described cross-reactivity is with respect to any single specific antigenic or immunogenic polypeptide, or combination(s) of 2, 3, 4, 5, or more of the specific antigenic and/or immunogenic polypeptides disclosed herein. Further included in the present invention are antibodies which bind polypeptides encoded by polynucleotides which hybridize to a polynucleotide of the present invention under stringent hybridization conditions (as described herein). Antibodies of the present invention may also be described or specified in terms of their binding affinity to a polypeptide of the invention. Preferred binding affinities include those with a dissociation constant or Kd less than 5 X 10^{-2} M, 10^{-2} M, 5 X 10^{-3} M, 10^{-3} M, 5 X 10^{-4} M, 10^{-4} M, 5 X 10^{-5} M, 10^{-5} M, 5 X 10^{-6} M, 10^{-6}M, 5 X 10^{-7} M, 10^{7} M, 5 X 10^{-8} M, 10^{-8} M, 5 X 10^{-9} M, 10^{-9} M, 5 X 10^{-10} M, 10^{-10} M, 5 X 10^{-11} M, 10^{-11} M, 5 X 10^{-12} M, $^{10-12}$ M, 5 X 10^{-13} M, 10^{-13} M, 5 X 10^{-14} M, 10^{-14} M, 5 X 10^{-15} M, or $^{10-15}$ M.

The invention also provides antibodies that competitively inhibit binding of an antibody to an epitope of the invention as determined by any method known in the art for determining competitive binding, for example, the immunoassays described herein. In preferred embodiments, the antibody competitively inhibits binding to the epitope by at least 95%, at least 90%, at least 85 %, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50%.

Antibodies of the present invention may act as agonists or antagonists of the polypeptides of the present invention. For example, the present invention includes antibodies which disrupt the receptor/ligand interactions with the polypeptides of the invention either partially or fully. Preferrably, antibodies of the present invention bind an antigenic epitope disclosed herein, or a portion thereof. The invention features both receptor-specific antibodies and ligand-specific antibodies. The invention also features receptor-specific antibodies which do not prevent ligand binding but prevent receptor activation. Receptor activation (i.e., signaling) may be determined by techniques described herein or otherwise known in the art. For example, receptor activation can be determined by detecting the phosphorylation (e.g., tyrosine or serine/threonine) of the receptor or its substrate by immunoprecipitation followed by western blot analysis (for example, as described supra). In specific embodiments, antibodies are provided that inhibit ligand activity or receptor activity by at least 95%, at least 90%, at least 85%, at least 80%, at least 75%, at least 70%, at least 60%, or at least 50% of the activity in absence of the antibody.

The invention also features receptor-specific antibodies which both prevent ligand binding and receptor activation as well as antibodies that recognize the receptor-ligand complex, and, preferably, do not specifically recognize the unbound receptor or the unbound ligand. Likewise, included in the invention are neutralizing antibodies which bind the ligand and prevent binding of the ligand to the receptor, as well as antibodies which bind the ligand, thereby preventing receptor activation, but do not prevent the ligand from binding the receptor. Further included in the invention are antibodies which activate the receptor. These antibodies may act as receptor agonists, i.e., potentiate or activate either all or a subset of the biological activities of the ligand-mediated receptor activation, for example, by inducing dimerization of the receptor. The antibodies may be specified as agonists, antagonists or inverse agonists for biological activities comprising the specific biological activities of the peptides of the invention disclosed herein. The above antibody agonists can be made using methods known in the art. See, e.g., PCT publication WO 96/40281; U.S. Patent No. 5,811,097; Deng et al., Blood 92(6):1981-1988 (1998); Chen et al., Cancer Res.

58(16):3668-3678 (1998); Harrop et al., J. Immunol. 161(4):1786-1794 (1998); Zhu et al., Cancer Res. 58(15):3209-3214 (1998); Yoon et al., J. Immunol. 160(7):3170-3179 (1998); Prat et al., J. Cell. Sci. 111(Pt2):237-247 (1998); Pitard et al., J. Immunol. Methods 205(2):177-190 (1997); Liautard et al., Cytokine 9(4):233-241 (1997); Carlson et al., J. Biol. Chem. 272(17):11295-11301 (1997); Taryman et al., Neuron 14(4):755-762 (1995); Muller et al., Structure 6(9):1153-1167 (1998); Bartunek et al., Cytokine 8(1):14-20 (1996) (which are all incorporated by reference herein in their entireties).

Antibodies of the present invention may be used, for example, but not limited to, to purify, detect, and target the polypeptides of the present invention, including both in vitro and in vivo diagnostic and therapeutic methods. For example, the antibodies have use in immunoassays for qualitatively and quantitatively measuring levels of the polypeptides of the present invention in biological samples. See, e.g., Harlow et al., Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988) (incorporated by reference herein in its entirety).

As discussed in more detail below, the antibodies of the present invention may be used either alone or in combination with other compositions. The antibodies may further be recombinantly fused to a heterologous polypeptide at the N- or C-terminus or chemically conjugated (including covalently and non-covalently conjugations) to polypeptides or other compositions. For example, antibodies of the present invention may be recombinantly fused or conjugated to molecules useful as labels in detection assays and effector molecules such as heterologous polypeptides, drugs, radionuclides, or toxins. See, e.g., PCT publications WO 92/08495; WO 91/14438; WO 89/12624; U.S. Patent No. 5,314,995; and EP 396,387.

The antibodies of the invention include derivatives that are modified, i.e, by the covalent attachment of any type of molecule to the antibody such that covalent attachment does not prevent the antibody from generating an anti-idiotypic response. For example, but not by way of limitation, the antibody derivatives include antibodies that have been modified, e.g., by glycosylation, acetylation, pegylation, phosphylation, amidation, derivatization by known protecting/blocking groups,

proteolytic cleavage, linkage to a cellular ligand or other protein, etc. Any of numerous chemical modifications may be carried out by known techniques, including, but not limited to specific chemical cleavage, acetylation, formylation, metabolic synthesis of tunicamycin, etc. Additionally, the derivative may contain one or more non-classical amino acids.

The antibodies of the present invention may be generated by any suitable method known in the art. Polyclonal antibodies to an antigen-of- interest can be produced by various procedures well known in the art. For example, a polypeptide of the invention can be administered to various host animals including, but not limited to, rabbits, mice, rats, etc. to induce the production of sera containing polyclonal antibodies specific for the antigen. Various adjuvants may be used to increase the immunological response, depending on the host species, and include but are not limited to, Freund's (complete and incomplete), mineral gels such as aluminum hydroxide, surface active substances such as lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, keyhole limpet hemocyanins, dinitrophenol, and potentially useful human adjuvants such as BCG (bacille Calmette-Guerin) and corynebacterium parvum. Such adjuvants are also well known in the art.

Monoclonal antibodies can be prepared using a wide variety of techniques known in the art including the use of hybridoma, recombinant, and phage display technologies, or a combination thereof. For example, monoclonal antibodies can be produced using hybridoma techniques including those known in the art and taught, for example, in Harlow et al., Antibodies: A Laboratory Manual, (Cold Spring Harbor Laboratory Press, 2nd ed. 1988); Hammerling, et al., in: Monoclonal Antibodies and T-Cell Hybridomas 563-681 (Elsevier, N.Y., 1981) (said references incorporated by reference in their entireties). The term "monoclonal antibody" as used herein is not limited to antibodies produced through hybridoma technology. The term "monoclonal antibody" refers to an antibody that is derived from a single clone, including any eukaryotic, prokaryotic, or phage clone, and not the method by which it is produced.

Methods for producing and screening for specific antibodies using hybridoma technology are routine and well known in the art and are discussed in detail in the Examples. In a non-limiting example, mice can be immunized with a polypeptide of the invention or a cell expressing such peptide. Once an immune response is detected, e.g., antibodies specific for the antigen are detected in the mouse serum, the mouse spleen is harvested and splenocytes isolated. The splenocytes are then fused by well known techniques to any suitable myeloma cells, for example cells from cell line SP20 available from the ATCC. Hybridomas are selected and cloned by limited dilution. The hybridoma clones are then assayed by methods known in the art for cells that secrete antibodies capable of binding a polypeptide of the invention. Ascites fluid, which generally contains high levels of antibodies, can be generated by immunizing mice with positive hybridoma clones.

Accordingly, the present invention provides methods of generating monoclonal antibodies as well as antibodies produced by the method comprising culturing a hybridoma cell secreting an antibody of the invention wherein, preferably, the hybridoma is generated by fusing splenocytes isolated from a mouse immunized with an antigen of the invention with myeloma cells and then screening the hybridomas resulting from the fusion for hybridoma clones that secrete an antibody able to bind a polypeptide of the invention.

Antibody fragments which recognize specific epitopes may be generated by known techniques. For example, Fab and F(ab')2 fragments of the invention may be produced by proteolytic cleavage of immunoglobulin molecules, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce F(ab')2 fragments). F(ab')2 fragments contain the variable region, the light chain constant region and the CH1 domain of the heavy chain.

For example, the antibodies of the present invention can also be generated using various phage display methods known in the art. In phage display methods, functional antibody domains are displayed on the surface of phage particles which carry the polynucleotide sequences encoding them. In a particular embodiment, such phage can be utilized to display antigen binding domains expressed from a repertoire

or combinatorial antibody library (e.g., human or murine). Phage expressing an antigen binding domain that binds the antigen of interest can be selected or identified with antigen, e.g., using labeled antigen or antigen bound or captured to a solid surface or bead. Phage used in these methods are typically filamentous phage including fd and M13 binding domains expressed from phage with Fab, Fv or disulfide stabilized Fv antibody domains recombinantly fused to either the phage gene III or gene VIII protein. Examples of phage display methods that can be used to make the antibodies of the present invention include those disclosed in Brinkman et al., J. Immunol. Methods 182:41-50 (1995); Ames et al., J. Immunol. Methods 184:177-186 (1995); Kettleborough et al., Eur. J. Immunol. 24:952-958 (1994); Persic et al., Gene 187 9-18 (1997); Burton et al., Advances in Immunology 57:191-280 (1994); PCT application No. PCT/GB91/01134; PCT publications WO 90/02809; WO 91/10737; WO 92/01047; WO 92/18619; WO 93/11236; WO 95/15982; WO 95/20401; and U.S. Patent Nos. 5,698,426; 5,223,409; 5,403,484; 5,580,717; 5,427,908; 5,750,753; 5,821,047; 5,571,698; 5,427,908; 5,516,637; 5,780,225; 5,658,727; 5,733,743 and 5,969,108; each of which is incorporated herein by reference in its entirety.

As described in the above references, after phage selection, the antibody coding regions from the phage can be isolated and used to generate whole antibodies, including human antibodies, or any other desired antigen binding fragment, and expressed in any desired host, including mammalian cells, insect cells, plant cells, yeast, and bacteria, e.g., as described in detail below. For example, techniques to recombinantly produce Fab, Fab' and F(ab')2 fragments can also be employed using methods known in the art such as those disclosed in PCT publication WO 92/22324; Mullinax et al., BioTechniques 12(6):864-869 (1992); and Sawai et al., AJRI 34:26-34 (1995); and Better et al., Science 240:1041-1043 (1988) (said references incorporated by reference in their entireties).

Examples of techniques which can be used to produce single-chain Fvs and antibodies include those described in U.S. Patents 4,946,778 and 5,258,498; Huston et al., Methods in Enzymology 203:46-88 (1991); Shu et al., PNAS 90:7995-7999

(1993); and Skerra et al., Science 240:1038-1040 (1988). For some uses, including in vivo use of antibodies in humans and in vitro detection assays, it may be preferable to use chimeric, humanized, or human antibodies. A chimeric antibody is a molecule in which different portions of the antibody are derived from different animal species, such as antibodies having a variable region derived from a murine monoclonal antibody and a human immunoglobulin constant region. Methods for producing chimeric antibodies are known in the art. See e.g., Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Gillies et al., (1989) J. Immunol. Methods 125:191-202; U.S. Patent Nos. 5,807,715; 4,816,567; and 4,816397, which are incorporated herein by reference in their entirety. Humanized antibodies are antibody molecules from non-human species antibody that binds the desired antigen having one or more complementarity determining regions (CDRs) from the non-human species and a framework regions from a human immunoglobulin molecule. Often, framework residues in the human framework regions will be substituted with the corresponding residue from the CDR donor antibody to alter, preferably improve, antigen binding. These framework substitutions are identified by methods well known in the art, e.g., by modeling of the interactions of the CDR and framework residues to identify framework residues important for antigen binding and sequence comparison to identify unusual framework residues at particular positions. (See, e.g., Queen et al., U.S. Patent No. 5,585,089; Riechmann et al., Nature 332:323 (1988), which are incorporated herein by reference in their entireties.) Antibodies can be humanized using a variety of techniques known in the art including, for example, CDR-grafting (EP 239,400; PCT publication WO 91/09967; U.S. Patent Nos. 5,225,539; 5,530,101; and 5,585,089), veneering or resurfacing (EP 592,106; EP 519,596; Padlan, Molecular Immunology 28(4/5):489-498 (1991); Studnicka et al., Protein Engineering 7(6):805-814 (1994); Roguska. et al., PNAS 91:969-973 (1994)), and chain shuffling (U.S. Patent No. 5,565,332).

Completely human antibodies are particularly desirable for therapeutic treatment of human patients. Human antibodies can be made by a variety of methods known in the art including phage display methods described above using antibody

libraries derived from human immunoglobulin sequences. See also, U.S. Patent Nos. 4,444,887 and 4,716,111; and PCT publications WO 98/46645, WO 98/50433, WO 98/24893, WO 98/16654, WO 96/34096, WO 96/33735, and WO 91/10741; each of which is incorporated herein by reference in its entirety.

Human antibodies can also be produced using transgenic mice which are incapable of expressing functional endogenous immunoglobulins, but which can express human immunoglobulin genes. For example, the human heavy and light chain immunoglobulin gene complexes may be introduced randomly or by homologous recombination into mouse embryonic stem cells. Alternatively, the human variable region, constant region, and diversity region may be introduced into mouse embryonic stem cells in addition to the human heavy and light chain genes. The mouse heavy and light chain immunoglobulin genes may be rendered non-functional separately or simultaneously with the introduction of human immunoglobulin loci by homologous recombination. In particular, homozygous deletion of the JH region prevents endogenous antibody production. The modified embryonic stem cells are expanded and microinjected into blastocysts to produce chimeric mice. The chimeric mice are then bred to produce homozygous offspring which express human antibodies. The transgenic mice are immunized in the normal fashion with a selected antigen, e.g., all or a portion of a polypeptide of the invention. Monoclonal antibodies directed against the antigen can be obtained from the immunized, transgenic mice using conventional hybridoma technology. The human immunoglobulin transgenes harbored by the transgenic mice rearrange during B cell differentiation, and subsequently undergo class switching and somatic mutation. Thus, using such a technique, it is possible to produce therapeutically useful IgG, IgA, IgM and IgE antibodies. For an overview of this technology for producing human antibodies, see Lonberg and Huszar, Int. Rev. Immunol. 13:65-93 (1995). For a detailed discussion of this technology for producing human antibodies and human monoclonal antibodies and protocols for producing such antibodies, see, e.g., PCT publications WO 98/24893; WO 92/01047; WO 96/34096; WO 96/33735; European Patent No. 0 598 877; U.S. Patent Nos. 5,413,923; 5,625,126; 5,633,425; 5,569,825;

5,661,016: 5,545,806; 5,814,318; 5,885,793; 5,916,771; and 5,939,598, which are incorporated by reference herein in their entirety. In addition, companies such as Abgenix, Inc. (Freemont, CA) and Genpharm (San Jose, CA) can be engaged to provide human antibodies directed against a selected antigen using technology similar to that described above.

Completely human antibodies which recognize a selected epitope can be generated using a technique referred to as "guided selection." In this approach a selected non-human monoclonal antibody, e.g., a mouse antibody, is used to guide the selection of a completely human antibody recognizing the same epitope. (Jespers et al., Bio/technology 12:899-903 (1988)).

Further, antibodies to the polypeptides of the invention can, in turn, be utilized to generate anti-idiotype antibodies that "mimic" polypeptides of the invention using techniques well known to those skilled in the art. (See, e.g., Greenspan & Bona, FASEB J. 7(5):437-444; (1989) and Nissinoff, J. Immunol. 147(8):2429-2438 (1991)). For example, antibodies which bind to and competitively inhibit polypeptide multimerization and/or binding of a polypeptide of the invention to a ligand can be used to generate anti-idiotypes that "mimic" the polypeptide multimerization and/or binding domain and, as a consequence, bind to and neutralize polypeptide and/or its ligand. Such neutralizing anti-idiotypes or Fab fragments of such anti-idiotypes can be used in therapeutic regimens to neutralize polypeptide ligand. For example, such anti-idiotypic antibodies can be used to bind a polypeptide of the invention and/or to bind its ligands/receptors, and thereby block its biological activity.

Polynucleotides Encoding Antibodies

The invention further provides polynucleotides comprising a nucleotide sequence encoding an antibody of the invention and fragments thereof. The invention also encompasses polynucleotides that hybridize under stringent or alternatively, under lower stringency hybridization conditions, e.g., as defined supra, to polynucleotides that encode an antibody, preferably, that specifically binds to a

polypeptide of the invention, preferably, an antibody that binds to a polypeptide having the amino acid sequence of SEQ ID NO:Y.

The polynucleotides may be obtained, and the nucleotide sequence of the polynucleotides determined, by any method known in the art. For example, if the nucleotide sequence of the antibody is known, a polynucleotide encoding the antibody may be assembled from chemically synthesized oligonucleotides (e.g., as described in Kutmeier et al., BioTechniques 17:242 (1994)), which, briefly, involves the synthesis of overlapping oligonucleotides containing portions of the sequence encoding the antibody, annealing and ligating of those oligonucleotides, and then amplification of the ligated oligonucleotides by PCR.

Alternatively, a polynucleotide encoding an antibody may be generated from nucleic acid from a suitable source. If a clone containing a nucleic acid encoding a particular antibody is not available, but the sequence of the antibody molecule is known, a nucleic acid encoding the immunoglobulin may be chemically synthesized or obtained from a suitable source (e.g., an antibody cDNA library, or a cDNA library generated from, or nucleic acid, preferably poly A+ RNA, isolated from, any tissue or cells expressing the antibody, such as hybridoma cells selected to express an antibody of the invention) by PCR amplification using synthetic primers hybridizable to the 3' and 5' ends of the sequence or by cloning using an oligonucleotide probe specific for the particular gene sequence to identify, e.g., a cDNA clone from a cDNA library that encodes the antibody. Amplified nucleic acids generated by PCR may then be cloned into replicable cloning vectors using any method well known in the art.

Once the nucleotide sequence and corresponding amino acid sequence of the antibody is determined, the nucleotide sequence of the antibody may be manipulated using methods well known in the art for the manipulation of nucleotide sequences, e.g., recombinant DNA techniques, site directed mutagenesis, PCR, etc. (see, for example, the techniques described in Sambrook et al., 1990, Molecular Cloning, A Laboratory Manual, 2d Ed., Cold Spring Harbor Laboratory, Cold Spring Harbor, NY and Ausubel et al., eds., 1998, Current Protocols in Molecular Biology, John Wiley &

Sons, NY, which are both incorporated by reference herein in their entireties), to generate antibodies having a different amino acid sequence, for example to create amino acid substitutions, deletions, and/or insertions.

In a specific embodiment, the amino acid sequence of the heavy and/or light chain variable domains may be inspected to identify the sequences of the complementarity determining regions (CDRs) by methods that are well know in the art, e.g., by comparison to known amino acid sequences of other heavy and light chain variable regions to determine the regions of sequence hypervariability. Using routine recombinant DNA techniques, one or more of the CDRs may be inserted within framework regions, e.g., into human framework regions to humanize a non-human antibody, as described supra. The framework regions may be naturally occurring or consensus framework regions, and preferably human framework regions (see, e.g., Chothia et al., J. Mol. Biol. 278: 457-479 (1998) for a listing of human framework regions). Preferably, the polynucleotide generated by the combination of the framework regions and CDRs encodes an antibody that specifically binds a polypeptide of the invention. Preferably, as discussed supra, one or more amino acid substitutions may be made within the framework regions, and, preferably, the amino acid substitutions improve binding of the antibody to its antigen. Additionally, such methods may be used to make amino acid substitutions or deletions of one or more variable region cysteine residues participating in an intrachain disulfide bond to generate antibody molecules lacking one or more intrachain disulfide bonds. Other alterations to the polynucleotide are encompassed by the present invention and within the skill of the art.

In addition, techniques developed for the production of "chimeric antibodies" (Morrison et al., Proc. Natl. Acad. Sci. 81:851-855 (1984); Neuberger et al., Nature 312:604-608 (1984); Takeda et al., Nature 314:452-454 (1985)) by splicing genes from a mouse antibody molecule of appropriate antigen specificity together with genes from a human antibody molecule of appropriate biological activity can be used. As described supra, a chimeric antibody is a molecule in which different portions are derived from different animal species, such as those having a variable region derived

from a murine mAb and a human immunoglobulin constant region, e.g., humanized antibodies.

Alternatively, techniques described for the production of single chain antibodies (U.S. Patent No. 4,946,778; Bird, Science 242:423- 42 (1988); Huston et al., Proc. Natl. Acad. Sci. USA 85:5879-5883 (1988); and Ward et al., Nature 334:544-54 (1989)) can be adapted to produce single chain antibodies. Single chain antibodies are formed by linking the heavy and light chain fragments of the Fv region via an amino acid bridge, resulting in a single chain polypeptide. Techniques for the assembly of functional Fv fragments in E. coli may also be used (Skerra et al., Science 242:1038- 1041 (1988)).

Methods of Producing Antibodies

The antibodies of the invention can be produced by any method known in the art for the synthesis of antibodies, in particular, by chemical synthesis or preferably, by recombinant expression techniques.

Recombinant expression of an antibody of the invention, or fragment, derivative or analog thereof, (e.g., a heavy or light chain of an antibody of the invention or a single chain antibody of the invention), requires construction of an expression vector containing a polynucleotide that encodes the antibody. Once a polynucleotide encoding an antibody molecule or a heavy or light chain of an antibody, or portion thereof (preferably containing the heavy or light chain variable domain), of the invention has been obtained, the vector for the production of the antibody molecule may be produced by recombinant DNA technology using techniques well known in the art. Thus, methods for preparing a protein by expressing a polynucleotide containing an antibody encoding nucleotide sequence are described herein. Methods which are well known to those skilled in the art can be used to construct expression vectors containing antibody coding sequences and appropriate transcriptional and translational control signals. These methods include, for example, in vitro recombinant DNA techniques, synthetic techniques, and in vivo genetic recombination. The invention, thus, provides replicable vectors comprising a

nucleotide sequence encoding an antibody molecule of the invention, or a heavy or light chain thereof, or a heavy or light chain variable domain, operably linked to a promoter. Such vectors may include the nucleotide sequence encoding the constant region of the antibody molecule (see, e.g., PCT Publication WO 86/05807; PCT Publication WO 89/01036; and U.S. Patent No. 5,122,464) and the variable domain of the antibody may be cloned into such a vector for expression of the entire heavy or light chain.

The expression vector is transferred to a host cell by conventional techniques and the transfected cells are then cultured by conventional techniques to produce an antibody of the invention. Thus, the invention includes host cells containing a polynucleotide encoding an antibody of the invention, or a heavy or light chain thereof, or a single chain antibody of the invention, operably linked to a heterologous promoter. In preferred embodiments for the expression of double-chained antibodies, vectors encoding both the heavy and light chains may be co-expressed in the host cell for expression of the entire immunoglobulin molecule, as detailed below.

A variety of host-expression vector systems may be utilized to express the antibody molecules of the invention. Such host-expression systems represent vehicles by which the coding sequences of interest may be produced and subsequently purified, but also represent cells which may, when transformed or transfected with the appropriate nucleotide coding sequences, express an antibody molecule of the invention in situ. These include but are not limited to microorganisms such as bacteria (e.g., E. coli, B. subtilis) transformed with recombinant bacteriophage DNA, plasmid DNA or cosmid DNA expression vectors containing antibody coding sequences; yeast (e.g., Saccharomyces, Pichia) transformed with recombinant yeast expression vectors containing antibody coding sequences; insect cell systems infected with recombinant virus expression vectors (e.g., baculovirus) containing antibody coding sequences; plant cell systems infected with recombinant virus expression vectors (e.g., cauliflower mosaic virus, CaMV; tobacco mosaic virus, TMV) or transformed with recombinant plasmid expression vectors (e.g., Ti plasmid) containing antibody coding sequences; or mammalian cell systems (e.g., COS, CHO,

BHK, 293, 3T3 cells) harboring recombinant expression constructs containing promoters derived from the genome of mammalian cells (e.g., metallothionein promoter) or from mammalian viruses (e.g., the adenovirus late promoter; the vaccinia virus 7.5K promoter). Preferably, bacterial cells such as Escherichia coli, and more preferably, eukaryotic cells, especially for the expression of whole recombinant antibody molecule, are used for the expression of a recombinant antibody molecule. For example, mammalian cells such as Chinese hamster ovary cells (CHO), in conjunction with a vector such as the major intermediate early gene promoter element from human cytomegalovirus is an effective expression system for antibodies (Foecking et al., Gene 45:101 (1986); Cockett et al., Bio/Technology 8:2 (1990)).

In bacterial systems, a number of expression vectors may be advantageously selected depending upon the use intended for the antibody molecule being expressed. For example, when a large quantity of such a protein is to be produced, for the generation of pharmaceutical compositions of an antibody molecule, vectors which direct the expression of high levels of fusion protein products that are readily purified may be desirable. Such vectors include, but are not limited, to the E. coli expression vector pUR278 (Ruther et al., EMBO J. 2:1791 (1983)), in which the antibody coding sequence may be ligated individually into the vector in frame with the lac Z coding region so that a fusion protein is produced; pIN vectors (Inouye & Inouye, Nucleic Acids Res. 13:3101-3109 (1985); Van Heeke & Schuster, J. Biol. Chem. 24:5503-5509 (1989)); and the like. pGEX vectors may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption and binding to matrix glutathione-agarose beads followed by elution in the presence of free glutathione. The pGEX vectors are designed to include thrombin or factor Xa protease cleavage sites so that the cloned target gene product can be released from the GST moiety.

In an insect system, Autographa californica nuclear polyhedrosis virus (AcNPV) is used as a vector to express foreign genes. The virus grows in

Spodoptera frugiperda cells. The antibody coding sequence may be cloned individually into non-essential regions (for example the polyhedrin gene) of the virus and placed under control of an AcNPV promoter (for example the polyhedrin promoter).

In mammalian host cells, a number of viral-based expression systems may be utilized. In cases where an adenovirus is used as an expression vector, the antibody coding sequence of interest may be ligated to an adenovirus transcription/translation control complex, e.g., the late promoter and tripartite leader sequence. This chimeric gene may then be inserted in the adenovirus genome by in vitro or in vivo recombination. Insertion in a non- essential region of the viral genome (e.g., region E1 or E3) will result in a recombinant virus that is viable and capable of expressing the antibody molecule in infected hosts. (e.g., see Logan & Shenk, Proc. Natl. Acad. Sci. USA 81:355-359 (1984)). Specific initiation signals may also be required for efficient translation of inserted antibody coding sequences. These signals include the ATG initiation codon and adjacent sequences. Furthermore, the initiation codon must be in phase with the reading frame of the desired coding sequence to ensure translation of the entire insert. These exogenous translational control signals and initiation codons can be of a variety of origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of appropriate transcription enhancer elements, transcription terminators, etc. (see Bittner et al., Methods in Enzymol. 153:51-544 (1987)).

In addition, a host cell strain may be chosen which modulates the expression of the inserted sequences, or modifies and processes the gene product in the specific fashion desired. Such modifications (e.g., glycosylation) and processing (e.g., cleavage) of protein products may be important for the function of the protein. Different host cells have characteristic and specific mechanisms for the post-translational processing and modification of proteins and gene products. Appropriate cell lines or host systems can be chosen to ensure the correct modification and processing of the foreign protein expressed. To this end, eukaryotic host cells which possess the cellular machinery for proper processing of the primary transcript,

glycosylation, and phosphorylation of the gene product may be used. Such mammalian host cells include but are not limited to CHO, VERY, BHK, Hela, COS, MDCK, 293, 3T3, WI38, and in particular, breast cancer cell lines such as, for example, BT483, Hs578T, HTB2, BT20 and T47D, and normal mammary gland cell line such as, for example, CRL7030 and Hs578Bst.

For long-term, high-yield production of recombinant proteins, stable expression is preferred. For example, cell lines which stably express the antibody molecule may be engineered. Rather than using expression vectors which contain viral origins of replication, host cells can be transformed with DNA controlled by appropriate expression control elements (e.g., promoter, enhancer, sequences, transcription terminators, polyadenylation sites, etc.), and a selectable marker. Following the introduction of the foreign DNA, engineered cells may be allowed to grow for 1-2 days in an enriched media, and then are switched to a selective media. The selectable marker in the recombinant plasmid confers resistance to the selection and allows cells to stably integrate the plasmid into their chromosomes and grow to form foci which in turn can be cloned and expanded into cell lines. This method may advantageously be used to engineer cell lines which express the antibody molecule. Such engineered cell lines may be particularly useful in screening and evaluation of compounds that interact directly or indirectly with the antibody molecule.

A number of selection systems may be used, including but not limited to the herpes simplex virus thymidine kinase (Wigler et al., Cell 11:223 (1977)), hypoxanthine-guanine phosphoribosyltransferase (Szybalska & Szybalski, Proc. Natl. Acad. Sci. USA 48:202 (1992)), and adenine phosphoribosyltransferase (Lowy et al., Cell 22:817 (1980)) genes can be employed in tk-, hgprt- or aprt- cells, respectively. Also, antimetabolite resistance can be used as the basis of selection for the following genes: dhfr, which confers resistance to methotrexate (Wigler et al., Natl. Acad. Sci. USA 77:357 (1980); O'Hare et al., Proc. Natl. Acad. Sci. USA 78:1527 (1981)); gpt, which confers resistance to mycophenolic acid (Mulligan & Berg, Proc. Natl. Acad. Sci. USA 78:2072 (1981)); neo, which confers resistance to the aminoglycoside G-418 Clinical Pharmacy 12:488-505; Wu and Wu, Biotherapy 3:87-95 (1991);

Tolstoshev. Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science 260:926-932 (1993); and Morgan and Anderson, Ann. Rev. Biochem. 62:191-217 (1993); May, 1993, TIB TECH 11(5):155-215); and hygro, which confers resistance to hygromycin (Santerre et al., Gene 30:147 (1984)). Methods commonly known in the art of recombinant DNA technology may be routinely applied to select the desired recombinant clone, and such methods are described, for example, in Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY (1993); Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990); and in Chapters 12 and 13, Dracopoli et al. (eds), Current Protocols in Human Genetics, John Wiley & Sons, NY (1994); Colberre-Garapin et al., J. Mol. Biol. 150:1 (1981), which are incorporated by reference herein in their entireties.

The expression levels of an antibody molecule can be increased by vector amplification (for a review, see Bebbington and Hentschel, The use of vectors based on gene amplification for the expression of cloned genes in mammalian cells in DNA cloning, Vol.3. (Academic Press, New York, 1987)). When a marker in the vector system expressing antibody is amplifiable, increase in the level of inhibitor present in culture of host cell will increase the number of copies of the marker gene. Since the amplified region is associated with the antibody gene, production of the antibody will also increase (Crouse et al., Mol. Cell. Biol. 3:257 (1983)).

The host cell may be co-transfected with two expression vectors of the invention, the first vector encoding a heavy chain derived polypeptide and the second vector encoding a light chain derived polypeptide. The two vectors may contain identical selectable markers which enable equal expression of heavy and light chain polypeptides. Alternatively, a single vector may be used which encodes, and is capable of expressing, both heavy and light chain polypeptides. In such situations, the light chain should be placed before the heavy chain to avoid an excess of toxic free heavy chain (Proudfoot, Nature 322:52 (1986); Kohler, Proc. Natl. Acad. Sci. USA 77:2197 (1980)). The coding sequences for the heavy and light chains may comprise cDNA or genomic DNA.

Once an antibody molecule of the invention has been produced by an animal, chemically synthesized, or recombinantly expressed, it may be purified by any method known in the art for purification of an immunoglobulin molecule, for example, by chromatography (e.g., ion exchange, affinity, particularly by affinity for the specific antigen after Protein A, and sizing column chromatography), centrifugation, differential solubility, or by any other standard technique for the purification of proteins. In addition, the antibodies of the present invention or fragments thereof can be fused to heterologous polypeptide sequences described herein or otherwise known in the art, to facilitate purification.

The present invention encompasses antibodies recombinantly fused or chemically conjugated (including both covalently and non-covalently conjugations) to a polypeptide (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention to generate fusion proteins. The fusion does not necessarily need to be direct, but may occur through linker sequences. The antibodies may be specific for antigens other than polypeptides (or portion thereof, preferably at least 10, 20, 30, 40, 50, 60, 70, 80, 90 or 100 amino acids of the polypeptide) of the present invention. For example, antibodies may be used to target the polypeptides of the present invention to particular cell types, either in vitro or in vivo, by fusing or conjugating the polypeptides of the present invention to antibodies specific for particular cell surface receptors. Antibodies fused or conjugated to the polypeptides of the present invention may also be used in in vitro immunoassays and purification methods using methods known in the art. See e.g., Harbor et al., supra, and PCT publication WO 93/21232; EP 439,095; Naramura et al., Immunol. Lett. 39:91-99 (1994); U.S. Patent 5,474,981; Gillies et al., PNAS 89:1428-1432 (1992); Fell et al., J. Immunol. 146:2446-2452(1991), which are incorporated by reference in their entireties.

The present invention further includes compositions comprising the polypeptides of the present invention fused or conjugated to antibody domains other than the variable regions. For example, the polypeptides of the present invention may be fused or conjugated to an antibody Fc region, or portion thereof. The antibody

portion fused to a polypeptide of the present invention may comprise the constant region, hinge region, CH1 domain, CH2 domain, and CH3 domain or any combination of whole domains or portions thereof. The polypeptides may also be fused or conjugated to the above antibody portions to form multimers. For example, Fc portions fused to the polypeptides of the present invention can form dimers through disulfide bonding between the Fc portions. Higher multimeric forms can be made by fusing the polypeptides to portions of IgA and IgM. Methods for fusing or conjugating the polypeptides of the present invention to antibody portions are known in the art. See, e.g., U.S. Patent Nos. 5,336,603; 5,622,929; 5,359,046; 5,349,053; 5,447,851; 5,112,946; EP 307,434; EP 367,166; PCT publications WO 96/04388; WO 91/06570; Ashkenazi et al., Proc. Natl. Acad. Sci. USA 88:10535-10539 (1991); Zheng et al., J. Immunol. 154:5590-5600 (1995); and Vil et al., Proc. Natl. Acad. Sci. USA 89:11337- 11341(1992) (said references incorporated by reference in their entireties).

As discussed, supra, the polypeptides corresponding to a polypeptide, polypeptide fragment, or a variant of SEQ ID NO:Y may be fused or conjugated to the above antibody portions to increase the in vivo half life of the polypeptides or for use in immunoassays using methods known in the art. Further, the polypeptides corresponding to SEQ ID NO:Y may be fused or conjugated to the above antibody portions to facilitate purification. One reported example describes chimeric proteins consisting of the first two domains of the human CD4-polypeptide and various domains of the constant regions of the heavy or light chains of mammalian immunoglobulins. (EP 394,827; Traunecker et al., Nature 331:84-86 (1988). The polypeptides of the present invention fused or conjugated to an antibody having disulfide- linked dimeric structures (due to the IgG) may also be more efficient in binding and neutralizing other molecules, than the monomeric secreted protein or protein fragment alone. (Fountoulakis et al., J. Biochem. 270:3958-3964 (1995)). In many cases, the Fc part in a fusion protein is beneficial in therapy and diagnosis, and thus can result in, for example, improved pharmacokinetic properties. (EP A 232,262). Alternatively, deleting the Fc part after the fusion protein has been

expressed, detected, and purified, would be desired. For example, the Fc portion may hinder therapy and diagnosis if the fusion protein is used as an antigen for immunizations. In drug discovery, for example, human proteins, such as hIL-5, have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists of hIL-5. (See, Bennett et al., J. Molecular Recognition 8:52-58 (1995); Johanson et al., J. Biol. Chem. 270:9459-9471 (1995).

Moreover, the antibodies or fragments thereof of the present invention can be fused to marker sequences, such as a peptide to facilitate purification. In preferred embodiments, the marker amino acid sequence is a hexa-histidine peptide, such as the tag provided in a pQE vector (QIAGEN, Inc., 9259 Eton Avenue, Chatsworth, CA, 91311), among others, many of which are commercially available. As described in Gentz et al., Proc. Natl. Acad. Sci. USA 86:821-824 (1989), for instance, hexa-histidine provides for convenient purification of the fusion protein. Other peptide tags useful for purification include, but are not limited to, the "HA" tag, which corresponds to an epitope derived from the influenza hemagglutinin protein (Wilson et al., Cell 37:767 (1984)) and the "flag" tag.

The present invention further encompasses antibodies or fragments thereof conjugated to a diagnostic or therapeutic agent. The antibodies can be used diagnostically to, for example, monitor the development or progression of a tumor as part of a clinical testing procedure to, e.g., determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, radioactive materials, positron emitting metals using various positron emission tomographies, and nonradioactive paramagnetic metal ions. The detectable substance may be coupled or conjugated either directly to the antibody (or fragment thereof) or indirectly, through an intermediate (such as, for example, a linker known in the art) using techniques known in the art. See, for example, U.S. Patent No. 4,741,900 for metal ions which can be conjugated to antibodies for use as diagnostics according to the present invention. Examples of suitable enzymes include horseradish

peroxidase, alkaline phosphatase, beta-galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin; and examples of suitable radioactive material include 125I, 131I, 111In or 99Tc.

Further, an antibody or fragment thereof may be conjugated to a therapeutic moiety such as a cytotoxin, e.g., a cytostatic or cytocidal agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, 213Bi. A cytotoxin or cytotoxic agent includes any agent that is detrimental to cells. Examples include paclitaxol, cytochalasin B, gramicidin D, ethidium bromide, emetine, mitomycin, etoposide, tenoposide, vincristine, vinblastine, colchicin, doxorubicin, daunorubicin, dihydroxy anthracin dione, mitoxantrone, mithramycin, actinomycin D, 1-dehydrotestosterone, glucocorticoids, procaine, tetracaine, lidocaine, propranolol, and puromycin and analogs or homologs thereof. Therapeutic agents include, but are not limited to, antimetabolites (e.g., methotrexate, 6-mercaptopurine, 6-thioguanine, cytarabine, 5-fluorouracil decarbazine), alkylating agents (e.g., mechlorethamine, thioepa chlorambucil, melphalan, carmustine (BSNU) and lomustine (CCNU), cyclothosphamide, busulfan, dibromomannitol, streptozotocin, mitomycin C, and cis-dichlorodiamine platinum (II) (DDP) cisplatin), anthracyclines (e.g., daunorubicin (formerly daunomycin) and doxorubicin), antibiotics (e.g., dactinomycin (formerly actinomycin), bleomycin, mithramycin, and anthramycin (AMC)), and anti-mitotic agents (e.g., vincristine and vinblastine).

The conjugates of the invention can be used for modifying a given biological response, the therapeutic agent or drug moiety is not to be construed as limited to classical chemical therapeutic agents. For example, the drug moiety may be a protein or polypeptide possessing a desired biological activity. Such proteins may include, for example, a toxin such as abrin, ricin A, pseudomonas exotoxin, or diphtheria

toxin; a protein such as tumor necrosis factor, a-interferon, ß-interferon, nerve growth factor, platelet derived growth factor, tissue plasminogen activator, an apoptotic agent, e.g., TNF-alpha, TNF-beta, AIM I (See, International Publication No. WO 97/33899), AIM II (See, International Publication No. WO 97/34911), Fas Ligand (Takahashi *et al., Int. Immunol., 6*:1567-1574 (1994)), VEGI (See, International Publication No. WO 99/23105), a thrombotic agent or an anti-angiogenic agent, e.g., angiostatin or endostatin; or, biological response modifiers such as, for example, lymphokines, interleukin-1 ("IL-1"), interleukin-2 ("IL-2"), interleukin-6 ("IL-6"), granulocyte macrophage colony stimulating factor ("GM-CSF"), granulocyte colony stimulating factor ("G-CSF"), or other growth factors.

Antibodies may also be attached to solid supports, which are particularly useful for immunoassays or purification of the target antigen. Such solid supports include, but are not limited to, glass, cellulose, polyacrylamide, nylon, polystyrene, polyvinyl chloride or polypropylene.

Techniques for conjugating such therapeutic moiety to antibodies are well known, see, e.g., Arnon et al., "Monoclonal Antibodies For Immunotargeting Of Drugs In Cancer Therapy", in Monoclonal Antibodies And Cancer Therapy, Reisfeld et al. (eds.), pp. 243-56 (Alan R. Liss, Inc. 1985); Hellstrom et al., "Antibodies For Drug Delivery", in Controlled Drug Delivery (2nd Ed.), Robinson et al. (eds.), pp. 623-53 (Marcel Dekker, Inc. 1987); Thorpe, "Antibody Carriers Of Cytotoxic Agents In Cancer Therapy: A Review", in Monoclonal Antibodies '84: Biological And Clinical Applications, Pinchera et al. (eds.), pp. 475-506 (1985); "Analysis, Results, And Future Prospective Of The Therapeutic Use Of Radiolabeled Antibody In Cancer Therapy", in Monoclonal Antibodies For Cancer Detection And Therapy, Baldwin et al. (eds.), pp. 303-16 (Academic Press 1985), and Thorpe et al., "The Preparation And Cytotoxic Properties Of Antibody-Toxin Conjugates", Immunol. Rev. 62:119-58 (1982).

Alternatively, an antibody can be conjugated to a second antibody to form an antibody heteroconjugate as described by Segal in U.S. Patent No. 4,676,980, which is incorporated herein by reference in its entirety.

An antibody, with or without a therapeutic moiety conjugated to it, administered alone or in combination with cytotoxic factor(s) and/or cytokine(s) can be used as a therapeutic.

Immunophenotyping

The antibodies of the invention may be utilized for immunophenotyping of cell lines and biological samples. The translation product of the gene of the present invention may be useful as a cell specific marker, or more specifically as a cellular marker that is differentially expressed at various stages of differentiation and/or maturation of particular cell types. Monoclonal antibodies directed against a specific epitope, or combination of epitopes, will allow for the screening of cellular populations expressing the marker. Various techniques can be utilized using monoclonal antibodies to screen for cellular populations expressing the marker(s), and include magnetic separation using antibody-coated magnetic beads, "panning" with antibody attached to a solid matrix (i.e., plate), and flow cytometry (See, e.g., U.S. Patent 5,985,660; and Morrison *et al., Cell, 96*:737-49 (1999)).

These techniques allow for the screening of particular populations of cells, such as might be found with hematological malignancies (i.e. minimal residual disease (MRD) in acute leukemic patients) and "non-self" cells in transplantations to prevent Graft-versus-Host Disease (GVHD). Alternatively, these techniques allow for the screening of hematopoietic stem and progenitor cells capable of undergoing proliferation and/or differentiation, as might be found in human umbilical cord blood.

Assays For Antibody Binding

The antibodies of the invention may be assayed for immunospecific binding by any method known in the art. The immunoassays which can be used include but are not limited to competitive and non-competitive assay systems using techniques such as western blots, radioimmunoassays, ELISA (enzyme linked immunosorbent assay), "sandwich" immunoassays, immunoprecipitation assays, precipitin reactions, gel diffusion precipitin reactions, immunodiffusion assays, agglutination assays,

complement-fixation assays, immunoradiometric assays, fluorescent immunoassays, protein A immunoassays, to name but a few. Such assays are routine and well known in the art (see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York, which is incorporated by reference herein in its entirety). Exemplary immunoassays are described briefly below (but are not intended by way of limitation).

Immunoprecipitation protocols generally comprise lysing a population of cells in a lysis buffer such as RIPA buffer (1% NP-40 or Triton X- 100, 1% sodium deoxycholate, 0.1% SDS, 0.15 M NaCl, 0.01 M sodium phosphate at pH 7.2, 1% Trasylol) supplemented with protein phosphatase and/or protease inhibitors (e.g., EDTA, PMSF, aprotinin, sodium vanadate), adding the antibody of interest to the cell lysate, incubating for a period of time (e.g., 1-4 hours) at 4° C, adding protein A and/or protein G sepharose beads to the cell lysate, incubating for about an hour or more at 4° C, washing the beads in lysis buffer and resuspending the beads in SDS/sample buffer. The ability of the antibody of interest to immunoprecipitate a particular antigen can be assessed by, e.g., western blot analysis. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the binding of the antibody to an antigen and decrease the background (e.g., pre-clearing the cell lysate with sepharose beads). For further discussion regarding immunoprecipitation protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.16.1.

Western blot analysis generally comprises preparing protein samples, electrophoresis of the protein samples in a polyacrylamide gel (e.g., 8%- 20% SDS-PAGE depending on the molecular weight of the antigen), transferring the protein sample from the polyacrylamide gel to a membrane such as nitrocellulose, PVDF or nylon, blocking the membrane in blocking solution (e.g., PBS with 3% BSA or non-fat milk), washing the membrane in washing buffer (e.g., PBS-Tween 20), blocking the membrane with primary antibody (the antibody of interest) diluted in blocking buffer, washing the membrane in washing buffer, blocking the membrane with a secondary antibody (which recognizes the primary antibody, e.g., an anti-human

antibody) conjugated to an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) or radioactive molecule (e.g., 32P or 125I) diluted in blocking buffer, washing the membrane in wash buffer, and detecting the presence of the antigen. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected and to reduce the background noise. For further discussion regarding western blot protocols see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 10.8.1.

ELISAs comprise preparing antigen, coating the well of a 96 well microtiter plate with the antigen, adding the antibody of interest conjugated to a detectable compound such as an enzymatic substrate (e.g., horseradish peroxidase or alkaline phosphatase) to the well and incubating for a period of time, and detecting the presence of the antigen. In ELISAs the antibody of interest does not have to be conjugated to a detectable compound; instead, a second antibody (which recognizes the antibody of interest) conjugated to a detectable compound may be added to the well. Further, instead of coating the well with the antigen, the antibody may be coated to the well. In this case, a second antibody conjugated to a detectable compound may be added following the addition of the antigen of interest to the coated well. One of skill in the art would be knowledgeable as to the parameters that can be modified to increase the signal detected as well as other variations of ELISAs known in the art. For further discussion regarding ELISAs see, e.g., Ausubel et al, eds, 1994, Current Protocols in Molecular Biology, Vol. 1, John Wiley & Sons, Inc., New York at 11.2.1.

The binding affinity of an antibody to an antigen and the off-rate of an antibody-antigen interaction can be determined by competitive binding assays. One example of a competitive binding assay is a radioimmunoassay comprising the incubation of labeled antigen (e.g., 3H or 125I) with the antibody of interest in the presence of increasing amounts of unlabeled antigen, and the detection of the antibody bound to the labeled antigen. The affinity of the antibody of interest for a particular antigen and the binding off-rates can be determined from the data by

scatchard plot analysis. Competition with a second antibody can also be determined using radioimmunoassays. In this case, the antigen is incubated with antibody of interest conjugated to a labeled compound (e.g., 3H or 125I) in the presence of increasing amounts of an unlabeled second antibody.

Therapeutic Uses

The present invention is further directed to antibody-based therapies which involve administering antibodies of the invention to an animal, preferably a mammal, and most preferably a human, patient for treating one or more of the disclosed diseases, disorders, or conditions. Therapeutic compounds of the invention include, but are not limited to, antibodies of the invention (including fragments, analogs and derivatives thereof as described herein) and nucleic acids encoding antibodies of the invention (including fragments, analogs and derivatives thereof and anti-idiotypic antibodies as described herein). The antibodies of the invention can be used to treat, inhibit or prevent diseases, disorders or conditions associated with aberrant expression and/or activity of a polypeptide of the invention, including, but not limited to, any one or more of the diseases, disorders, or conditions described herein. The treatment and/or prevention of diseases, disorders, or conditions associated with aberrant expression and/or activity of a polypeptide of the invention includes, but is not limited to, alleviating symptoms associated with those diseases, disorders or conditions. Antibodies of the invention may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors (such as, e.g., IL-2, IL-3 and IL-7), for example, which serve to increase the number or activity of effector cells which interact with the antibodies.

The antibodies of the invention may be administered alone or in combination with other types of treatments (e.g., radiation therapy, chemotherapy, hormonal therapy, immunotherapy and anti-tumor agents). Generally, administration of products of a species origin or species reactivity (in the case of antibodies) that is the same species as that of the patient is preferred. Thus, in a preferred embodiment, human antibodies, fragments derivatives, analogs, or nucleic acids, are administered to a human patient for therapy or prophylaxis.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragments thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides of the invention, including fragments thereof. Preferred binding affinities include those with a dissociation constant or Kd less than 5×10^{-2} M, 10^{-2} M, 5×10^{-3} M, 10^{-3} M, 5×10^{-4} M, 10^{-4} M, 5×10^{-5} M, 10^{-5} M, 5×10^{-6} M, 10^{-6} M, 5×10^{-7} M, 10^{-7} M, 5×10^{-8} M, 10^{-8} M, 5×10^{-9} M, 10^{-9} M, 5×10^{-10} M, 10^{-10} M, 5×10^{-11} M, 10^{-11} M, 5×10^{-12} M, 10^{-12} M, 5×10^{-13} M, 10^{-13} M, 5×10^{-14} M, 10^{-14} M, 5×10^{-15} M, and 10^{-15} M.

Gene Therapy

In a specific embodiment, nucleic acids comprising sequences encoding antibodies or functional derivatives thereof, are administered to treat, inhibit or prevent a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention, by way of gene therapy. Gene therapy refers to therapy performed by the administration to a subject of an expressed or expressible nucleic

acid. In this embodiment of the invention, the nucleic acids produce their encoded protein that mediates a therapeutic effect.

Any of the methods for gene therapy available in the art can be used according to the present invention. Exemplary methods are described below.

For general reviews of the methods of gene therapy, see Goldspiel et al., Clinical Pharmacy 12:488-505 (1993); Wu and Wu, Biotherapy 3:87-95 (1991); Tolstoshev, Ann. Rev. Pharmacol. Toxicol. 32:573-596 (1993); Mulligan, Science 260:926-932 (1993); and Morgan and Anderson, Ann. Rev. Biochem. 62:191-217 (1993); May, TIBTECH 11(5):155-215 (1993). Methods commonly known in the art of recombinant DNA technology which can be used are described in Ausubel et al. (eds.), Current Protocols in Molecular Biology, John Wiley & Sons, NY (1993); and Kriegler, Gene Transfer and Expression, A Laboratory Manual, Stockton Press, NY (1990).

In a preferred aspect, the compound comprises nucleic acid sequences encoding an antibody, said nucleic acid sequences being part of expression vectors that express the antibody or fragments or chimeric proteins or heavy or light chains thereof in a suitable host. In particular, such nucleic acid sequences have promoters operably linked to the antibody coding region, said promoter being inducible or constitutive, and, optionally, tissue-specific. In another particular embodiment, nucleic acid molecules are used in which the antibody coding sequences and any other desired sequences are flanked by regions that promote homologous recombination at a desired site in the genome, thus providing for intrachromosomal expression of the antibody encoding nucleic acids (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989). In specific embodiments, the expressed antibody molecule is a single chain antibody; alternatively, the nucleic acid sequences include sequences encoding both the heavy and light chains, or fragments thereof, of the antibody.

Delivery of the nucleic acids into a patient may be either direct, in which case the patient is directly exposed to the nucleic acid or nucleic acid- carrying vectors, or indirect, in which case, cells are first transformed with the nucleic acids in vitro, then

transplanted into the patient. These two approaches are known, respectively, as in vivo or ex vivo gene therapy.

In a specific embodiment, the nucleic acid sequences are directly administered in vivo, where it is expressed to produce the encoded product. This can be accomplished by any of numerous methods known in the art, e.g., by constructing them as part of an appropriate nucleic acid expression vector and administering it so that they become intracellular, e.g., by infection using defective or attenuated retrovirals or other viral vectors (see U.S. Patent No. 4,980,286), or by direct injection of naked DNA, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, encapsulation in liposomes, microparticles, or microcapsules, or by administering them in linkage to a peptide which is known to enter the nucleus, by administering it in linkage to a ligand subject to receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)) (which can be used to target cell types specifically expressing the receptors), etc. In another embodiment, nucleic acid-ligand complexes can be formed in which the ligand comprises a fusogenic viral peptide to disrupt endosomes, allowing the nucleic acid to avoid lysosomal degradation. In yet another embodiment, the nucleic acid can be targeted in vivo for cell specific uptake and expression, by targeting a specific receptor (see, e.g., PCT Publications WO 92/06180; WO 92/22635; WO92/20316; WO93/14188, WO 93/20221). Alternatively, the nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination (Koller and Smithies, Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); Zijlstra et al., Nature 342:435-438 (1989)).

In a specific embodiment, viral vectors that contains nucleic acid sequences encoding an antibody of the invention are used. For example, a retroviral vector can be used (see Miller et al., Meth. Enzymol. 217:581-599 (1993)). These retroviral vectors contain the components necessary for the correct packaging of the viral genome and integration into the host cell DNA. The nucleic acid sequences encoding the antibody to be used in gene therapy are cloned into one or more vectors, which

facilitates delivery of the gene into a patient. More detail about retroviral vectors can be found in Boesen et al., Biotherapy 6:291-302 (1994), which describes the use of a retroviral vector to deliver the mdr1 gene to hematopoietic stem cells in order to make the stem cells more resistant to chemotherapy. Other references illustrating the use of retroviral vectors in gene therapy are: Clowes et al., J. Clin. Invest. 93:644-651 (1994); Kiem et al., Blood 83:1467-1473 (1994); Salmons and Gunzberg, Human Gene Therapy 4:129-141 (1993); and Grossman and Wilson, Curr. Opin. in Genetics and Devel. 3:110-114 (1993).

Adenoviruses are other viral vectors that can be used in gene therapy. Adenoviruses are especially attractive vehicles for delivering genes to respiratory epithelia. Adenoviruses naturally infect respiratory epithelia where they cause a mild disease. Other targets for adenovirus-based delivery systems are liver, the central nervous system, endothelial cells, and muscle. Adenoviruses have the advantage of being capable of infecting non-dividing cells. Kozarsky and Wilson, Current Opinion in Genetics and Development 3:499-503 (1993) present a review of adenovirus-based gene therapy. Bout et al., Human Gene Therapy 5:3-10 (1994) demonstrated the use of adenovirus vectors to transfer genes to the respiratory epithelia of rhesus monkeys. Other instances of the use of adenoviruses in gene therapy can be found in Rosenfeld et al., Science 252:431-434 (1991); Rosenfeld et al., Cell 68:143- 155 (1992); Mastrangeli et al., J. Clin. Invest. 91:225-234 (1993); PCT Publication WO94/12649; and Wang, et al., Gene Therapy 2:775-783 (1995). In a preferred embodiment, adenovirus vectors are used.

Adeno-associated virus (AAV) has also been proposed for use in gene therapy (Walsh et al., Proc. Soc. Exp. Biol. Med. 204:289-300 (1993); U.S. Patent No. 5,436,146).

Another approach to gene therapy involves transferring a gene to cells in tissue culture by such methods as electroporation, lipofection, calcium phosphate mediated transfection, or viral infection. Usually, the method of transfer includes the transfer of a selectable marker to the cells. The cells are then placed under selection

to isolate those cells that have taken up and are expressing the transferred gene. Those cells are then delivered to a patient.

In this embodiment, the nucleic acid is introduced into a cell prior to administration in vivo of the resulting recombinant cell. Such introduction can be carried out by any method known in the art, including but not limited to transfection, electroporation, microinjection, infection with a viral or bacteriophage vector containing the nucleic acid sequences, cell fusion, chromosome-mediated gene transfer, microcell-mediated gene transfer, spheroplast fusion, etc. Numerous techniques are known in the art for the introduction of foreign genes into cells (see, e.g., Loeffler and Behr, Meth. Enzymol. 217:599-618 (1993); Cohen et al., Meth. Enzymol. 217:618-644 (1993); Cline, Pharmac. Ther. 29:69-92m (1985) and may be used in accordance with the present invention, provided that the necessary developmental and physiological functions of the recipient cells are not disrupted. The technique should provide for the stable transfer of the nucleic acid to the cell, so that the nucleic acid is expressible by the cell and preferably heritable and expressible by its cell progeny.

The resulting recombinant cells can be delivered to a patient by various methods known in the art. Recombinant blood cells (e.g., hematopoietic stem or progenitor cells) are preferably administered intravenously. The amount of cells envisioned for use depends on the desired effect, patient state, etc., and can be determined by one skilled in the art.

Cells into which a nucleic acid can be introduced for purposes of gene therapy encompass any desired, available cell type, and include but are not limited to epithelial cells, endothelial cells, keratinocytes, fibroblasts, muscle cells, hepatocytes; blood cells such as Tlymphocytes, Blymphocytes, monocytes, macrophages, neutrophils, eosinophils, megakaryocytes, granulocytes; various stem or progenitor cells, in particular hematopoietic stem or progenitor cells, e.g., as obtained from bone marrow, umbilical cord blood, peripheral blood, fetal liver, etc.

In a preferred embodiment, the cell used for gene therapy is autologous to the patient.

In an embodiment in which recombinant cells are used in gene therapy, nucleic acid sequences encoding an antibody are introduced into the cells such that they are expressible by the cells or their progeny, and the recombinant cells are then administered in vivo for therapeutic effect. In a specific embodiment, stem or progenitor cells are used. Any stem and/or progenitor cells which can be isolated and maintained in vitro can potentially be used in accordance with this embodiment of the present invention (see e.g. PCT Publication WO 94/08598; Stemple and Anderson, Cell 71:973-985 (1992); Rheinwald, Meth. Cell Bio. 21A:229 (1980); and Pittelkow and Scott, Mayo Clinic Proc. 61:771 (1986)).

In a specific embodiment, the nucleic acid to be introduced for purposes of gene therapy comprises an inducible promoter operably linked to the coding region, such that expression of the nucleic acid is controllable by controlling the presence or absence of the appropriate inducer of transcription. Demonstration of Therapeutic or Prophylactic Activity

The compounds or pharmaceutical compositions of the invention are preferably tested in vitro, and then in vivo for the desired therapeutic or prophylactic activity, prior to use in humans. For example, in vitro assays to demonstrate the therapeutic or prophylactic utility of a compound or pharmaceutical composition include, the effect of a compound on a cell line or a patient tissue sample. The effect of the compound or composition on the cell line and/or tissue sample can be determined utilizing techniques known to those of skill in the art including, but not limited to, rosette formation assays and cell lysis assays. In accordance with the invention, in vitro assays which can be used to determine whether administration of a specific compound is indicated, include in vitro cell culture assays in which a patient tissue sample is grown in culture, and exposed to or otherwise administered a compound, and the effect of such compound upon the tissue sample is observed.

Therapeutic/Prophylactic Administration and Composition

The invention provides methods of treatment, inhibition and prophylaxis by administration to a subject of an effective amount of a compound or pharmaceutical

composition of the invention, preferably a polypeptide or antibody of the invention. In a preferred aspect, the compound is substantially purified (e.g., substantially free from substances that limit its effect or produce undesired side-effects). The subject is preferably an animal, including but not limited to animals such as cows, pigs, horses, chickens, cats, dogs, etc., and is preferably a mammal, and most preferably human.

Formulations and methods of administration that can be employed when the compound comprises a nucleic acid or an immunoglobulin are described above; additional appropriate formulations and routes of administration can be selected from among those described herein below.

Various delivery systems are known and can be used to administer a compound of the invention, e.g., encapsulation in liposomes, microparticles, microcapsules, recombinant cells capable of expressing the compound, receptor-mediated endocytosis (see, e.g., Wu and Wu, J. Biol. Chem. 262:4429-4432 (1987)), construction of a nucleic acid as part of a retroviral or other vector, etc. Methods of introduction include but are not limited to intradermal, intramuscular, intraperitoneal, intravenous, subcutaneous, intranasal, epidural, and oral routes. The compounds or compositions may be administered by any convenient route, for example by infusion or bolus injection, by absorption through epithelial or mucocutaneous linings (e.g., oral mucosa, rectal and intestinal mucosa, etc.) and may be administered together with other biologically active agents. Administration can be systemic or local. In addition, it may be desirable to introduce the pharmaceutical compounds or compositions of the invention into the central nervous system by any suitable route, including intraventricular and intrathecal injection; intraventricular injection may be facilitated by an intraventricular catheter, for example, attached to a reservoir, such as an Ommaya reservoir. Pulmonary administration can also be employed, e.g., by use of an inhaler or nebulizer, and formulation with an aerosolizing agent.

In a specific embodiment, it may be desirable to administer the pharmaceutical compounds or compositions of the invention locally to the area in need of treatment; this may be achieved by, for example, and not by way of limitation, local infusion during surgery, topical application, e.g., in conjunction with a wound dressing after

surgery, by injection, by means of a catheter, by means of a suppository, or by means of an implant, said implant being of a porous, non-porous, or gelatinous material, including membranes, such as sialastic membranes, or fibers. Preferably, when administering a protein, including an antibody, of the invention, care must be taken to use materials to which the protein does not absorb.

In another embodiment, the compound or composition can be delivered in a vesicle, in particular a liposome (see Langer, Science 249:1527-1533 (1990); Treat et al., in Liposomes in the Therapy of Infectious Disease and Cancer, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 353- 365 (1989); Lopez-Berestein, ibid., pp. 317-327; see generally ibid.)

In yet another embodiment, the compound or composition can be delivered in a controlled release system. In one embodiment, a pump may be used (see Langer, supra; Sefton, CRC Crit. Ref. Biomed. Eng. 14:201 (1987); Buchwald et al., Surgery 88:507 (1980); Saudek et al., N. Engl. J. Med. 321:574 (1989)). In another embodiment, polymeric materials can be used (see Medical Applications of Controlled Release, Langer and Wise (eds.), CRC Pres., Boca Raton, Florida (1974); Controlled Drug Bioavailability, Drug Product Design and Performance, Smolen and Ball (eds.), Wiley, New York (1984); Ranger and Peppas, J., Macromol. Sci. Rev. Macromol. Chem. 23:61 (1983); see also Levy et al., Science 228:190 (1985); During et al., Ann. Neurol. 25:351 (1989); Howard et al., J.Neurosurg. 71:105 (1989)). In yet another embodiment, a controlled release system can be placed in proximity of the therapeutic target, i.e., the brain, thus requiring only a fraction of the systemic dose (see, e.g., Goodson, in Medical Applications of Controlled Release, supra, vol. 2, pp. 115-138 (1984)).

Other controlled release systems are discussed in the review by Langer (Science 249:1527-1533 (1990)).

In a specific embodiment where the compound of the invention is a nucleic acid encoding a protein, the nucleic acid can be administered in vivo to promote expression of its encoded protein, by constructing it as part of an appropriate nucleic acid expression vector and administering it so that it becomes intracellular, e.g., by

use of a retroviral vector (see U.S. Patent No. 4,980,286), or by direct injection, or by use of microparticle bombardment (e.g., a gene gun; Biolistic, Dupont), or coating with lipids or cell-surface receptors or transfecting agents, or by administering it in linkage to a homeobox- like peptide which is known to enter the nucleus (see e.g., Joliot et al., Proc. Natl. Acad. Sci. USA 88:1864-1868 (1991)), etc. Alternatively, a nucleic acid can be introduced intracellularly and incorporated within host cell DNA for expression, by homologous recombination.

The present invention also provides pharmaceutical compositions. Such compositions comprise a therapeutically effective amount of a compound, and a pharmaceutically acceptable carrier. In a specific embodiment, the term "pharmaceutically acceptable" means approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, and more particularly in humans. The term "carrier" refers to a diluent, adjuvant, excipient, or vehicle with which the therapeutic is administered. Such pharmaceutical carriers can be sterile liquids, such as water and oils, including those of petroleum, animal, vegetable or synthetic origin, such as peanut oil, soybean oil, mineral oil, sesame oil and the like. Water is a preferred carrier when the pharmaceutical composition is administered intravenously. Saline solutions and aqueous dextrose and glycerol solutions can also be employed as liquid carriers, particularly for injectable solutions. Suitable pharmaceutical excipients include starch, glucose, lactose, sucrose, gelatin, malt, rice, flour, chalk, silica gel, sodium stearate, glycerol monostearate, talc, sodium chloride, dried skim milk, glycerol, propylene, glycol, water, ethanol and the like. The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. These compositions can take the form of solutions, suspensions, emulsion, tablets, pills, capsules, powders, sustained-release formulations and the like. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, etc. Examples of suitable

pharmaceutical carriers are described in "Remington's Pharmaceutical Sciences" by E.W. Martin. Such compositions will contain a therapeutically effective amount of the compound, preferably in purified form, together with a suitable amount of carrier so as to provide the form for proper administration to the patient. The formulation should suit the mode of administration.

In a preferred embodiment, the composition is formulated in accordance with routine procedures as a pharmaceutical composition adapted for intravenous administration to human beings. Typically, compositions for intravenous administration are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic such as lignocaine to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampoule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water or saline. Where the composition is administered by injection, an ampoule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

The compounds of the invention can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with anions such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with cations such as those derived from sodium, potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The amount of the compound of the invention which will be effective in the treatment, inhibition and prevention of a disease or disorder associated with aberrant expression and/or activity of a polypeptide of the invention can be determined by standard clinical techniques. In addition, in vitro assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of

the disease or disorder, and should be decided according to the judgment of the practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from in vitro or animal model test systems.

For antibodies, the dosage administered to a patient is typically 0.1 mg/kg to 100 mg/kg of the patient's body weight. Preferably, the dosage administered to a patient is between 0.1 mg/kg and 20 mg/kg of the patient's body weight, more preferably 1 mg/kg to 10 mg/kg of the patient's body weight. Generally, human antibodies have a longer half-life within the human body than antibodies from other species due to the immune response to the foreign polypeptides. Thus, lower dosages of human antibodies and less frequent administration is often possible. Further, the dosage and frequency of administration of antibodies of the invention may be reduced by enhancing uptake and tissue penetration (e.g., into the brain) of the antibodies by modifications such as, for example, lipidation.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration.

Diagnosis and Imaging

Labeled antibodies, and derivatives and analogs thereof, which specifically bind to a polypeptide of interest can be used for diagnostic purposes to detect, diagnose, or monitor diseases, disorders, and/or conditions associated with the aberrant expression and/or activity of a polypeptide of the invention. The invention provides for the detection of aberrant expression of a polypeptide of interest, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level,

whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of aberrant expression.

The invention provides a diagnostic assay for diagnosing a disorder, comprising (a) assaying the expression of the polypeptide of interest in cells or body fluid of an individual using one or more antibodies specific to the polypeptide interest and (b) comparing the level of gene expression with a standard gene expression level, whereby an increase or decrease in the assayed polypeptide gene expression level compared to the standard expression level is indicative of a particular disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Antibodies of the invention can be used to assay protein levels in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, et al., J. Cell . Biol. 105:3087-3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine (125I, 121I), carbon (14C), sulfur (35S), tritium (3H), indium (112In), and technetium (99Tc); luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

One aspect of the invention is the detection and diagnosis of a disease or disorder associated with aberrant expression of a polypeptide of interest in an animal, preferably a mammal and most preferably a human. In one embodiment, diagnosis comprises: a) administering (for example, parenterally, subcutaneously, or intraperitoneally) to a subject an effective amount of a labeled molecule which specifically binds to the polypeptide of interest; b) waiting for a time interval

following the administering for permitting the labeled molecule to preferentially concentrate at sites in the subject where the polypeptide is expressed (and for unbound labeled molecule to be cleared to background level); c) determining background level; and d) detecting the labeled molecule in the subject, such that detection of labeled molecule above the background level indicates that the subject has a particular disease or disorder associated with aberrant expression of the polypeptide of interest. Background level can be determined by various methods including, comparing the amount of labeled molecule detected to a standard value previously determined for a particular system.

It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of 99mTc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which contain the specific protein. In vivo tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments." (Chapter 13 in Tumor Imaging: The Radiochemical Detection of Cancer, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982).

Depending on several variables, including the type of label used and the mode of administration, the time interval following the administration for permitting the labeled molecule to preferentially concentrate at sites in the subject and for unbound labeled molecule to be cleared to background level is 6 to 48 hours or 6 to 24 hours or 6 to 12 hours. In another embodiment the time interval following administration is 5 to 20 days or 5 to 10 days.

In an embodiment, monitoring of the disease or disorder is carried out by repeating the method for diagnosing the disease or disease, for example, one month after initial diagnosis, six months after initial diagnosis, one year after initial diagnosis, etc.

Presence of the labeled molecule can be detected in the patient using methods known in the art for in vivo scanning. These methods depend upon the type of label used. Skilled artisans will be able to determine the appropriate method for detecting a particular label. Methods and devices that may be used in the diagnostic methods of the invention include, but are not limited to, computed tomography (CT), whole body scan such as position emission tomography (PET), magnetic resonance imaging (MRI), and sonography.

In a specific embodiment, the molecule is labeled with a radioisotope and is detected in the patient using a radiation responsive surgical instrument (Thurston et al., U.S. Patent No. 5,441,050). In another embodiment, the molecule is labeled with a fluorescent compound and is detected in the patient using a fluorescence responsive scanning instrument. In another embodiment, the molecule is labeled with a positron emitting metal and is detected in the patent using positron emission-tomography. In yet another embodiment, the molecule is labeled with a paramagnetic label and is detected in a patient using magnetic resonance imaging (MRI).

Kits

The present invention provides kits that can be used in the above methods. In one embodiment, a kit comprises an antibody of the invention, preferably a purified antibody, in one or more containers. In a specific embodiment, the kits of the present invention contain a substantially isolated polypeptide comprising an epitope which is specifically immunoreactive with an antibody included in the kit. Preferably, the kits of the present invention further comprise a control antibody which does not react with the polypeptide of interest. In another specific embodiment, the kits of the present invention contain a means for detecting the binding of an antibody to a polypeptide of interest (e.g., the antibody may be conjugated to a detectable substrate such as a fluorescent compound, an enzymatic substrate, a radioactive compound or a luminescent compound, or a second antibody which recognizes the first antibody may be conjugated to a detectable substrate).

In another specific embodiment of the present invention, the kit is a diagnostic kit for use in screening serum containing antibodies specific against proliferative and/or cancerous polynucleotides and polypeptides. Such a kit may include a control antibody that does not react with the polypeptide of interest. Such a kit may include a substantially isolated polypeptide antigen comprising an epitope which is specifically immunoreactive with at least one anti-polypeptide antigen antibody. Further, such a kit includes means for detecting the binding of said antibody to the antigen (e.g., the antibody may be conjugated to a fluorescent compound such as fluorescein or rhodamine which can be detected by flow cytometry). In specific embodiments, the kit may include a recombinantly produced or chemically synthesized polypeptide antigen. The polypeptide antigen of the kit may also be attached to a solid support.

In a more specific embodiment the detecting means of the above-described kit includes a solid support to which said polypeptide antigen is attached. Such a kit may also include a non-attached reporter-labeled anti-human antibody. In this embodiment, binding of the antibody to the polypeptide antigen can be detected by binding of the said reporter-labeled antibody.

In an additional embodiment, the invention includes a diagnostic kit for use in screening serum containing antigens of the polypeptide of the invention. The diagnostic kit includes a substantially isolated antibody specifically immunoreactive with polypeptide or polynucleotide antigens, and means for detecting the binding of the polynucleotide or polypeptide antigen to the antibody. In one embodiment, the antibody is attached to a solid support. In a specific embodiment, the antibody may be a monoclonal antibody. The detecting means of the kit may include a second, labeled monoclonal antibody. Alternatively, or in addition, the detecting means may include a labeled, competing antigen.

In one diagnostic configuration, test serum is reacted with a solid phase reagent having a surface-bound antigen obtained by the methods of the present invention. After binding with specific antigen antibody to the reagent and removing unbound serum components by washing, the reagent is reacted with reporter-labeled anti-human antibody to bind reporter to the reagent in proportion to the amount of

bound anti-antigen antibody on the solid support. The reagent is again washed to remove unbound labeled antibody, and the amount of reporter associated with the reagent is determined. Typically, the reporter is an enzyme which is detected by incubating the solid phase in the presence of a suitable fluorometric, luminescent or colorimetric substrate (Sigma, St. Louis, MO).

The solid surface reagent in the above assay is prepared by known techniques for attaching protein material to solid support material, such as polymeric beads, dip sticks, 96-well plate or filter material. These attachment methods generally include non-specific adsorption of the protein to the support or covalent attachment of the protein, typically through a free amine group, to a chemically reactive group on the solid support, such as an activated carboxyl, hydroxyl, or aldehyde group. Alternatively, streptavidin coated plates can be used in conjunction with biotinylated antigen(s).

Thus, the invention provides an assay system or kit for carrying out this diagnostic method. The kit generally includes a support with surface- bound recombinant antigens, and a reporter-labeled anti-human antibody for detecting surface-bound anti-antigen antibody.

<u>Uses of the Polynucleotides</u>

Each of the polynucleotides identified herein can be used in numerous ways as reagents. The following description should be considered exemplary and utilizes known techniques.

The cancer antigen polynucleotides of the present invention are useful for chromosome identification. There exists an ongoing need to identify new chromosome markers, since few chromosome marking reagents, based on actual sequence data (repeat polymorphisms), are presently available. Each sequence is specifically targeted to and can hybridize with a particular location on an individual human chromosome, thus each polynucleotide of the present invention can routinely be used as a chromosome marker using techniques known in the art.

Briefly, sequences can be mapped to chromosomes by preparing PCR primers (preferably at least 15 bp (e.g., 15-25 bp) from the sequences shown in SEQ ID NO:X, or the complement thereto. Primers can optionally be selected using computer analysis so that primers do not span more than one predicted exon in the genomic DNA. These primers are then used for PCR screening of somatic cell hybrids containing individual human chromosomes. Only those hybrids containing the human gene corresponding to SEQ ID NO:X will yield an amplified fragment.

Similarly, somatic hybrids provide a rapid method of PCR mapping the polynucleotides to particular chromosomes. Three or more clones can be assigned per day using a single thermal cycler. Moreover, sublocalization of the polynucleotides can be achieved with panels of specific chromosome fragments. Other gene mapping strategies that can be used include in situ hybridization, prescreening with labeled flow-sorted chromosomes, preselection by hybridization to construct chromosome specific-cDNA libraries, and computer mapping techniques (See, e.g., Shuler, Trends Biotechnol 16:456-459 (1998) which is hereby incorporated by reference in its entirety).

Precise chromosomal location of the polynucleotides can also be achieved using fluorescence in situ hybridization (FISH) of a metaphase chromosomal spread. This technique uses polynucleotides as short as 500 or 600 bases; however, polynucleotides 2,000-4,000 bp are preferred. For a review of this technique, see Verma et al., "Human Chromosomes: a Manual of Basic Techniques," Pergamon Press, New York (1988).

For chromosome mapping, the polynucleotides can be used individually (to mark a single chromosome or a single site on that chromosome) or in panels (for marking multiple sites and/or multiple chromosomes).

Thus, the present invention also provides a method for chromosomal localization which involves (a) preparing PCR primers from the polynucleotide sequences in Table 3 and SEQ ID NO:X and (b) screening somatic cell hybrids containing individual chromosomes.

The polynucleotides of the present invention would likewise be useful for radiation hybrid mapping, HAPPY mapping, and long range restriction mapping. For a review of these techniques and others known in the art, see, e.g. Dear, "Genome Mapping: A Practical Approach," IRL Press at Oxford University Press, London (1997); Aydin, J. Mol. Med. 77:691-694 (1999); Hacia et al., Mol. Psychiatry 3:483-492 (1998); Herrick et al., Chromosome Res. 7:409-423 (1999); Hamilton et al., Methods Cell Biol. 62:265-280 (2000); and/or Ott, J. Hered. 90:68-70 (1999) each of which is hereby incorporated by reference in its entirety.

Once a polynucleotide has been mapped to a precise chromosomal location, the physical position of the polynucleotide can be used in linkage analysis. Linkage analysis establishes coinheritance between a chromosomal location and presentation of a particular disease. (Disease mapping data are found, for example, in V. McKusick, Mendelian Inheritance in Man (available on line through Johns Hopkins University Welch Medical Library).) Assuming 1 megabase mapping resolution and one gene per 20 kb, a cDNA precisely localized to a chromosomal region associated with the disease could be one of 50-500 potential causative genes.

Thus, once coinheritance is established, differences in a polynucleotide of the invention and the corresponding gene between affected and unaffected individuals can be examined. First, visible structural alterations in the chromosomes, such as deletions or translocations, are examined in chromosome spreads or by PCR. If no structural alterations exist, the presence of point mutations are ascertained. Mutations observed in some or all affected individuals, but not in normal individuals, indicates that the mutation may cause the disease. However, complete sequencing of the polypeptide and the corresponding gene from several normal individuals is required to distinguish the mutation from a polymorphism. If a new polymorphism is identified, this polymorphic polypeptide can be used for further linkage analysis.

Furthermore, increased or decreased expression of the gene in affected individuals as compared to unaffected individuals can be assessed using the polynucleotides of the invention. Any of these alterations (altered expression,

chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

Thus, the invention provides a method of detecting increased or decreased expression levels of the cancer polynucleotides in affected individuals as compared to unaffected individuals using polynucleotides of the present invention and techniques known in the art, including but not limited to the method described in Example 11. Any of these alterations (altered expression, chromosomal rearrangement, or mutation) can be used as a diagnostic or prognostic marker.

Thus, the invention also provides a diagnostic method useful during diagnosis of a tissue specific disorder, including cancer, involving measuring the expression level of cancer polynucleotides in tissues or other cells or body fluid from an individual and comparing the measured gene expression level with a standard cancer polynucleotide expression level, whereby an increase or decrease in the gene expression level compared to the standard is indicative of a tissue specific disorder.

In still another embodiment, the invention includes a kit for analyzing samples for the presence of proliferative and/or cancerous polynucleotides derived from a test subject. In a general embodiment, the kit includes at least one polynucleotide probe containing a nucleotide sequence that will specifically hybridize with a polynucleotide of the invention and a suitable container. In a specific embodiment, the kit includes two polynucleotide probes defining an internal region of the polynucleotide of the invention, where each probe has one strand containing a 31'mer-end internal to the region. In a further embodiment, the probes may be useful as primers for polymerase chain reaction amplification.

Where a diagnosis of a tissue specific disorder, including, for example, diagnosis of a tumor, has already been made according to conventional methods, the present invention is useful as a prognostic indicator, whereby patients exhibiting enhanced or depressed cancer polynucleotide expression will experience a worse clinical outcome relative to patients expressing the gene at a level nearer the standard level.

By "measuring the expression level of cancer polynucleotides" is intended qualitatively or quantitatively measuring or estimating the level of the cancer polypeptide or the level of the mRNA encoding the cancer polypeptide in a first biological sample either directly (e.g., by determining or estimating absolute protein level or mRNA level) or relatively (e.g., by comparing to the cancer polypeptide level or mRNA level in a second biological sample). Preferably, the cancer polypeptide level or mRNA level in the first biological sample is measured or estimated and compared to a standard cancer polypeptide level or mRNA level, the standard being taken from a second biological sample obtained from an individual not having the tissue specific disorder or being determined by averaging levels from a population of individuals not having the tissue specific disorder. As will be appreciated in the art, once a standard cancer polypeptide level or mRNA level is known, it can be used repeatedly as a standard for comparison.

By "biological sample" is intended any biological sample obtained from an individual, body fluid, cell line, tissue culture, or other source which contains a cancer polypeptide or the corresponding mRNA. As indicated, biological samples include body fluids (such as sputum, breast milk, vaginal pool, bile, semen, lymph, sera, plasma, urine, synovial fluid and spinal fluid) which contain the cancer polypeptide, and other tissue sources found to express the cancer polypeptide. Methods for obtaining tissue biopsies and body fluids from mammals are well known in the art. Where the biological sample is to include mRNA, a tissue biopsy is the preferred source.

The method(s) provided above may preferrably be applied in a diagnostic method and/or kits in which polynucleotides and/or polypeptides of the invention are attached to a solid support. In one exemplary method, the support may be a "gene chip" or a "biological chip" as described in US Patents 5,837,832, 5,874,219, and 5,856,174. Further, such a gene chip with cancer antigen polynucleotides attached may be used to identify polymorphisms between the cancer antigen polynucleotide sequences, with polynucleotides isolated from a test subject. The knowledge of such polymorphisms (i.e. their location, as well as, their existence) would be beneficial in

identifying disease loci for many disorders, such as for example, in neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions. Such a method is described in US Patents 5,858,659 and 5,856,104. The US Patents referenced supra are hereby incorporated by reference in their entirety herein.

The present invention encompasses cancer polynucleotides that are chemically synthesized, or reproduced as peptide nucleic acids (PNA), or according to other methods known in the art. The use of PNAs would serve as the preferred form if the polynucleotides of the invention are incorporated onto a solid support, or gene chip. For the purposes of the present invention, a peptide nucleic acid (PNA) is a polyamide type of DNA analog and the monomeric units for adenine, guanine, thymine and cytosine are available commercially (Perceptive Biosystems). Certain components of DNA, such as phosphorus, phosphorus oxides, or deoxyribose derivatives, are not present in PNAs. As disclosed by P. E. Nielsen, M. Egholm, R. H. Berg and O. Buchardt, Science 254, 1497 (1991); and M. Egholm, O. Buchardt, L.Christensen, C. Behrens, S. M. Freier, D. A. Driver, R. H. Berg, S. K. Kim, B. Norden, and P. E. Nielsen, Nature 365, 666 (1993), PNAs bind specifically and tightly to complementary DNA strands and are not degraded by nucleases. In fact, PNA binds more strongly to DNA than DNA itself does. This is probably because there is no electrostatic repulsion between the two strands, and also the polyamide backbone is more flexible. Because of this, PNA/DNA duplexes bind under a wider range of stringency conditions than DNA/DNA duplexes, making it easier to perform multiplex hybridization. Smaller probes can be used than with DNA due to the strong binding. In addition, it is more likely that single base mismatches can be determined with PNA/DNA hybridization because a single mismatch in a PNA/DNA 15-mer lowers the melting point (T.sub.m) by 8°-20° C, vs. 4°-16° C for the DNA/DNA 15-mer duplex. Also, the absence of charge groups in PNA means that hybridization can be done at low ionic strengths and reduce possible interference by salt during the analysis.

The present invention have uses which include, but are not limited to, detecting cancer in mammals. In particular the invention is useful during diagnosis of pathological cell proliferative neoplasias which include, but are not limited to: acute myelogenous leukemias including acute monocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute erythroleukemia, acute megakaryocytic leukemia, and acute undifferentiated leukemia, etc.; and chronic myelogenous leukemias including chronic myelomonocytic leukemia, chronic granulocytic leukemia, etc. Preferred mammals include monkeys, apes, cats, dogs, cows, pigs, horses, rabbits and humans. Particularly preferred are humans.

Pathological cell proliferative disorders are often associated with inappropriate activation of proto-oncogenes. (Gelmann, E. P. et al., "The Etiology of Acute Leukemia: Molecular Genetics and Viral Oncology," in Neoplastic Diseases of the Blood, Vol 1., Wiernik, P. H. et al. eds., 161-182 (1985)). Neoplasias are now believed to result from the qualitative alteration of a normal cellular gene product, or from the quantitative modification of gene expression by insertion into the chromosome of a viral sequence, by chromosomal translocation of a gene to a more actively transcribed region, or by some other mechanism. (Gelmann et al., supra) It is likely that mutated or altered expression of specific genes is involved in the pathogenesis of some leukemias, among other tissues and cell types. (Gelmann et al., supra) Indeed, the human counterparts of the oncogenes involved in some animal neoplasias have been amplified or translocated in some cases of human leukemia and carcinoma. (Gelmann et al., supra)

For example, c-myc expression is highly amplified in the non-lymphocytic leukemia cell line HL-60. When HL-60 cells are chemically induced to stop proliferation, the level of c-myc is found to be downregulated. (International Publication Number WO 91/15580). However, it has been shown that exposure of HL-60 cells to a DNA construct that is complementary to the 5' end of c-myc or c-myb blocks translation of the corresponding mRNAs which downregulates expression of the c-myc or c-myb proteins and causes arrest of cell proliferation and

differentiation of the treated cells. (International Publication Number WO 91/15580; Wickstrom et al., Proc. Natl. Acad. Sci. 85:1028 (1988); Anfossi et al., Proc. Natl. Acad. Sci. 86:3379 (1989)). However, the skilled artisan would appreciate the present invention's usefulness is not limited to treatment of proliferative disorders of hematopoietic cells and tissues, in light of the numerous cells and cell types of varying origins which are known to exhibit proliferative phenotypes.

In addition to the foregoing, a cancer antigen polynucleotide can be used to control gene expression through triple helix formation or through antisense DNA or RNA. Antisense techniques are discussed, for example, in Okano, J. Neurochem. 56: 560 (1991); "Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance Lee et al., Nucleic Acids Research 6: 3073 (1979); Cooney et al., Science 241: 456 (1988); and Dervan et al., Science 251: 1360 (1991). Both methods rely on binding of the polynucleotide to a complementary DNA or RNA. For these techniques, preferred polynucleotides are usually oligonucleotides 20 to 40 bases in length and complementary to either the region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res. 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1360 (1991)) or to the mRNA itself (antisense - Okano, J. Neurochem. 56:560 (1991); Oligodeoxy-nucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988).) Triple helix formation optimally results in a shut-off of RNA transcription from DNA, while antisense RNA hybridization blocks translation of an mRNA molecule into polypeptide. The oligonucleotide described above can also be delivered to cells such that the antisense RNA or DNA may be expressed in vivo to inhibit production of polypeptide of the present invention antigens. Both techniques are effective in model systems, and the information disclosed herein can be used to design antisense or triple helix polynucleotides in an effort to treat disease, and in particular, for the treatment of proliferative diseases and/or conditions.

Polynucleotides of the present invention are also useful in gene therapy. One goal of gene therapy is to insert a normal gene into an organism having a defective

gene, in an effort to correct the genetic defect. The polynucleotides disclosed in the present invention offer a means of targeting such genetic defects in a highly accurate manner. Another goal is to insert a new gene that was not present in the host genome, thereby producing a new trait in the host cell.

The polynucleotides are also useful for identifying individuals from minute biological samples. The United States military, for example, is considering the use of restriction fragment length polymorphism (RFLP) for identification of its personnel. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identifying personnel. This method does not suffer from the current limitations of "Dog Tags" which can be lost, switched, or stolen, making positive identification difficult. The polynucleotides of the present invention can be used as additional DNA markers for RFLP.

The polynucleotides of the present invention can also be used as an alternative to RFLP, by determining the actual base-by-base DNA sequence of selected portions of an individual's genome. These sequences can be used to prepare PCR primers for amplifying and isolating such selected DNA, which can then be sequenced. Using this technique, individuals can be identified because each individual will have a unique set of DNA sequences. Once an unique ID database is established for an individual, positive identification of that individual, living or dead, can be made from extremely small tissue samples.

Forensic biology also benefits from using DNA-based identification techniques as disclosed herein. DNA sequences taken from very small biological samples such as tissues, e.g., hair or skin, or body fluids, e.g., blood, saliva, semen, synovial fluid, amniotic fluid, breast milk, lymph, pulmonary sputum or surfactant, urine, fecal matter, etc., can be amplified using PCR. In one prior art technique, gene sequences amplified from polymorphic loci, such as DQa class II HLA gene, are used in forensic biology to identify individuals. (Erlich, H., PCR Technology, Freeman and Co. (1992).) Once these specific polymorphic loci are amplified, they are digested with one or more restriction enzymes, yielding an identifying set of bands on

a Southern blot probed with DNA corresponding to the DQa class II HLA gene. Similarly, polynucleotides of the present invention can be used as polymorphic markers for forensic purposes.

There is also a need for reagents capable of identifying the source of a particular tissue. Such need arises, for example, in forensics when presented with tissue of unknown origin. Appropriate reagents can comprise, for example, DNA probes or primers specific to cancer polynucleotides prepared from the sequences of the present invention. Panels of such reagents can identify tissue by species and/or by organ type. In a similar fashion, these reagents can be used to screen tissue cultures for contamination.

The polynucleotides of the present invention are also useful as hybridization probes for differential identification of the tissue(s) or cell type(s) present in a biological sample. Similarly, polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of the tissue(s) (e.g., immunohistochemistry assays) or cell type(s) (e.g., immunocytochemistry assays). In addition, for a number of disorders of the above tissues or cells, significantly higher or lower levels of gene expression of the polynucleotides/polypeptides of the present invention may be detected in certain tissues (e.g., tissues expressing polypeptides and/or polynucleotides of the present invention, cancer tissues and/or cancerous and/or wounded tissues) or bodily fluids (e.g., semen, vaginal pool, breast milk, bile, lymph, serum, plasma, urine, synovial fluid or spinal fluid) taken from an individual having such a disorder, relative to a "standard" gene expression level, i.e., the expression level in healthy tissue from an individual not having the disorder.

Thus, the invention provides a diagnostic method of a disorder, which involves: (a) assaying gene expression level in cells or body fluid of an individual; (b) comparing the gene expression level with a standard gene expression level, whereby an increase or decrease in the assayed gene expression level compared to the standard expression level is indicative of a disorder.

In the very least, the polynucleotides of the present invention can be used as molecular weight markers on Southern gels, as diagnostic probes for the presence of a specific mRNA in a particular cell type, as a probe to "subtract-out" known sequences in the process of discovering novel polynucleotides, for selecting and making oligomers for attachment to a "gene chip" or other support, to raise anti-DNA antibodies using DNA immunization techniques, and as an antigen to elicit an immune response.

Uses of the Polypeptides

Each of the polypeptides identified herein can be used in numerous ways. The following description should be considered exemplary and utilizes known techniques.

Polypeptides and antibodies directed to polypeptides of the present invention are useful to provide immunological probes for differential identification of the tissue(s) (e.g., immunohistochemistry assays such as, for example, ABC immunoperoxidase (Hsu et al., J. Histochem. Cytochem. 29:577-580 (1981)) or cell type(s) (e.g., immunocytochemistry assays).

Antibodies can be used to assay levels of polypeptides encoded by polynucleotides of the invention in a biological sample using classical immunohistological methods known to those of skill in the art (e.g., see Jalkanen, et al., J. Cell. Biol. 101:976-985 (1985); Jalkanen, et al., J. Cell. Biol. 105:3087-3096 (1987)). Other antibody-based methods useful for detecting protein gene expression include immunoassays, such as the enzyme linked immunosorbent assay (ELISA) and the radioimmunoassay (RIA). Suitable antibody assay labels are known in the art and include enzyme labels, such as, glucose oxidase; radioisotopes, such as iodine (^{131}I, ^{125}I, ^{123}I, ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^{3}H), indium (^{115m}In, ^{113m}In, ^{112}In, ^{111}In), and technetium (^{99}Tc, ^{99m}Tc), thallium (^{201}Ti), gallium (^{68}Ga, ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F), ^{153}Sm, ^{177}Lu, ^{159}Gd, ^{149}Pm, ^{140}La, ^{175}Yb, ^{166}Ho, ^{90}Y, ^{47}Sc, ^{186}Re, ^{188}Re, ^{142}Pr, ^{105}Rh, ^{97}Ru; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

In addition to assaying levels of polypeptide of the present invention in a biological sample, proteins can also be detected in vivo by imaging. Antibody labels or markers for in vivo imaging of protein include those detectable by X-radiography, NMR or ESR. For X-radiography, suitable labels include radioisotopes such as barium or cesium, which emit detectable radiation but are not overtly harmful to the subject. Suitable markers for NMR and ESR include those with a detectable characteristic spin, such as deuterium, which may be incorporated into the antibody by labeling of nutrients for the relevant hybridoma.

A protein-specific antibody or antibody fragment which has been labeled with an appropriate detectable imaging moiety, such as a radioisotope (for example, ^{131}I, ^{112}In, ^{99m}Tc, (^{131}I, ^{125}I, ^{123}I, ^{121}I), carbon (^{14}C), sulfur (^{35}S), tritium (^{3}H), indium (^{115m}In, ^{113m}In, ^{112}In, ^{111}In), and technetium (^{99}Tc, ^{99m}Tc), thallium (^{201}Ti), gallium (^{68}Ga, ^{67}Ga), palladium (^{103}Pd), molybdenum (^{99}Mo), xenon (^{133}Xe), fluorine (^{18}F, ^{153}Sm, ^{177}Lu, ^{159}Gd, ^{149}Pm, ^{140}La, ^{175}Yb, ^{166}Ho, ^{90}Y, ^{47}Sc, ^{186}Re, ^{188}Re, ^{142}Pr, ^{105}Rh, ^{97}Ru), a radio-opaque substance, or a material detectable by nuclear magnetic resonance, is introduced (for example, parenterally, subcutaneously or intraperitoneally) into the mammal to be examined for immune system disorder. It will be understood in the art that the size of the subject and the imaging system used will determine the quantity of imaging moiety needed to produce diagnostic images. In the case of a radioisotope moiety, for a human subject, the quantity of radioactivity injected will normally range from about 5 to 20 millicuries of ^{99m}Tc. The labeled antibody or antibody fragment will then preferentially accumulate at the location of cells which express the polypeptide encoded by a polynucleotide of the invention. *In vivo* tumor imaging is described in S.W. Burchiel et al., "Immunopharmacokinetics of Radiolabeled Antibodies and Their Fragments" (Chapter 13 in *Tumor Imaging: The Radiochemical Detection of Cancer*, S.W. Burchiel and B. A. Rhodes, eds., Masson Publishing Inc. (1982)).

In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (e.g., polypeptides encoded by polynucleotides of the invention and/or

antibodies) that are associated with heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention in association with toxins or cytotoxic prodrugs.

By "toxin" is meant one or more compounds that bind and activate endogenous cytotoxic effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNAse, alpha toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. "Toxin" also includes a cytostatic or cytocidal agent, a therapeutic agent or a radioactive metal ion, e.g., alpha-emitters such as, for example, ^{213}Bi, or other radioisotopes such as, for example, ^{103}Pd, ^{133}Xe, ^{131}I, ^{68}Ge, ^{57}Co, ^{65}Zn, ^{85}Sr, ^{32}P, ^{35}S, ^{90}Y, ^{153}Sm, ^{153}Gd, ^{169}Yb, ^{51}Cr, ^{54}Mn, ^{75}Se, ^{113}Sn, ^{90}Yttrium, ^{117}Tin, ^{186}Rhenium, ^{166}Holmium, and ^{188}Rhenium; luminescent labels, such as luminol; and fluorescent labels, such as fluorescein and rhodamine, and biotin.

Techniques known in the art may be applied to label polypeptides of the invention (including antibodies). Such techniques include, but are not limited to, the use of bifunctional conjugating agents (see e.g., U.S. Patent Nos. 5,756,065; 5,714,631; 5,696,239; 5,652,361; 5,505,931; 5,489,425; 5,435,990; 5,428,139;

5,342,604; 5,274,119; 4,994,560; and 5,808,003; the contents of each of which are hereby incorporated by reference in its entirety).

Thus, the invention provides a diagnostic method of a disorder, which involves (a) assaying the expression level of a cancer polypeptide of the present invention in cells or body fluid of an individual; and (b) comparing the assayed polypeptide expression level with a standard polypeptide expression level, whereby an increase or decrease in the assayed polypeptide expression level compared to the standard expression level is indicative of a disorder. With respect to cancer, the presence of a relatively high amount of transcript in biopsied tissue from an individual may indicate a predisposition for the development of the disease, or may provide a means for detecting the disease prior to the appearance of actual clinical symptoms. A more definitive diagnosis of this type may allow health professionals to employ preventative measures or aggressive treatment earlier thereby preventing the development or further progression of the cancer.

Moreover, cancer antigen polypeptides of the present invention can be used to treat or prevent diseases or conditions such as, for example, neural disorders, immune system disorders, muscular disorders, reproductive disorders, gastrointestinal disorders, pulmonary disorders, cardiovascular disorders, renal disorders, proliferative disorders, and/or cancerous diseases and conditions. For example, patients can be administered a polypeptide of the present invention in an effort to replace absent or decreased levels of the polypeptide (e.g., insulin), to supplement absent or decreased levels of a different polypeptide (e.g., hemoglobin S for hemoglobin B, SOD, catalase, DNA repair proteins), to inhibit the activity of a polypeptide (e.g., an oncogene or tumor supressor), to activate the activity of a polypeptide (e.g., by binding to a receptor), to reduce the activity of a membrane bound receptor by competing with it for free ligand (e.g., soluble TNF receptors used in reducing inflammation), or to bring about a desired response (e.g., blood vessel growth inhibition, enhancement of the immune response to proliferative cells or tissues).

Similarly, antibodies directed to a polypeptide of the present invention can also be used to treat disease (as described supra, and elsewhere herein). For example,

administration of an antibody directed to a polypeptide of the present invention can bind, and/or neutralize the polypeptide, and/or reduce overproduction of the polypeptide. Similarly, administration of an antibody can activate the polypeptide, such as by binding to a polypeptide bound to a membrane (receptor).

At the very least, the polypeptides of the present invention can be used as molecular weight markers on SDS-PAGE gels or on molecular sieve gel filtration columns using methods well known to those of skill in the art. Polypeptides can also be used to raise antibodies, which in turn are used to measure protein expression from a recombinant cell, as a way of assessing transformation of the host cell. Moreover, the polypeptides of the present invention can be used to test the following biological activities.

Gene Therapy Methods

Another aspect of the present invention is to gene therapy methods for treating or preventing disorders, diseases and conditions. The gene therapy methods relate to the introduction of nucleic acid (DNA, RNA and antisense DNA or RNA) sequences into an animal to achieve expression of the polypeptide of the present invention. This method requires a polynucleotide which codes for a polypeptide of the present invention operatively linked to a promoter and any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques are known in the art, see, for example, WO90/11092, which is herein incorporated by reference.

Thus, for example, cells from a patient may be engineered with a polynucleotide (DNA or RNA) comprising a promoter operably linked to a polynucleotide of the present invention ex vivo, with the engineered cells then being provided to a patient to be treated with the polypeptide of the present invention. Such methods are well-known in the art. For example, see Belldegrun, A., et al., J. Natl. Cancer Inst. 85: 207-216 (1993); Ferrantini, M. et al., Cancer Research 53: 1107-1112 (1993); Ferrantini, M. et al., J. Immunology 153: 4604-4615 (1994); Kaido, T., et al., Int. J. Cancer 60: 221-229 (1995); Ogura, H., et al., Cancer Research 50: 5102-5106

(1990); Santodonato, L., et al., Human Gene Therapy 7:1-10 (1996); Santodonato, L., et al., Gene Therapy 4:1246-1255 (1997); and Zhang, J.-F. et al., Cancer Gene Therapy 3: 31-38 (1996)), which are herein incorporated by reference. In one embodiment, the cells which are engineered are arterial cells. The arterial cells may be reintroduced into the patient through direct injection to the artery, the tissues surrounding the artery, or through catheter injection.

As discussed in more detail below, the polynucleotide constructs can be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, and the like). The polynucleotide constructs may be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

In one embodiment, the polynucleotide of the present invention is delivered as a naked polynucleotide. The term "naked" polynucleotide, DNA or RNA refers to sequences that are free from any delivery vehicle that acts to assist, promote or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotide of the present invention can also be delivered in liposome formulations and lipofectin formulations and the like can be prepared by methods well known to those skilled in the art. Such methods are described, for example, in U.S. Patent Nos. 5,593,972, 5,589,466, and 5,580,859, which are herein incorporated by reference.

The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that allow for replication. Appropriate vectors include pWLNEO, pSV2CAT, pOG44, pXT1 and pSG available from Stratagene; pSVK3, pBPV, pMSG and pSVL available from Pharmacia; and pEF1/V5, pcDNA3.1, and pRc/CMV2 available from Invitrogen. Other suitable vectors will be readily apparent to the skilled artisan.

Any strong promoter known to those skilled in the art can be used for driving the expression of the polynucleotide sequence. Suitable promoters include adenoviral

promoters, such as the adenoviral major late promoter; or heterologous promoters, such as the cytomegalovirus (CMV) promoter; the respiratory syncytial virus (RSV) promoter; inducible promoters, such as the MMT promoter, the metallothionein promoter; heat shock promoters; the albumin promoter; the ApoAI promoter; human globin promoters; viral thymidine kinase promoters, such as the Herpes Simplex thymidine kinase promoter; retroviral LTRs; the b-actin promoter; and human growth hormone promoters. The promoter also may be the native promoter for the polynucleotide of the present invention.

Unlike other gene therapy techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular, fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. In vivo muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked nucleic acid sequence injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 mg/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration.

The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked DNA constructs can be delivered to arteries during angioplasty by the catheter used in the procedure.

The naked polynucleotides are delivered by any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, and so-called "gene guns". These delivery methods are known in the art.

The constructs may also be delivered with delivery vehicles such as viral sequences, viral particles, liposome formulations, lipofectin, precipitating agents, etc. Such methods of delivery are known in the art.

In certain embodiments, the polynucleotide constructs are complexed in a liposome preparation. Liposomal preparations for use in the instant invention include cationic (positively charged), anionic (negatively charged) and neutral preparations. However, cationic liposomes are particularly preferred because a tight charge complex can be formed between the cationic liposome and the polyanionic nucleic acid. Cationic liposomes have been shown to mediate intracellular delivery of plasmid DNA (Felgner et al., Proc. Natl. Acad. Sci. USA (1987) 84:7413-7416, which is herein incorporated by reference); mRNA (Malone et al., Proc. Natl. Acad. Sci. USA (1989) 86:6077-6081, which is herein incorporated by reference); and purified

transcription factors (Debs et al., J. Biol. Chem. (1990) 265:10189-10192, which is herein incorporated by reference), in functional form.

Cationic liposomes are readily available. For example, N[1-2,3-dioleyloxy)propyl]-N,N,N-triethylammonium (DOTMA) liposomes are particularly useful and are available under the trademark Lipofectin, from GIBCO BRL, Grand Island, N.Y. (See, also, Felgner et al., Proc. Natl Acad. Sci. USA (1987) 84:7413-7416, which is herein incorporated by reference). Other commercially available liposomes include transfectace (DDAB/DOPE) and DOTAP/DOPE (Boehringer).

Other cationic liposomes can be prepared from readily available materials using techniques well known in the art. See, e.g. PCT Publication No. WO 90/11092 (which is herein incorporated by reference) for a description of the synthesis of DOTAP (1,2-bis(oleoyloxy)-3-(trimethylammonio)propane) liposomes. Preparation of DOTMA liposomes is explained in the literature, see, e.g., P. Felgner et al., Proc. Natl. Acad. Sci. USA 84:7413-7417, which is herein incorporated by reference. Similar methods can be used to prepare liposomes from other cationic lipid materials.

Similarly, anionic and neutral liposomes are readily available, such as from Avanti Polar Lipids (Birmingham, Ala.), or can be easily prepared using readily available materials. Such materials include phosphatidyl, choline, cholesterol, phosphatidyl ethanolamine, dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), dioleoylphoshatidyl ethanolamine (DOPE), among others. These materials can also be mixed with the DOTMA and DOTAP starting materials in appropriate ratios. Methods for making liposomes using these materials are well known in the art.

For example, commercially dioleoylphosphatidyl choline (DOPC), dioleoylphosphatidyl glycerol (DOPG), and dioleoylphosphatidyl ethanolamine (DOPE) can be used in various combinations to make conventional liposomes, with or without the addition of cholesterol. Thus, for example, DOPG/DOPC vesicles can be prepared by drying 50 mg each of DOPG and DOPC under a stream of nitrogen gas into a sonication vial. The sample is placed under a vacuum pump overnight and

is hydrated the following day with deionized water. The sample is then sonicated for 2 hours in a capped vial, using a Heat Systems model 350 sonicator equipped with an inverted cup (bath type) probe at the maximum setting while the bath is circulated at 15EC. Alternatively, negatively charged vesicles can be prepared without sonication to produce multilamellar vesicles or by extrusion through nucleopore membranes to produce unilamellar vesicles of discrete size. Other methods are known and available to those of skill in the art.

The liposomes can comprise multilamellar vesicles (MLVs), small unilamellar vesicles (SUVs), or large unilamellar vesicles (LUVs), with SUVs being preferred. The various liposome-nucleic acid complexes are prepared using methods well known in the art. See, e.g., Straubinger et al., Methods of Immunology (1983), 101:512-527, which is herein incorporated by reference. For example, MLVs containing nucleic acid can be prepared by depositing a thin film of phospholipid on the walls of a glass tube and subsequently hydrating with a solution of the material to be encapsulated. SUVs are prepared by extended sonication of MLVs to produce a homogeneous population of unilamellar liposomes. The material to be entrapped is added to a suspension of preformed MLVs and then sonicated. When using liposomes containing cationic lipids, the dried lipid film is resuspended in an appropriate solution such as sterile water or an isotonic buffer solution such as 10 mM Tris/NaCl, sonicated, and then the preformed liposomes are mixed directly with the DNA. The liposome and DNA form a very stable complex due to binding of the positively charged liposomes to the cationic DNA. SUVs find use with small nucleic acid fragments. LUVs are prepared by a number of methods, well known in the art. Commonly used methods include Ca^{2+}-EDTA chelation (Papahadjopoulos et al., Biochim. Biophys. Acta (1975) 394:483; Wilson et al., Cell (1979) 17:77); ether injection (Deamer, D. and Bangham, A., Biochim. Biophys. Acta (1976) 443:629; Ostro et al., Biochem. Biophys. Res. Commun. (1977) 76:836; Fraley et al., Proc. Natl. Acad. Sci. USA (1979) 76:3348); detergent dialysis (Enoch, H. and Strittmatter, P., Proc. Natl. Acad. Sci. USA (1979) 76:145); and reverse-phase evaporation (REV) (Fraley et al., J. Biol. Chem. (1980) 255:10431; Szoka, F. and Papahadjopoulos, D., Proc. Natl. Acad. Sci.

USA (1978) 75:145; Schaefer-Ridder et al., Science (1982) 215:166), which are herein incorporated by reference.

Generally, the ratio of DNA to liposomes will be from about 10:1 to about 1:10. Preferably, the ration will be from about 5:1 to about 1:5. More preferably, the ration will be about 3:1 to about 1:3. Still more preferably, the ratio will be about 1:1.

U.S. Patent No. 5,676,954 (which is herein incorporated by reference) reports on the injection of genetic material, complexed with cationic liposomes carriers, into mice. U.S. Patent Nos. 4,897,355, 4,946,787, 5,049,386, 5,459,127, 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 (which are herein incorporated by reference) provide cationic lipids for use in transfecting DNA into cells and mammals. U.S. Patent Nos. 5,589,466, 5,693,622, 5,580,859, 5,703,055, and international publication no. WO 94/9469 (which are herein incorporated by reference) provide methods for delivering DNA-cationic lipid complexes to mammals.

In certain embodiments, cells are engineered, ex vivo or in vivo, using a retroviral particle containing RNA which comprises a sequence encoding a polypeptide of the present invention. Retroviruses from which the retroviral plasmid vectors may be derived include, but are not limited to, Moloney Murine Leukemia Virus, spleen necrosis virus, Rous sarcoma Virus, Harvey Sarcoma Virus, avian leukosis virus, gibbon ape leukemia virus, human immunodeficiency virus, Myeloproliferative Sarcoma Virus, and mammary tumor virus.

The retroviral plasmid vector is employed to transduce packaging cell lines to form producer cell lines. Examples of packaging cells which may be transfected include, but are not limited to, the PE501, PA317, R-2, R-AM, PA12, T19-14X, VT-19-17-H2, RCRE, RCRIP, GP+E-86, GP+envAm12, and DAN cell lines as described in Miller, Human Gene Therapy 1:5-14 (1990), which is incorporated herein by reference in its entirety. The vector may transduce the packaging cells through any means known in the art. Such means include, but are not limited to, electroporation, the use of liposomes, and $CaPO_4$ precipitation. In one alternative, the retroviral

plasmid vector may be encapsulated into a liposome, or coupled to a lipid, and then administered to a host.

The producer cell line generates infectious retroviral vector particles which include polynucleotide encoding a polypeptide of the present invention. Such retroviral vector particles then may be employed, to transduce eukaryotic cells, either in vitro or in vivo. The transduced eukaryotic cells will express a polypeptide of the present invention.

In certain other embodiments, cells are engineered, ex vivo or in vivo, with polynucleotide contained in an adenovirus vector. Adenovirus can be manipulated such that it encodes and expresses a polypeptide of the present invention, and at the same time is inactivated in terms of its ability to replicate in a normal lytic viral life cycle. Adenovirus expression is achieved without integration of the viral DNA into the host cell chromosome, thereby alleviating concerns about insertional mutagenesis. Furthermore, adenoviruses have been used as live enteric vaccines for many years with an excellent safety profile (Schwartz, A. R. et al. (1974) Am. Rev. Respir. Dis.109:233-238). Finally, adenovirus mediated gene transfer has been demonstrated in a number of instances including transfer of alpha-1-antitrypsin and CFTR to the lungs of cotton rats (Rosenfeld, M. A. et al. (1991) Science 252:431-434; Rosenfeld et al., (1992) Cell 68:143-155). Furthermore, extensive studies to attempt to establish adenovirus as a causative agent in human cancer were uniformly negative (Green, M. et al. (1979) Proc. Natl. Acad. Sci. USA 76:6606).

Suitable adenoviral vectors useful in the present invention are described, for example, in Kozarsky and Wilson, Curr. Opin. Genet. Devel. 3:499-503 (1993); Rosenfeld et al., Cell 68:143-155 (1992); Engelhardt et al., Human Genet. Ther. 4:759-769 (1993); Yang et al., Nature Genet. 7:362-369 (1994); Wilson et al., Nature 365:691-692 (1993); and U.S. Patent No. 5,652,224, which are herein incorporated by reference. For example, the adenovirus vector Ad2 is useful and can be grown in human 293 cells. These cells contain the El region of adenovirus and constitutively express Ela and Elb, which complement the defective adenoviruses by providing the

products of the genes deleted from the vector. In addition to Ad2, other varieties of adenovirus (e.g., Ad3, Ad5, and Ad7) are also useful in the present invention.

Preferably, the adenoviruses used in the present invention are replication deficient. Replication deficient adenoviruses require the aid of a helper virus and/or packaging cell line to form infectious particles. The resulting virus is capable of infecting cells and can express a polynucleotide of interest which is operably linked to a promoter, but cannot replicate in most cells. Replication deficient adenoviruses may be deleted in one or more of all or a portion of the following genes: E1a, E1b, E3, E4, E2a, or L1 through L5.

In certain other embodiments, the cells are engineered, ex vivo or in vivo, using an adeno-associated virus (AAV). AAVs are naturally occurring defective viruses that require helper viruses to produce infectious particles (Muzyczka, N., Curr. Topics in Microbiol. Immunol. 158:97 (1992)). It is also one of the few viruses that may integrate its DNA into non-dividing cells. Vectors containing as little as 300 base pairs of AAV can be packaged and can integrate, but space for exogenous DNA is limited to about 4.5 kb. Methods for producing and using such AAVs are known in the art. See, for example, U.S. Patent Nos. 5,139,941, 5,173,414, 5,354,678, 5,436,146, 5,474,935, 5,478,745, and 5,589,377.

For example, an appropriate AAV vector for use in the present invention will include all the sequences necessary for DNA replication, encapsidation, and host-cell integration. The polynucleotide construct is inserted into the AAV vector using standard cloning methods, such as those found in Sambrook et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press (1989). The recombinant AAV vector is then transfected into packaging cells which are infected with a helper virus, using any standard technique, including lipofection, electroporation, calcium phosphate precipitation, etc. Appropriate helper viruses include adenoviruses, cytomegaloviruses, vaccinia viruses, or herpes viruses. Once the packaging cells are transfected and infected, they will produce infectious AAV viral particles which contain the polynucleotide construct. These viral particles are then used to transduce eukaryotic cells, either ex vivo or in vivo. The transduced cells will contain the

polynucleotide construct integrated into its genome, and will express a polypeptide of the invention.

Another method of gene therapy involves operably associating heterologous control regions and endogenous polynucleotide sequences (e.g. encoding a polypeptide of the present invention) via homologous recombination (see, e.g., U.S. Patent No. 5,641,670, issued June 24, 1997; International Publication No. WO 96/29411, published September 26, 1996; International Publication No. WO 94/12650, published August 4, 1994; Koller et al., Proc. Natl. Acad. Sci. USA 86:8932-8935 (1989); and Zijlstra et al., Nature 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not normally expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made, using standard techniques known in the art, which contain the promoter with targeting sequences flanking the promoter. Suitable promoters are described herein. The targeting sequence is sufficiently complementary to an endogenous sequence to permit homologous recombination of the promoter-targeting sequence with the endogenous sequence. The targeting sequence will be sufficiently near the 5' end of the desired endogenous polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination.

The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter. The amplified promoter and targeting sequences are digested and ligated together.

The promoter-targeting sequence construct is delivered to the cells, either as naked polynucleotide, or in conjunction with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, whole viruses, lipofection, precipitating agents, etc., described in more detail above. The P promoter-targeting sequence can

be delivered by any method, included direct needle injection, intravenous injection, topical administration, catheter infusion, particle accelerators, etc. The methods are described in more detail below.

The promoter-targeting sequence construct is taken up by cells. Homologous recombination between the construct and the endogenous sequence takes place, such that an endogenous sequence is placed under the control of the promoter. The promoter then drives the expression of the endogenous sequence.

Preferably, the polynucleotide encoding a polypeptide of the present invention contains a secretory signal sequence that facilitates secretion of the protein. Typically, the signal sequence is positioned in the coding region of the polynucleotide to be expressed towards or at the 5' end of the coding region. The signal sequence may be homologous or heterologous to the polynucleotide of interest and may be homologous or heterologous to the cells to be transfected. Additionally, the signal sequence may be chemically synthesized using methods known in the art.

Any mode of administration of any of the above-described polynucleotides constructs can be used so long as the mode results in the expression of one or more molecules in an amount sufficient to provide a therapeutic effect. This includes direct needle injection, systemic injection, catheter infusion, biolistic injectors, particle accelerators (i.e., "gene guns"), gelfoam sponge depots, other commercially available depot materials, osmotic pumps (e.g., Alza minipumps), oral or suppositorial solid (tablet or pill) pharmaceutical formulations, and decanting or topical applications during surgery. For example, direct injection of naked calcium phosphate-precipitated plasmid into rat liver and rat spleen or a protein-coated plasmid into the portal vein has resulted in gene expression of the foreign gene in the rat livers (Kaneda et al., Science 243:375 (1989)).

A preferred method of local administration is by direct injection. Preferably, a recombinant molecule of the present invention complexed with a delivery vehicle is administered by direct injection into or locally within the area of arteries. Administration of a composition locally within the area of arteries refers to injecting the composition centimeters and preferably, millimeters within arteries.

Another method of local administration is to contact a polynucleotide construct of the present invention in or around a surgical wound. For example, a patient can undergo surgery and the polynucleotide construct can be coated on the surface of tissue inside the wound or the construct can be injected into areas of tissue inside the wound.

Therapeutic compositions useful in systemic administration, include recombinant molecules of the present invention complexed to a targeted delivery vehicle of the present invention. Suitable delivery vehicles for use with systemic administration comprise liposomes comprising ligands for targeting the vehicle to a particular site.

Preferred methods of systemic administration, include intravenous injection, aerosol, oral and percutaneous (topical) delivery. Intravenous injections can be performed using methods standard in the art. Aerosol delivery can also be performed using methods standard in the art (see, for example, Stribling et al., Proc. Natl. Acad. Sci. USA 189:11277-11281, 1992, which is incorporated herein by reference). Oral delivery can be performed by complexing a polynucleotide construct of the present invention to a carrier capable of withstanding degradation by digestive enzymes in the gut of an animal. Examples of such carriers, include plastic capsules or tablets, such as those known in the art. Topical delivery can be performed by mixing a polynucleotide construct of the present invention with a lipophilic reagent (e.g., DMSO) that is capable of passing into the skin.

Determining an effective amount of substance to be delivered can depend upon a number of factors including, for example, the chemical structure and biological activity of the substance, the age and weight of the animal, the precise condition requiring treatment and its severity, and the route of administration. The frequency of treatments depends upon a number of factors, such as the amount of polynucleotide constructs administered per dose, as well as the health and history of the subject. The precise amount, number of doses, and timing of doses will be determined by the attending physician or veterinarian.

Therapeutic compositions of the present invention can be administered to any animal, preferably to mammals and birds. Preferred mammals include humans, dogs, cats, mice, rats, rabbits sheep, cattle, horses and pigs, with humans being particularly preferred.

Biological Activities

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, can be used in assays to test for one or more biological activities. If these polynucleotides or polypeptides, or agonists or antagonists of the present invention, do exhibit activity in a particular assay, it is likely that these molecules may be involved in the diseases associated with the biological activity. Thus, the polynucleotides and polypeptides, and agonists or antagonists could be used to treat the associated disease.

Immune Activity

A polypeptide or polynucleotide, or agonists or antagonists of the present invention may be useful in treating deficiencies or disorders of the immune system, by activating or inhibiting the proliferation, differentiation, or mobilization (chemotaxis) of immune cells. Immune cells develop through a process called hematopoiesis, producing myeloid (platelets, red blood cells, neutrophils, and macrophages) and lymphoid (B and T lymphocytes) cells from pluripotent stem cells. The etiology of these immune deficiencies or disorders may be genetic, somatic, such as cancer or some autoimmune disorders, acquired (e.g., by chemotherapy or toxins), or infectious. Moreover, polynucleotides or polypeptides, or agonists or antagonists of the present invention can be used as a marker or detector of a particular immune system disease or disorder.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may be useful in treating or detecting deficiencies or disorders of hematopoietic cells. Polynucleotides or polypeptides, or agonists or antagonists of the present invention could be used to increase differentiation and proliferation of

hematopoietic cells, including the pluripotent stem cells, in an effort to treat those disorders associated with a decrease in certain (or many) types hematopoietic cells. Examples of immunologic deficiency syndromes include, but are not limited to: blood protein disorders (e.g. agammaglobulinemia, dysgammaglobulinemia), ataxia telangiectasia, common variable immunodeficiency, Digeorge Syndrome, HIV infection, HTLV-BLV infection, leukocyte adhesion deficiency syndrome, lymphopenia, phagocyte bactericidal dysfunction, severe combined immunodeficiency (SCIDs), Wiskott-Aldrich Disorder, anemia, thrombocytopenia, or hemoglobinuria.

Moreover, polynucleotides or polypeptides, or agonists or antagonists of the present invention could also be used to modulate hemostatic (the stopping of bleeding) or thrombolytic activity (clot formation). For example, by increasing hemostatic or thrombolytic activity, polynucleotides or polypeptides, or agonists or antagonists of the present invention could be used to treat blood coagulation disorders (e.g., afibrinogenemia, factor deficiencies), blood platelet disorders (e.g. thrombocytopenia), or wounds resulting from trauma, surgery, or other causes. Alternatively, polynucleotides or polypeptides, or agonists or antagonists of the present invention that can decrease hemostatic or thrombolytic activity could be used to inhibit or dissolve clotting. These molecules could be important in the treatment of heart attacks (infarction), strokes, or scarring.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be useful in treating or detecting autoimmune disorders. Many autoimmune disorders result from inappropriate recognition of self as foreign material by immune cells. This inappropriate recognition results in an immune response leading to the destruction of the host tissue. Therefore, the administration of polynucleotides or polypeptides, or agonists or antagonists of the present invention that can inhibit an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing autoimmune disorders.

Examples of autoimmune disorders that can be treated or detected include, but are not limited to: Addison's Disease, hemolytic anemia, antiphospholipid syndrome, rheumatoid arthritis, dermatitis, allergic encephalomyelitis, glomerulonephritis, Goodpasture's Syndrome, Graves' Disease, Multiple Sclerosis, Myasthenia Gravis, Neuritis, Ophthalmia, Bullous Pemphigoid, Pemphigus, Polyendocrinopathies, Purpura, Reiter's Disease, Stiff-Man Syndrome, Autoimmune Thyroiditis, Systemic Lupus Erythematosus, Autoimmune Pulmonary Inflammation, Guillain-Barre Syndrome, insulin dependent diabetes mellitis, and autoimmune inflammatory eye disease.

Similarly, allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems, may also be treated by polynucleotides or polypeptides, or agonists or antagonists of the present invention. Moreover, these molecules can be used to treat anaphylaxis, hypersensitivity to an antigenic molecule, or blood group incompatibility.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to treat and/or prevent organ rejection or graft-versus-host disease (GVHD). Organ rejection occurs by host immune cell destruction of the transplanted tissue through an immune response. Similarly, an immune response is also involved in GVHD, but, in this case, the foreign transplanted immune cells destroy the host tissues. The administration of polynucleotides or polypeptides, or agonists or antagonists of the present invention that inhibits an immune response, particularly the proliferation, differentiation, or chemotaxis of T-cells, may be an effective therapy in preventing organ rejection or GVHD.

Similarly, polynucleotides or polypeptides, or agonists or antagonists of the present invention may also be used to modulate inflammation. For example, polynucleotides or polypeptides, or agonists or antagonists of the present invention may inhibit the proliferation and differentiation of cells involved in an inflammatory response. These molecules can be used to treat inflammatory conditions, both chronic and acute conditions, including chronic prostatitis, granulomatous prostatitis and malacoplakia, inflammation associated with infection (e.g., septic shock, sepsis, or

systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine induced lung injury, inflammatory bowel disease, Crohn's disease, or resulting from over production of cytokines (e.g., TNF or IL-1.)

Hyperproliferative Disorders

Polynucleotides or polypeptides, or agonists or antagonists of the present invention can be used to treat or detect hyperproliferative disorders, including neoplasms. Polynucleotides or polypeptides, or agonists or antagonists of the present invention may inhibit the proliferation of the disorder through direct or indirect interactions. Alternatively, Polynucleotides or polypeptides, or agonists or antagonists of the present invention may proliferate other cells which can inhibit the hyperproliferative disorder.

For example, by increasing an immune response, particularly increasing antigenic qualities of the hyperproliferative disorder or by proliferating, differentiating, or mobilizing T-cells, hyperproliferative disorders can be treated. This immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, decreasing an immune response may also be a method of treating hyperproliferative disorders, such as a chemotherapeutic agent.

Examples of hyperproliferative disorders that can be treated or detected by Polynucleotides or polypeptides, or agonists or antagonists of the present invention include, but are not limited to neoplasms located in the: colon, abdomen, bone, breast, digestive system, liver, pancreas, peritoneum, endocrine glands (adrenal, parathyroid, pituitary, testicles, ovary, thymus, thyroid), eye, head and neck, nervous (central and peripheral), lymphatic system, pelvic, skin, soft tissue, spleen, thoracic, and urogenital.

Similarly, other hyperproliferative disorders can also be treated or detected by polynucleotides or polypeptides, or agonists or antagonists of the present invention. Examples of such hyperproliferative disorders include, but are not limited to:

hypergammaglobulinemia, lymphoproliferative disorders, paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstron's Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other hyperproliferative disease, besides neoplasia, located in an organ system listed above.

One preferred embodiment utilizes polynucleotides of the present invention to inhibit aberrant cellular division, by gene therapy using the present invention, and/or protein fusions or fragments thereof.

Thus, the present invention provides a method for treating cell proliferative disorders by inserting into an abnormally proliferating cell a polynucleotide of the present invention, wherein said polynucleotide represses said expression.

Another embodiment of the present invention provides a method of treating cell-proliferative disorders in individuals comprising administration of one or more active gene copies of the present invention to an abnormally proliferating cell or cells. In a preferred embodiment, polynucleotides of the present invention is a DNA construct comprising a recombinant expression vector effective in expressing a DNA sequence encoding said polynucleotides. In another preferred embodiment of the present invention, the DNA construct encoding the poynucleotides of the present invention is inserted into cells to be treated utilizing a retrovirus, or more preferrably an adenoviral vector (See G J. Nabel, et. al., PNAS 1999 96: 324-326, which is hereby incorporated by reference). In a most preferred embodiment, the viral vector is defective and will not transform non-proliferating cells, only proliferating cells. Moreover, in a preferred embodiment, the polynucleotides of the present invention inserted into proliferating cells either alone, or in combination with or fused to other polynucleotides, can then be modulated via an external stimulus (i.e. magnetic, specific small molecule, chemical, or drug administration, etc.), which acts upon the promoter upstream of said polynucleotides to induce expression of the encoded protein product. As such the beneficial therapeutic affect of the present invention may be expressly modulated (i.e. to increase, decrease, or inhibit expression of the present invention) based upon said external stimulus.

Polynucleotides of the present invention may be useful in repressing expression of oncogenic genes or antigens. By "repressing expression of the oncogenic genes " is intended the suppression of the transcription of the gene, the degradation of the gene transcript (pre-message RNA), the inhibition of splicing, the destruction of the messenger RNA, the prevention of the post-translational modifications of the protein, the destruction of the protein, or the inhibition of the normal function of the protein.

For local administration to abnormally proliferating cells, polynucleotides of the present invention may be administered by any method known to those of skill in the art including, but not limited to transfection, electroporation, microinjection of cells, or in vehicles such as liposomes, lipofectin, or as naked polynucleotides, or any other method described throughout the specification. The polynucleotide of the present invention may be delivered by known gene delivery systems such as, but not limited to, retroviral vectors (Gilboa, J. Virology 44:845 (1982); Hocke, Nature 320:275 (1986); Wilson, et al., Proc. Natl. Acad. Sci. U.S.A. 85:3014), vaccinia virus system (Chakrabarty et al., Mol. Cell Biol. 5:3403 (1985) or other efficient DNA delivery systems (Yates et al., Nature 313:812 (1985)) known to those skilled in the art. These references are exemplary only and are hereby incorporated by reference. In order to specifically deliver or transfect cells which are abnormally proliferating and spare non-dividing cells, it is preferable to utilize a retrovirus, or adenoviral (as described in the art and elsewhere herein) delivery system known to those of skill in the art. Since host DNA replication is required for retroviral DNA to integrate and the retrovirus will be unable to self replicate due to the lack of the retrovirus genes needed for its life cycle. Utilizing such a retroviral delivery system for polynucleotides of the present invention will target said gene and constructs to abnormally proliferating cells and will spare the non-dividing normal cells.

The polynucleotides of the present invention may be delivered directly to cell proliferative disorder/disease sites in internal organs, body cavities and the like by use of imaging devices used to guide an injecting needle directly to the disease site. The

polynucleotides of the present invention may also be administered to disease sites at the time of surgical intervention.

By "cell proliferative disease" is meant any human or animal disease or disorder, affecting any one or any combination of organs, cavities, or body parts, which is characterized by single or multiple local abnormal proliferations of cells, groups of cells, or tissues, whether benign or malignant.

Any amount of the polynucleotides of the present invention may be administered as long as it has a biologically inhibiting effect on the proliferation of the treated cells. Moreover, it is possible to administer more than one of the polynucleotide of the present invention simultaneously to the same site. By "biologically inhibiting" is meant partial or total growth inhibition as well as decreases in the rate of proliferation or growth of the cells. The biologically inhibitory dose may be determined by assessing the effects of the polynucleotides of the present invention on target malignant or abnormally proliferating cell growth in tissue culture, tumor growth in animals and cell cultures, or any other method known to one of ordinary skill in the art.

The present invention is further directed to antibody-based therapies which involve administering of anti-polypeptides and anti-polynucleotide antibodies to a mammalian, preferably human, patient for treating one or more of the described disorders. Methods for producing anti-polypeptides and anti-polynucleotide antibodies polyclonal and monoclonal antibodies are described in detail elsewhere herein. Such antibodies may be provided in pharmaceutically acceptable compositions as known in the art or as described herein.

A summary of the ways in which the antibodies of the present invention may be used therapeutically includes binding polynucleotides or polypeptides of the present invention locally or systemically in the body or by direct cytotoxicity of the antibody, e.g. as mediated by complement (CDC) or by effector cells (ADCC). Some of these approaches are described in more detail below. Armed with the teachings provided herein, one of ordinary skill in the art will know how to use the antibodies of

the present invention for diagnostic, monitoring or therapeutic purposes without undue experimentation.

In particular, the antibodies, fragments and derivatives of the present invention are useful for treating a subject having or developing cell proliferative and/or differentiation disorders as described herein. Such treatment comprises administering a single or multiple doses of the antibody, or a fragment, derivative, or a conjugate thereof.

The antibodies of this invention may be advantageously utilized in combination with other monoclonal or chimeric antibodies, or with lymphokines or hematopoietic growth factors, for example., which serve to increase the number or activity of effector cells which interact with the antibodies.

It is preferred to use high affinity and/or potent in vivo inhibiting and/or neutralizing antibodies against polypeptides or polynucleotides of the present invention, fragments or regions thereof, for both immunoassays directed to and therapy of disorders related to polynucleotides or polypeptides, including fragements thereof, of the present invention. Such antibodies, fragments, or regions, will preferably have an affinity for polynucleotides or polypeptides, including fragements thereof. Preferred binding affinities include those with a dissociation constant or Kd less than $5X10^{-6}M$, $10^{-6}M$, $5X10^{-7}M$, $10^{-7}M$, $5X10^{-8}M$, $10^{-8}M$, $5X10^{-9}M$, $10^{-9}M$, $5X10^{-10}M$, $10^{-10}M$, $5X10^{-11}M$, $10^{-11}M$, $5X10^{-12}M$, $10^{-12}M$, $5X10^{-13}M$, $10^{-13}M$, $5X10^{-14}M$, $10^{-14}M$, $5X10^{-15}M$, and $10^{-15}M$.

Moreover, polypeptides of the present invention are useful in inhibiting the angiogenesis of proliferative cells or tissues, either alone, as a protein fusion, or in combination with other polypeptides directly or indirectly, as described elsewhere herein. In a most preferred embodiment, said anti-angiogenesis effect may be achieved indirectly, for example, through the inhibition of hematopoietic, tumor-specific cells, such as tumor-associated macrophages (See Joseph IB, et al. J Natl Cancer Inst, 90(21):1648-53 (1998), which is hereby incorporated by reference). Antibodies directed to polypeptides or polynucleotides of the present invention may also result in inhibition of angiogenesis directly, or indirectly (See Witte L, et al.,

Cancer Metastasis Rev. 17(2):155-61 (1998), which is hereby incorporated by reference)).

Polypeptides, including protein fusions, of the present invention, or fragments thereof may be useful in inhibiting proliferative cells or tissues through the induction of apoptosis. Said polypeptides may act either directly, or indirectly to induce apoptosis of proliferative cells and tissues, for example in the activation of a death-domain receptor, such as tumor necrosis factor (TNF) receptor-1, CD95 (Fas/APO-1), TNF-receptor-related apoptosis-mediated protein (TRAMP) and TNF-related apoptosis-inducing ligand (TRAIL) receptor-1 and -2 (See Schulze-Osthoff K, et.al., Eur J Biochem 254(3):439-59 (1998), which is hereby incorporated by reference). Moreover, in another preferred embodiment of the present invention, said polypeptides may induce apoptosis through other mechanisms, such as in the activation of other proteins which will activate apoptosis, or through stimulating the expression of said proteins, either alone or in combination with small molecule drugs or adjuviants, such as apoptonin, galectins, thioredoxins, antiinflammatory proteins (See for example, Mutat Res 400(1-2):447-55 (1998), Med Hypotheses.50(5):423-33 (1998), Chem Biol Interact. Apr 24;111-112:23-34 (1998), J Mol Med.76(6):402-12 (1998), Int J Tissue React;20(1):3-15 (1998), which are all hereby incorporated by reference).

Polypeptides, including protein fusions to, or fragments thereof, of the present invention are useful in inhibiting the metastasis of proliferative cells or tissues. Inhibition may occur as a direct result of administering polypeptides, or antibodies directed to said polypeptides as described elsewere herein, or indirectly, such as activating the expression of proteins known to inhibit metastasis, for example alpha 4 integrins, (See, e.g., Curr Top Microbiol Immunol 1998;231:125-41, which is hereby incorporated by reference). Such thereapeutic affects of the present invention may be achieved either alone, or in combination with small molecule drugs or adjuvants.

In another embodiment, the invention provides a method of delivering compositions containing the polypeptides of the invention (e.g., compositions containing polypeptides or polypeptide antibodes associated with heterologous

polypeptides, heterologous nucleic acids, toxins, or prodrugs) to targeted cells expressing the polypeptide of the present invention. Polypeptides or polypeptide antibodes of the invention may be associated with with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. Polypeptides, protein fusions to, or fragments thereof, of the present invention are useful in enhancing the immunogenicity and/or antigenicity of proliferating cells or tissues, either directly, such as would occur if the polypeptides of the present invention 'vaccinated' the immune response to respond to proliferative antigens and immunogens, or indirectly, such as in activating the expression of proteins known to enhance the immune response (e.g. chemokines), to said antigens and immunogens.

Cardiovascular Disorders

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, may be used to treat cardiovascular disorders, including peripheral artery disease, such as limb ischemia.

Cardiovascular disorders include cardiovascular abnormalities, such as arterio-arterial fistula, arteriovenous fistula, cerebral arteriovenous malformations, congenital heart defects, pulmonary atresia, and Scimitar Syndrome. Congenital heart defects include aortic coarctation, cor triatriatum, coronary vessel anomalies, crisscross heart, dextrocardia, patent ductus arteriosus, Ebstein's anomaly, Eisenmenger complex, hypoplastic left heart syndrome, levocardia, tetralogy of fallot, transposition of great vessels, double outlet right ventricle, tricuspid atresia, persistent truncus arteriosus, and heart septal defects, such as aortopulmonary septal defect, endocardial cushion defects, Lutembacher's Syndrome, trilogy of Fallot, ventricular heart septal defects.

Cardiovascular disorders also include heart disease, such as arrhythmias, carcinoid heart disease, high cardiac output, low cardiac output, cardiac tamponade, endocarditis (including bacterial), heart aneurysm, cardiac arrest, congestive heart failure, congestive cardiomyopathy, paroxysmal dyspnea, cardiac edema, heart hypertrophy, congestive cardiomyopathy, left ventricular hypertrophy, right

ventricular hypertrophy, post-infarction heart rupture, ventricular septal rupture, heart valve diseases, myocardial diseases, myocardial ischemia, pericardial effusion, pericarditis (including constrictive and tuberculous), pneumopericardium, postpericardiotomy syndrome, pulmonary heart disease, rheumatic heart disease, ventricular dysfunction, hyperemia, cardiovascular pregnancy complications, Scimitar Syndrome, cardiovascular syphilis, and cardiovascular tuberculosis.

Arrhythmias include sinus arrhythmia, atrial fibrillation, atrial flutter, bradycardia, extrasystole, Adams-Stokes Syndrome, bundle-branch block, sinoatrial block, long QT syndrome, parasystole, Lown-Ganong-Levine Syndrome, Mahaim-type pre-excitation syndrome, Wolff-Parkinson-White syndrome, sick sinus syndrome, tachycardias, and ventricular fibrillation. Tachycardias include paroxysmal tachycardia, supraventricular tachycardia, accelerated idioventricular rhythm, atrioventricular nodal reentry tachycardia, ectopic atrial tachycardia, ectopic junctional tachycardia, sinoatrial nodal reentry tachycardia, sinus tachycardia, Torsades de Pointes, and ventricular tachycardia.

Heart valve disease include aortic valve insufficiency, aortic valve stenosis, hear murmurs, aortic valve prolapse, mitral valve prolapse, tricuspid valve prolapse, mitral valve insufficiency, mitral valve stenosis, pulmonary atresia, pulmonary valve insufficiency, pulmonary valve stenosis, tricuspid atresia, tricuspid valve insufficiency, and tricuspid valve stenosis.

Myocardial diseases include alcoholic cardiomyopathy, congestive cardiomyopathy, hypertrophic cardiomyopathy, aortic subvalvular stenosis, pulmonary subvalvular stenosis, restrictive cardiomyopathy, Chagas cardiomyopathy, endocardial fibroelastosis, endomyocardial fibrosis, Kearns Syndrome, myocardial reperfusion injury, and myocarditis.

Myocardial ischemias include coronary disease, such as angina pectoris, coronary aneurysm, coronary arteriosclerosis, coronary thrombosis, coronary vasospasm, myocardial infarction and myocardial stunning.

Cardiovascular diseases also include vascular diseases such as aneurysms, angiodysplasia, angiomatosis, bacillary angiomatosis, Hippel-Lindau Disease,

Klippel-Trenaunay-Weber Syndrome. Sturge-Weber Syndrome, angioneurotic edema, aortic diseases, Takayasu's Arteritis, aortitis, Leriche's Syndrome, arterial occlusive diseases, arteritis, enarteritis, polyarteritis nodosa, cerebrovascular disorders, diabetic angiopathies, diabetic retinopathy, embolisms, thrombosis, erythromelalgia, hemorrhoids, hepatic veno-occlusive disease, hypertension, hypotension, ischemia, peripheral vascular diseases, phlebitis, pulmonary veno-occlusive disease, Raynaud's disease, CREST syndrome, retinal vein occlusion, Scimitar syndrome, superior vena cava syndrome, telangiectasia, atacia telangiectasia, hereditary hemorrhagic telangiectasia, varicocele, varicose veins, varicose ulcer, vasculitis, and venous insufficiency.

Aneurysms include dissecting aneurysms, false aneurysms, infected aneurysms, ruptured aneurysms, aortic aneurysms, cerebral aneurysms, coronary aneurysms, heart aneurysms, and iliac aneurysms.

Arterial occlusive diseases include arteriosclerosis, intermittent claudication, carotid stenosis, fibromuscular dysplasias, mesenteric vascular occlusion, Moyamoya disease, renal artery obstruction, retinal artery occlusion, and thromboangiitis obliterans.

Cerebrovascular disorders include carotid artery diseases, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral arteriovenous malformation, cerebral artery diseases, cerebral embolism and thrombosis, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, cerebral hemorrhage, epidural hematoma, subdural hematoma, subaraxhnoid hemorrhage, cerebral infarction, cerebral ischemia (including transient), subclavian steal syndrome, periventricular leukomalacia, vascular headache, cluster headache, migraine, and vertebrobasilar insufficiency.

Embolisms include air embolisms, amniotic fluid embolisms, cholesterol embolisms, blue toe syndrome, fat embolisms, pulmonary embolisms, and thromoboembolisms. Thrombosis include coronary thrombosis, hepatic vein thrombosis, retinal vein occlusion, carotid artery thrombosis, sinus thrombosis, Wallenberg's syndrome, and thrombophlebitis.

Ischemia includes cerebral ischemia, ischemic colitis, compartment syndromes, anterior compartment syndrome, myocardial ischemia, reperfusion injuries, and peripheral limb ischemia. Vasculitis includes aortitis, arteritis, Behcet's Syndrome, Churg-Strauss Syndrome, mucocutaneous lymph node syndrome, thromboangiitis obliterans, hypersensitivity vasculitis, Schoenlein-Henoch purpura, allergic cutaneous vasculitis, and Wegener's granulomatosis.

Polynucleotides or polypeptides, or agonists or antagonists of the present invention, are especially effective for the treatment of critical limb ischemia and coronary disease.

Polypeptides may be administered using any method known in the art, including, but not limited to, direct needle injection at the delivery site, intravenous injection, topical administration, catheter infusion, biolistic injectors, particle accelerators, gelfoam sponge depots, other commercially available depot materials, osmotic pumps, oral or suppositorial solid pharmaceutical formulations, decanting or topical applications during surgery, aerosol delivery. Such methods are known in the art. Polypeptides may be administered as part of a Therapeutic, described in more detail below. Methods of delivering polynucleotides are described in more detail herein.

Anti-Angiogenesis Activity

The naturally occurring balance between endogenous stimulators and inhibitors of angiogenesis is one in which inhibitory influences predominate. Rastinejad *et al., Cell 56*:345-355 (1989). In those rare instances in which neovascularization occurs under normal physiological conditions, such as wound healing, organ regeneration, embryonic development, and female reproductive processes, angiogenesis is stringently regulated and spatially and temporally delimited. Under conditions of pathological angiogenesis such as that characterizing solid tumor growth, these regulatory controls fail. Unregulated angiogenesis becomes pathologic and sustains progression of many neoplastic and non-neoplastic diseases. A number of serious diseases are dominated by abnormal neovascularization

including solid tumor growth and metastases, arthritis, some types of eye disorders, and psoriasis. See, e.g., reviews by Moses *et al., Biotech.* *9*:630-634 (1991); Folkman *et al., N. Engl. J. Med., 333*:1757-1763 (1995); Auerbach *et al., J. Microvasc. Res. 29*:401-411 (1985); Folkman, Advances in Cancer Research, eds. Klein and Weinhouse, Academic Press, New York, pp. 175-203 (1985); Patz, *Am. J. Opthalmol. 94*:715-743 (1982); and Folkman *et al.,* Science *221*:719-725 (1983). In a number of pathological conditions, the process of angiogenesis contributes to the disease state. For example, significant data have accumulated which suggest that the growth of solid tumors is dependent on angiogenesis. Folkman and Klagsbrun, *Science 235*:442-447 (1987).

The polynucleotides encoding a polypeptide of the present invention may be administered along with other polynucleotides encoding an angiogenic protein. Examples of angiogenic proteins include, but are not limited to, acidic and basic fibroblast growth factors, VEGF-1, VEGF-2, VEGF-3, epidermal growth factor alpha and beta, platelet-derived endothelial cell growth factor, platelet-derived growth factor, tumor necrosis factor alpha, hepatocyte growth factor, insulin like growth factor, colony stimulating factor, macrophage colony stimulating factor, granulocyte/macrophage colony stimulating factor, and nitric oxide synthase.

The present invention provides for treatment of diseases or disorders associated with neovascularization by administration of the polynucleotides and/or polypeptides of the invention, as well as agonists or antagonists of the present invention. Malignant and metastatic conditions which can be treated with the polynucleotides and polypeptides, or agonists or antagonists of the invention include, but are not limited to, malignancies, solid tumors, and cancers described herein and otherwise known in the art (for a review of such disorders, see Fishman *et al.,* Medicine, 2d Ed., J. B. Lippincott Co., Philadelphia (1985)).Thus, the present invention provides a method of treating an angiogenesis-related disease and/or disorder, comprising administering to an individual in need thereof a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist of the invention. For example, polynucleotides, polypeptides, antagonists and/or agonists

may be utilized in a variety of additional methods in order to therapeutically treat a cancer or tumor. Cancers which may be treated with polynucleotides, polypeptides, antagonists and/or agonists include, but are not limited to solid tumors, including prostate, lung, breast, ovarian, stomach, pancreas, larynx, esophagus, testes, liver, parotid, biliary tract, colon, rectum, cervix, uterus, endometrium, kidney, bladder, thyroid cancer; primary tumors and metastases; melanomas; glioblastoma; Kaposi's sarcoma; leiomyosarcoma; non- small cell lung cancer; colorectal cancer; advanced malignancies; and blood born tumors such as leukemias. For example, polynucleotides, polypeptides, antagonists and/or agonists may be delivered topically, in order to treat cancers such as skin cancer, head and neck tumors, breast tumors, and Kaposi's sarcoma.

Within yet other aspects, polynucleotides, polypeptides, antagonists and/or agonists may be utilized to treat superficial forms of bladder cancer by, for example, intravesical administration. Polynucleotides, polypeptides, antagonists and/or agonists may be delivered directly into the tumor, or near the tumor site, via injection or a catheter. Of course, as the artisan of ordinary skill will appreciate, the appropriate mode of administration will vary according to the cancer to be treated. Other modes of delivery are discussed herein.

Polynucleotides, polypeptides, antagonists and/or agonists may be useful in treating other disorders, besides cancers, which involve angiogenesis. These disorders include, but are not limited to: benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; artheroscleric plaques; ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, uvietis and Pterygia (abnormal blood vessel growth) of the eye; rheumatoid arthritis; psoriasis; delayed wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars (keloids); nonunion fractures; scleroderma; trachoma; vascular adhesions; myocardial angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous malformations; ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization;

telangiectasia; hemophiliac joints; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; and atherosclerosis.

For example, within one aspect of the present invention methods are provided for treating hypertrophic scars and keloids, comprising the step of administering a polynucleotide, polypeptide, antagonist and/or agonist of the invention to a hypertrophic scar or keloid.

Within one embodiment of the present invention polynucleotides, polypeptides, antagonists and/or agonists are directly injected into a hypertrophic scar or keloid, in order to prevent the progression of these lesions. This therapy is of particular value in the prophylactic treatment of conditions which are known to result in the development of hypertrophic scars and keloids (e.g., burns), and is preferably initiated after the proliferative phase has had time to progress (approximately 14 days after the initial injury), but before hypertrophic scar or keloid development. As noted above, the present invention also provides methods for treating neovascular diseases of the eye, including for example, corneal neovascularization, neovascular glaucoma, proliferative diabetic retinopathy, retrolental fibroplasia and macular degeneration.

Moreover, Ocular disorders associated with neovascularization which can be treated with the polynucleotides and polypeptides of the present invention (including agonists and/or antagonists) include, but are not limited to: neovascular glaucoma, diabetic retinopathy, retinoblastoma, retrolental fibroplasia, uveitis, retinopathy of prematurity macular degeneration, corneal graft neovascularization, as well as other eye inflammatory diseases, ocular tumors and diseases associated with choroidal or iris neovascularization. See, e.g., reviews by Waltman *et al., Am. J. Ophthal. 85*:704-710 (1978) and Gartner *et al., Surv. Ophthal. 22*:291-312 (1978).

Thus, within one aspect of the present invention methods are provided for treating neovascular diseases of the eye such as corneal neovascularization (including corneal graft neovascularization), comprising the step of administering to a patient a therapeutically effective amount of a compound (as described above) to the cornea, such that the formation of blood vessels is inhibited. Briefly, the cornea is a tissue which normally lacks blood vessels. In certain pathological conditions however,

capillaries may extend into the cornea from the pericorneal vascular plexus of the limbus. When the cornea becomes vascularized, it also becomes clouded, resulting in a decline in the patient's visual acuity. Visual loss may become complete if the cornea completely opacitates. A wide variety of disorders can result in corneal neovascularization, including for example, corneal infections (e.g., trachoma, herpes simplex keratitis, leishmaniasis and onchocerciasis), immunological processes (e.g., graft rejection and Stevens-Johnson's syndrome), alkali burns, trauma, inflammation (of any cause), toxic and nutritional deficiency states, and as a complication of wearing contact lenses.

Within particularly preferred embodiments of the invention, may be prepared for topical administration in saline (combined with any of the preservatives and antimicrobial agents commonly used in ocular preparations), and administered in eyedrop form. The solution or suspension may be prepared in its pure form and administered several times daily. Alternatively, anti-angiogenic compositions, prepared as described above, may also be administered directly to the cornea. Within preferred embodiments, the anti-angiogenic composition is prepared with a muco-adhesive polymer which binds to cornea. Within further embodiments, the anti-angiogenic factors or anti-angiogenic compositions may be utilized as an adjunct to conventional steroid therapy. Topical therapy may also be useful prophylactically in corneal lesions which are known to have a high probability of inducing an angiogenic response (such as chemical burns). In these instances the treatment, likely in combination with steroids, may be instituted immediately to help prevent subsequent complications.

Within other embodiments, the compounds described above may be injected directly into the corneal stroma by an ophthalmologist under microscopic guidance. The preferred site of injection may vary with the morphology of the individual lesion, but the goal of the administration would be to place the composition at the advancing front of the vasculature (i.e., interspersed between the blood vessels and the normal cornea). In most cases this would involve perilimbic corneal injection to "protect" the cornea from the advancing blood vessels. This method may also be utilized shortly

after a corneal insult in order to prophylactically prevent corneal neovascularization. In this situation the material could be injected in the perilimbic cornea interspersed between the corneal lesion and its undesired potential limbic blood supply. Such methods may also be utilized in a similar fashion to prevent capillary invasion of transplanted corneas. In a sustained-release form injections might only be required 2-3 times per year. A steroid could also be added to the injection solution to reduce inflammation resulting from the injection itself.

Within another aspect of the present invention, methods are provided for treating neovascular glaucoma, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. In one embodiment, the compound may be administered topically to the eye in order to treat early forms of neovascular glaucoma. Within other embodiments, the compound may be implanted by injection into the region of the anterior chamber angle. Within other embodiments, the compound may also be placed in any location such that the compound is continuously released into the aqueous humor. Within another aspect of the present invention, methods are provided for treating proliferative diabetic retinopathy, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eyes, such that the formation of blood vessels is inhibited.

Within particularly preferred embodiments of the invention, proliferative diabetic retinopathy may be treated by injection into the aqueous humor or the vitreous, in order to increase the local concentration of the polynucleotide, polypeptide, antagonist and/or agonist in the retina. Preferably, this treatment should be initiated prior to the acquisition of severe disease requiring photocoagulation.

Within another aspect of the present invention, methods are provided for treating retrolental fibroplasia, comprising the step of administering to a patient a therapeutically effective amount of a polynucleotide, polypeptide, antagonist and/or agonist to the eye, such that the formation of blood vessels is inhibited. The

compound may be administered topically, via intravitreous injection and/or via intraocular implants.

Additionally, disorders which can be treated with the polynucleotides, polypeptides, agonists and/or agonists include, but are not limited to, hemangioma, arthritis, psoriasis, angiofibroma, atherosclerotic plaques, delayed wound healing, granulations. hemophilic joints, hypertrophic scars, nonunion fractures, Osler-Weber syndrome, pyogenic granuloma, scleroderma, trachoma, and vascular adhesions.

Moreover, disorders and/or states, which can be treated with be treated with the the polynucleotides, polypeptides, agonists and/or agonists include, but are not limited to, solid tumors, blood born tumors such as leukemias, tumor metastasis, Kaposi's sarcoma, benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas, rheumatoid arthritis, psoriasis, ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, and uvietis, delayed wound healing, endometriosis, vascluogenesis, granulations, hypertrophic scars (keloids), nonunion fractures, scleroderma, trachoma, vascular adhesions, myocardial angiogenesis, coronary collaterals, cerebral collaterals, arteriovenous malformations, ischemic limb angiogenesis, Osler-Webber Syndrome, plaque neovascularization, telangiectasia, hemophiliac joints, angiofibroma fibromuscular dysplasia, wound granulation, Crohn's disease, atherosclerosis, birth control agent by preventing vascularization required for embryo implantation controlling menstruation, diseases that have angiogenesis as a pathologic consequence such as cat scratch disease (Rochele minalia quintosa), ulcers (Helicobacter pylori), Bartonellosis and bacillary angiomatosis.

In one aspect of the birth control method, an amount of the compound sufficient to block embryo implantation is administered before or after intercourse and fertilization have occurred, thus providing an effective method of birth control, possibly a "morning after" method. Polynucleotides, polypeptides, agonists and/or agonists may also be used in controlling menstruation or administered as either a

peritoneal lavage fluid or for peritoneal implantation in the treatment of endometriosis.

Polynucleotides, polypeptides, agonists and/or agonists of the present invention may be incorporated into surgical sutures in order to prevent stitch granulomas.

Polynucleotides, polypeptides, agonists and/or agonists may be utilized in a wide variety of surgical procedures. For example, within one aspect of the present invention a compositions (in the form of, for example, a spray or film) may be utilized to coat or spray an area prior to removal of a tumor, in order to isolate normal surrounding tissues from malignant tissue, and/or to prevent the spread of disease to surrounding tissues. Within other aspects of the present invention, compositions (e.g., in the form of a spray) may be delivered via endoscopic procedures in order to coat tumors, or inhibit angiogenesis in a desired locale. Within yet other aspects of the present invention, surgical meshes which have been coated with anti- angiogenic compositions of the present invention may be utilized in any procedure wherein a surgical mesh might be utilized. For example, within one embodiment of the invention a surgical mesh laden with an anti-angiogenic composition may be utilized during abdominal cancer resection surgery (e.g., subsequent to colon resection) in order to provide support to the structure, and to release an amount of the anti-angiogenic factor.

Within further aspects of the present invention, methods are provided for treating tumor excision sites, comprising administering a polynucleotide, polypeptide, agonist and/or agonist to the resection margins of a tumor subsequent to excision, such that the local recurrence of cancer and the formation of new blood vessels at the site is inhibited. Within one embodiment of the invention, the anti-angiogenic compound is administered directly to the tumor excision site (e.g., applied by swabbing, brushing or otherwise coating the resection margins of the tumor with the anti-angiogenic compound). Alternatively, the anti-angiogenic compounds may be incorporated into known surgical pastes prior to administration. Within particularly

preferred embodiments of the invention, the anti-angiogenic compounds are applied after hepatic resections for malignancy, and after neurosurgical operations.

Within one aspect of the present invention, polynucleotides, polypeptides, agonists and/or agonists may be administered to the resection margin of a wide variety of tumors, including for example, breast, colon, brain and hepatic tumors. For example, within one embodiment of the invention, anti-angiogenic compounds may be administered to the site of a neurological tumor subsequent to excision, such that the formation of new blood vessels at the site are inhibited.

The polynucleotides, polypeptides, agonists and/or agonists of the present invention may also be administered along with other anti-angiogenic factors. Representative examples of other anti-angiogenic factors include: Anti-Invasive Factor, retinoic acid and derivatives thereof, paclitaxel, Suramin, Tissue Inhibitor of Metalloproteinase-1, Tissue Inhibitor of Metalloproteinase-2, Plasminogen Activator Inhibitor-1, Plasminogen Activator Inhibitor-2, and various forms of the lighter "d group" transition metals.

Lighter "d group" transition metals include, for example, vanadium, molybdenum, tungsten, titanium, niobium, and tantalum species. Such transition metal species may form transition metal complexes. Suitable complexes of the above-mentioned transition metal species include oxo transition metal complexes.

Representative examples of vanadium complexes include oxo vanadium complexes such as vanadate and vanadyl complexes. Suitable vanadate complexes include metavanadate and orthovanadate complexes such as, for example, ammonium metavanadate, sodium metavanadate, and sodium orthovanadate. Suitable vanadyl complexes include, for example, vanadyl acetylacetonate and vanadyl sulfate including vanadyl sulfate hydrates such as vanadyl sulfate mono- and trihydrates.

Representative examples of tungsten and molybdenum complexes also include oxo complexes. Suitable oxo tungsten complexes include tungstate and tungsten oxide complexes. Suitable tungstate complexes include ammonium tungstate, calcium tungstate, sodium tungstate dihydrate, and tungstic acid. Suitable tungsten oxides include tungsten (IV) oxide and tungsten (VI) oxide. Suitable oxo

molybdenum complexes include molybdate, molybdenum oxide, and molybdenyl complexes. Suitable molybdate complexes includc ammonium molybdate and its hydrates, sodium molybdate and its hydrates, and potassium molybdate and its hydrates. Suitable molybdenum oxides include molybdenum (VI) oxide, molybdenum (VI) oxide, and molybdic acid. Suitable molybdenyl complexes include, for example, molybdenyl acetylacetonate. Other suitable tungsten and molybdenum complexes include hydroxo derivatives derived from, for example, glycerol, tartaric acid, and sugars.

A wide variety of other anti-angiogenic factors may also be utilized within the context of the present invention. Representative examples include platelet factor 4; protamine sulphate; sulphated chitin derivatives (prepared from queen crab shells), (Murata et al., Cancer Res. 51:22-26, 1991); Sulphated Polysaccharide Peptidoglycan Complex (SP- PG) (the function of this compound may be enhanced by the presence of steroids such as estrogen, and tamoxifen citrate); Staurosporine; modulators of matrix metabolism, including for example, proline analogs, cishydroxyproline, d,L-3,4-dehydroproline, Thiaproline, alpha,alpha-dipyridyl, aminopropionitrile fumarate; 4-propyl-5-(4-pyridinyl)-2(3H)-oxazolone; Methotrexate; Mitoxantrone; Heparin; Interferons; 2 Macroglobulin-serum; ChIMP-3 (Pavloff et al., J. Bio. Chem. 267:17321-17326, 1992); Chymostatin (Tomkinson et al., Biochem J. 286:475-480, 1992); Cyclodextrin Tetradecasulfate; Eponemycin; Camptothecin; Fumagillin (Ingber et al., Nature 348:555-557, 1990); Gold Sodium Thiomalate ("GST"; Matsubara and Ziff, J. Clin. Invest. 79:1440-1446, 1987); anticollagenase-serum; alpha2-antiplasmin (Holmes et al., J. Biol. Chem. 262(4):1659-1664, 1987); Bisantrene (National Cancer Institute); Lobenzarit disodium (N-(2)-carboxyphenyl-4-chloroanthronilic acid disodium or "CCA"; Takeuchi et al., Agents Actions 36:312-316, 1992); Thalidomide; Angostatic steroid; AGM-1470; carboxynaminolmidazole; and metalloproteinase inhibitors such as BB94.

Diseases at the Cellular Level

Diseases associated with increased cell survival or the inhibition of apoptosis that could be treated or detected by polynucleotides or polypeptides, as well as antagonists or agonists of the present invention, include cancers (such as follicular lymphomas, carcinomas with p53 mutations, and hormone-dependent tumors, including, but not limited to colon cancer, cardiac tumors, pancreatic cancer, melanoma, retinoblastoma, glioblastoma, lung cancer, intestinal cancer, testicular cancer, stomach cancer, neuroblastoma, myxoma, myoma, lymphoma, endothelioma, osteoblastoma, osteoclastoma, osteosarcoma, chondrosarcoma, adenoma, breast cancer, prostate cancer, Kaposi's sarcoma and ovarian cancer); autoimmune disorders (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) and viral infections (such as herpes viruses, pox viruses and adenoviruses), inflammation, graft v. host disease, acute graft rejection, and chronic graft rejection. In preferred embodiments, polynucleotides, polypeptides, and/or antagonists of the invention are used to inhibit growth, progression, and/or metasis of cancers, in particular those listed above.

Additional diseases or conditions associated with increased cell survival that could be treated or detected by polynucleotides or polypeptides, or agonists or antagonists of the present invention include, but are not limited to, progression, and/or metastases of malignancies and related disorders such as leukemia (including acute leukemias (e.g., acute lymphocytic leukemia, acute myelocytic leukemia (including myeloblastic, promyelocytic, myelomonocytic, monocytic, and erythroleukemia)) and chronic leukemias (e.g., chronic myelocytic (granulocytic) leukemia and chronic lymphocytic leukemia)), polycythemia vera, lymphomas (e.g., Hodgkin's disease and non-Hodgkin's disease), multiple myeloma, Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors including, but not limited to, sarcomas and carcinomas such as fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma,

lymphangiosarcoma, lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, bile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, testicular tumor, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma, melanoma, neuroblastoma, and retinoblastoma.

Diseases associated with increased apoptosis that could be treated or detected by polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, include AIDS; neurodegenerative disorders (such as Alzheimer's disease, Parkinson's disease, Amyotrophic lateral sclerosis, Retinitis pigmentosa, Cerebellar degeneration and brain tumor or prior associated disease); autoimmune disorders (such as, multiple sclerosis, Sjogren's syndrome, Hashimoto's thyroiditis, biliary cirrhosis, Behcet's disease, Crohn's disease, polymyositis, systemic lupus erythematosus and immune-related glomerulonephritis and rheumatoid arthritis) myelodysplastic syndromes (such as aplastic anemia), graft v. host disease, ischemic injury (such as that caused by myocardial infarction, stroke and reperfusion injury), liver injury (e.g., hepatitis related liver injury, ischemia/reperfusion injury, cholestosis (bile duct injury) and liver cancer); toxin-induced liver disease (such as that caused by alcohol), septic shock, cachexia and anorexia.

Wound Healing and Epithelial Cell Proliferation

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, for therapeutic purposes, for example, to stimulate epithelial cell proliferation and basal keratinocytes for the purpose of wound

healing, and to stimulate hair follicle production and healing of dermal wounds. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may be clinically useful in stimulating wound healing including surgical wounds, excisional wounds, deep wounds involving damage of the dermis and epidermis, eye tissue wounds, dental tissue wounds, oral cavity wounds, diabetic ulcers, dermal ulcers, cubitus ulcers, arterial ulcers, venous stasis ulcers, burns resulting from heat exposure or chemicals, and other abnormal wound healing conditions such as uremia, malnutrition, vitamin deficiencies and complications associted with systemic treatment with steroids, radiation therapy and antineoplastic drugs and antimetabolites. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to promote dermal reestablishment subsequent to dermal loss

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to increase the adherence of skin grafts to a wound bed and to stimulate re-epithelialization from the wound bed. The following are types of grafts that polynucleotides or polypeptides, agonists or antagonists of the present invention, could be used to increase adherence to a wound bed: autografts, artificial skin, allografts, autodermic graft, autoepdermic grafts, avacular grafts, Blair-Brown grafts, bone graft, brephoplastic grafts, cutis graft, delayed graft, dermic graft, epidermic graft, fascia graft, full thickness graft, heterologous graft, xenograft, homologous graft, hyperplastic graft, lamellar graft, mesh graft, mucosal graft, Ollier-Thiersch graft, omenpal graft, patch graft, pedicle graft, penetrating graft, split skin graft, thick split graft. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, can be used to promote skin strength and to improve the appearance of aged skin.

It is believed that polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, will also produce changes in hepatocyte proliferation, and epithelial cell proliferation in the lung, breast, pancreas, stomach, small intesting, and large intestine. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could promote proliferation of

epithelial cells such as sebocytes, hair follicles, hepatocytes, type II pneumocytes, mucin-producing goblet cells, and other epithelial cells and their progenitors contained within the skin, lung, liver, and gastrointestinal tract. Polynucleotides or polypeptides, agonists or antagonists of the present invention, may promote proliferation of endothelial cells, keratinocytes, and basal keratinocytes.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could also be used to reduce the side effects of gut toxicity that result from radiation, chemotherapy treatments or viral infections. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may have a cytoprotective effect on the small intestine mucosa. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may also stimulate healing of mucositis (mouth ulcers) that result from chemotherapy and viral infections.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could further be used in full regeneration of skin in full and partial thickness skin defects, including burns, (i.e., repopulation of hair follicles, sweat glands, and sebaceous glands), treatment of other skin defects such as psoriasis. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to treat epidermolysis bullosa, a defect in adherence of the epidermis to the underlying dermis which results in frequent, open and painful blisters by accelerating reepithelialization of these lesions. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could also be used to treat gastric and doudenal ulcers and help heal by scar formation of the mucosal lining and regeneration of glandular mucosa and duodenal mucosal lining more rapidly. Inflamamatory bowel diseases, such as Crohn's disease and ulcerative colitis, are diseases which result in destruction of the mucosal surface of the small or large intestine, respectively. Thus, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to promote the resurfacing of the mucosal surface to aid more rapid healing and to prevent progression of inflammatory bowel disease. Treatment with polynucleotides or polypeptides, agonists or antagonists of the present invention, is expected to have a significant effect on the

production of mucus throughout the gastrointestinal tract and could be used to protect the intestinal mucosa from injurious substances that are ingested or following surgery. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to treat diseases associate with the under expression.

Moreover, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to prevent and heal damage to the lungs due to various pathological states. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, which could stimulate proliferation and differentiation and promote the repair of alveoli and brochiolar epithelium to prevent or treat acute or chronic lung damage. For example, emphysema, which results in the progressive loss of aveoli, and inhalation injuries, i.e., resulting from smoke inhalation and burns, that cause necrosis of the bronchiolar epithelium and alveoli could be effectively treated using polynucleotides or polypeptides, agonists or antagonists of the present invention. Also, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to stimulate the proliferation of and differentiation of type II pneumocytes, which may help treat or prevent disease such as hyaline membrane diseases, such as infant respiratory distress syndrome and bronchopulmonary displasia, in premature infants.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could stimulate the proliferation and differentiation of hepatocytes and, thus, could be used to alleviate or treat liver diseases and pathologies such as fulminant liver failure caused by cirrhosis, liver damage caused by viral hepatitis and toxic substances (i.e., acetaminophen, carbon tetraholoride and other hepatotoxins known in the art).

In addition, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used treat or prevent the onset of diabetes mellitus. In patients with newly diagnosed Types I and II diabetes, where some islet cell function remains, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, could be used to maintain the islet function so as to alleviate, delay or prevent permanent manifestation of the disease. Also, polynucleotides or

polypeptides, as well as agonists or antagonists of the present invention, could be used as an auxiliary in islet cell transplantation to improve or promote islet cell function.

Neurological Diseases

In accordance with yet a further aspect of the present invention, there is provided a process for utilizing polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, for therapeutic purposes, for example, to stimulate neurological cell proliferation and/or differentiation. Therefore, polynucleotides, polypeptides, agonists and/or antagonists of the invention may be used to treat and/or detect neurologic diseases. Moreover, polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used as a marker or detector of a particular nervous system disease or disorder.

Examples of neurologic diseases which can be treated or detected with polynucleotides, polypeptides, agonists, and/or antagonists of the present invention include brain diseases, such as metabolic brain diseases which includes phenylketonuria such as maternal phenylketonuria, pyruvate carboxylase deficiency, pyruvate dehydrogenase complex deficiency, Wernicke's Encephalopathy, brain edema, brain neoplasms such as cerebellar neoplasms which include infratentorial neoplasms, cerebral ventricle neoplasms such as choroid plexus neoplasms, hypothalamic neoplasms, supratentorial neoplasms, canavan disease, cerebellar diseases such as cerebellar ataxia which include spinocerebellar degeneration such as ataxia telangiectasia, cerebellar dyssynergia, Friederich's Ataxia, Machado-Joseph Disease, olivopontocerebellar atrophy, cerebellar neoplasms such as infratentorial neoplasms, diffuse cerebral sclerosis such as encephalitis periaxialis, globoid cell leukodystrophy, metachromatic leukodystrophy and subacute sclerosing panencephalitis, cerebrovascular disorders (such as carotid artery diseases which include carotid artery thrombosis, carotid stenosis and Moyamoya Disease, cerebral amyloid angiopathy, cerebral aneurysm, cerebral anoxia, cerebral arteriosclerosis, cerebral arteriovenous malformations, cerebral artery diseases, cerebral embolism and

thrombosis such as carotid artery thrombosis, sinus thrombosis and Wallenberg's Syndrome, cerebral hemorrhage such as epidural hematoma, subdural hematoma and subarachnoid hemorrhage, cerebral infarction, cerebral ischemia such as transient cerebral ischemia, Subclavian Steal Syndrome and vertebrobasilar insufficiency, vascular dementia such as multi-infarct dementia, periventricular leukomalacia, vascular headache such as cluster headache, migraine, dementia such as AIDS Dementia Complex, presenile dementia such as Alzheimer's Disease and Creutzfeldt-Jakob Syndrome, senile dementia such as Alzheimer's Disease and progressive supranuclear palsy, vascular dementia such as multi-infarct dementia, encephalitis which include encephalitis periaxialis, viral encephalitis such as epidemic encephalitis, Japanese Encephalitis, St. Louis Encephalitis, tick-borne encephalitis and West Nile Fever, acute disseminated encephalomyelitis, meningoencephalitis such as uveomeningoencephalitic syndrome, Postencephalitic Parkinson Disease and subacute sclerosing panencephalitis, encephalomalacia such as periventricular leukomalacia, epilepsy such as generalized epilepsy which includes infantile spasms, absence epilepsy, myoclonic epilepsy which includes MERRF Syndrome, tonic-clonic epilepsy, partial epilepsy such as complex partial epilepsy, frontal lobe epilepsy and temporal lobe epilepsy, post-traumatic epilepsy, status epilepticus such as Epilepsia Partialis Continua, Hallervorden-Spatz Syndrome, hydrocephalus such as Dandy-Walker Syndrome and normal pressure hydrocephalus, hypothalamic diseases such as hypothalamic neoplasms, cerebral malaria, narcolepsy which includes cataplexy, bulbar poliomyelitis, cerebri pseudotumor, Rett Syndrome, Reye's Syndrome, thalamic diseases, cerebral toxoplasmosis, intracranial tuberculoma and Zellweger Syndrome, central nervous system infections such as AIDS Dementia Complex, Brain Abscess, subdural empyema, encephalomyelitis such as Equine Encephalomyelitis, Venezuelan Equine Encephalomyelitis, Necrotizing Hemorrhagic Encephalomyelitis, Visna, cerebral malaria, meningitis such as arachnoiditis, aseptic meningtitis such as viral meningtitis which includes lymphocytic choriomeningitis. Bacterial meningtitis which includes Haemophilus Meningtitis, Listeria Meningtitis, Meningococcal Meningtitis such as Waterhouse-Friderichsen Syndrome,

Pneumococcal Meningtitis and meningeal tuberculosis, fungal meningitis such as Cryptococcal Meningtitis, subdural effusion, meningoencephalitis such as uvemeningoencephalitic syndrome, myelitis such as transverse myelitis, neurosyphilis such as tabes dorsalis, poliomyelitis which includes bulbar poliomyelitis and postpoliomyelitis syndrome, prion diseases (such as Creutzfeldt-Jakob Syndrome, Bovine Spongiform Encephalopathy, Gerstmann-Straussler Syndrome, Kuru, Scrapie) cerebral toxoplasmosis, central nervous system neoplasms such as brain neoplasms that include cerebellear neoplasms such as infratentorial neoplasms, cerebral ventricle neoplasms such as choroid plexus neoplasms, hypothalamic neoplasms and supratentorial neoplasms, meningeal neoplasms, spinal cord neoplasms which include epidural neoplasms, demyelinating diseases such as Canavan Diseases, diffuse cerebral sceloris which includes adrenoleukodystrophy, encephalitis periaxialis, globoid cell leukodystrophy, diffuse cerebral sclerosis such as metachromatic leukodystrophy, allergic encephalomyelitis, necrotizing hemorrhagic encephalomyelitis, progressive multifocal leukoencephalopathy, multiple sclerosis, central pontine myelinolysis, transverse myelitis, neuromyelitis optica, Scrapie, Swayback, Chronic Fatigue Syndrome, Visna, High Pressure Nervous Syndrome, Meningism, spinal cord diseases such as amyotonia congenita, amyotrophic lateral sclerosis, spinal muscular atrophy such as Werdnig-Hoffmann Disease, spinal cord compression, spinal cord neoplasms such as epidural neoplasms, syringomyelia, Tabes Dorsalis, Stiff-Man Syndrome, mental retardation such as Angelman Syndrome, Cri-du-Chat Syndrome, De Lange's Syndrome, Down Syndrome, Gangliosidoses such as gangliosidoses G(M1), Sandhoff Disease, Tay-Sachs Disease, Hartnup Disease, homocystinuria, Laurence-Moon- Biedl Syndrome, Lesch-Nyhan Syndrome, Maple Syrup Urine Disease, mucolipidosis such as fucosidosis, neuronal ceroid-lipofuscinosis, oculocerebrorenal syndrome, phenylketonuria such as maternal phenylketonuria, Prader-Willi Syndrome, Rett Syndrome, Rubinstein-Taybi Syndrome, Tuberous Sclerosis, WAGR Syndrome, nervous system abnormalities such as holoprosencephaly, neural tube defects such as anencephaly which includes hydrangencephaly, Arnold-Chairi Deformity, encephalocele, meningocele,

meningomyelocele, spinal dysraphism such as spina bifida cystica and spina bifida occulta, hereditary motor and sensory neuropathies which include Charcot-Marie Disease, Hereditary optic atrophy, Refsum's Disease, hereditary spastic paraplegia, Werdnig-Hoffmann Disease, Hereditary Sensory and Autonomic Neuropathies such as Congenital Analgesia and Familial Dysautonomia, Neurologic manifestations (such as agnosia that include Gerstmann's Syndrome, Amnesia such as retrograde amnesia, apraxia, neurogenic bladder, cataplexy, communicative disorders such as hearing disorders that includes deafness, partial hearing loss, loudness recruitment and tinnitus, language disorders such as aphasia which include agraphia, anomia, broca aphasia, and Wernicke Aphasia, Dyslexia such as Acquired Dyslexia, language development disorders, speech disorders such as aphasia which includes anomia, broca aphasia and Wernicke Aphasia, articulation disorders, communicative disorders such as speech disorders which include dysarthria, echolalia, mutism and stuttering, voice disorders such as aphonia and hoarseness, decerebrate state, delirium, fasciculation, hallucinations, meningism, movement disorders such as angelman syndrome, ataxia, athetosis, chorea, dystonia, hypokinesia, muscle hypotonia, myoclonus, tic, torticollis and tremor, muscle hypertonia such as muscle rigidity such as stiff-man syndrome, muscle spasticity, paralysis such as facial paralysis which includes Herpes Zoster Oticus, Gastroparesis, Hemiplegia, ophthalmoplegia such as diplopia, Duane's Syndrome, Horner's Syndrome, Chronic progressive external ophthalmoplegia such as Kearns Syndrome, Bulbar Paralysis, Tropical Spastic Paraparesis, Paraplegia such as Brown-Sequard Syndrome, quadriplegia, respiratory paralysis and vocal cord paralysis, paresis, phantom limb, taste disorders such as ageusia and dysgeusia, vision disorders such as amblyopia, blindness, color vision defects, diplopia, hemianopsia, scotoma and subnormal vision, sleep disorders such as hypersomnia which includes Kleine-Levin Syndrome, insomnia, and somnambulism, spasm such as trismus, unconsciousness such as coma, persistent vegetative state and syncope and vertigo, neuromuscular diseases such as amyotonia congenita, amyotrophic lateral sclerosis, Lambert-Eaton Myasthenic Syndrome, motor neuron disease, muscular atrophy such as spinal muscular atrophy, Charcot-Marie Disease

and Werdnig-Hoffmann Disease, Postpoliomyelitis Syndrome, Muscular Dystrophy, Myasthenia Gravis, Myotonia Atrophica, Myotonia Confenita, Nemaline Myopathy, Familial Periodic Paralysis, Multiplex Paramyloclonus, Tropical Spastic Paraparesis and Stiff-Man Syndrome, peripheral nervous system diseases such as acrodynia, amyloid neuropathies, autonomic nervous system diseases such as Adie's Syndrome, Barre-Lieou Syndrome, Familial Dysautonomia, Horner's Syndrome, Reflex Sympathetic Dystrophy and Shy-Drager Syndrome, Cranial Nerve Diseases such as Acoustic Nerve Diseases such as Acoustic Neuroma which includes Neurofibromatosis 2, Facial Nerve Diseases such as Facial Neuralgia,Melkersson-Rosenthal Syndrome, ocular motility disorders which includes amblyopia, nystagmus, oculomotor nerve paralysis, ophthalmoplegia such as Duane's Syndrome, Horner's Syndrome, Chronic Progressive External Ophthalmoplegia which includes Kearns Syndrome, Strabismus such as Esotropia and Exotropia, Oculomotor Nerve Paralysis, Optic Nerve Diseases such as Optic Atrophy which includes Hereditary Optic Atrophy, Optic Disk Drusen, Optic Neuritis such as Neuromyelitis Optica, Papilledema, Trigeminal Neuralgia, Vocal Cord Paralysis, Demyelinating Diseases such as Neuromyelitis Optica and Swayback, Diabetic neuropathies such as diabetic foot, nerve compression syndromes such as carpal tunnel syndrome, tarsal tunnel syndrome, thoracic outlet syndrome such as cervical rib syndrome, ulnar nerve compression syndrome, neuralgia such as causalgia, cervico-brachial neuralgia, facial neuralgia and trigeminal neuralgia, neuritis such as experimental allergic neuritis, optic neuritis, polyneuritis, polyradiculoneuritis and radiculities such as polyradiculitis, hereditary motor and sensory neuropathies such as Charcot-Marie Disease, Hereditary Optic Atrophy, Refsum's Disease, Hereditary Spastic Paraplegia and Werdnig-Hoffmann Disease, Hereditary Sensory and Autonomic Neuropathies which include Congenital Analgesia and Familial Dysautonomia, POEMS Syndrome, Sciatica, Gustatory Sweating and Tetany).

Infectious Disease

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention can be used to treat or detect infectious agents. For example, by increasing the immune response, particularly increasing the proliferation and differentiation of B and/or T cells, infectious diseases may be treated. The immune response may be increased by either enhancing an existing immune response, or by initiating a new immune response. Alternatively, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may also directly inhibit the infectious agent, without necessarily eliciting an immune response.

Viruses are one example of an infectious agent that can cause disease or symptoms that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention. Examples of viruses, include, but are not limited to Examples of viruses, include, but are not limited to the following DNA and RNA viruses and viral families: Arbovirus, Adenoviridae, Arenaviridae, Arterivirus, Birnaviridae, Bunyaviridae, Caliciviridae, Circoviridae, Coronaviridae, Dengue, EBV, HIV, Flaviviridae, Hepadnaviridae (Hepatitis), Herpesviridae (such as, Cytomegalovirus, Herpes Simplex, Herpes Zoster), Mononegavirus (e.g., Paramyxoviridae, Morbillivirus, Rhabdoviridae), Orthomyxoviridae (e.g., Influenza A, Influenza B, and parainfluenza), Papiloma virus, Papovaviridae, Parvoviridae, Picornaviridae, Poxviridae (such as Smallpox or Vaccinia), Reoviridae (e.g., Rotavirus), Retroviridae (HTLV-I, HTLV-II, Lentivirus), and Togaviridae (e.g., Rubivirus). Viruses falling within these families can cause a variety of diseases or symptoms, including, but not limited to: arthritis, bronchiollitis, respiratory syncytial virus, encephalitis, eye infections (e.g., conjunctivitis, keratitis), chronic fatigue syndrome, hepatitis (A, B, C, E, Chronic Active, Delta), Japanese B encephalitis, Junin, Chikungunya, Rift Valley fever, yellow fever, meningitis, opportunistic infections (e.g., AIDS), pneumonia, Burkitt's Lymphoma, chickenpox, hemorrhagic fever, Measles, Mumps, Parainfluenza, Rabies, the common cold, Polio, leukemia, Rubella, sexually transmitted diseases, skin diseases (e.g., Kaposi's, warts), and viremia. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific

embodiments, polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat: meningitis, Dengue, EBV, and/or hepatitis (e.g., hepatitis B). In an additional specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat patients nonresponsive to one or more other commercially available hepatitis vaccines. In a further specific embodiment polynucleotides, polypeptides, or agonists or antagonists of the invention are used to treat AIDS.

Similarly, bacterial or fungal agents that can cause disease or symptoms and that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, include, but not limited to, the following Gram-Negative and Gram-positive bacteria and bacterial families and fungi: Actinomycetales (e.g., Corynebacterium, Mycobacterium, Norcardia), Cryptococcus neoformans, Aspergillosis, Bacillaceae (e.g., Anthrax, Clostridium), Bacteroidaceae, Blastomycosis, Bordetella, Borrelia (e.g., Borrelia burgdorferi, Brucellosis, Candidiasis, Campylobacter, Coccidioidomycosis, Cryptococcosis, Dermatocycoses, E. coli (e.g., Enterotoxigenic E. coli and Enterohemorrhagic E. coli), Enterobacteriaceae (Klebsiella, Salmonella (e.g., Salmonella typhi, and Salmonella paratyphi), Serratia, Yersinia), Erysipelothrix, Helicobacter, Legionellosis, Leptospirosis, Listeria, Mycoplasmatales, Mycobacterium leprae, Vibrio cholerae, Neisseriaceae (e.g., Acinetobacter, Gonorrhea, Menigococcal), Meisseria meningitidis, Pasteurellacea Infections (e.g., Actinobacillus, Heamophilus (e.g., Heamophilus influenza type B), Pasteurella), Pseudomonas, Rickettsiaceae, Chlamydiaceae, Syphilis, Shigella spp., Staphylococcal, Meningiococcal, Pneumococcal and Streptococcal (e.g., Streptococcus pneumoniae and Group B Streptococcus). These bacterial or fungal families can cause the following diseases or symptoms, including, but not limited to: bacteremia, endocarditis, eye infections (conjunctivitis, tuberculosis, uveitis), gingivitis, opportunistic infections (e.g., AIDS related infections), paronychia, prosthesis-related infections, Reiter's Disease, respiratory tract infections, such as Whooping Cough or Empyema, sepsis, Lyme Disease, Cat-Scratch Disease, Dysentery, Paratyphoid Fever, food poisoning,

Typhoid, pneumonia, Gonorrhea, meningitis (e.g., mengitis types A and B), Chlamydia, Syphilis, Diphtheria, Leprosy, Paratuberculosis, Tuberculosis, Lupus, Botulism, gangrene, tetanus, impetigo, Rheumatic Fever, Scarlet Fever, sexually transmitted diseases, skin diseases (e.g., cellulitis, dermatocycoses), toxemia, urinary tract infections, wound infections. Polynucleotides or polypeptides, agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases. In specific embodiments, Ppolynucleotides, polypeptides, agonists or antagonists of the invention are used to treat: tetanus, Diptheria, botulism, and/or meningitis type B.

Moreover, parasitic agents causing disease or symptoms that can be treated or detected by a polynucleotide or polypeptide and/or agonist or antagonist of the present invention include, but not limited to, the following families or class: Amebiasis, Babesiosis, Coccidiosis, Cryptosporidiosis, Dientamoebiasis, Dourine, Ectoparasitic, Giardiasis, Helminthiasis, Leishmaniasis, Theileriasis, Toxoplasmosis, Trypanosomiasis, and Trichomonas and Sporozoans (e.g., Plasmodium virax, Plasmodium falciparium, Plasmodium malariae and Plasmodium ovale). These parasites can cause a variety of diseases or symptoms, including, but not limited to: Scabies, Trombiculiasis, eye infections, intestinal disease (e.g., dysentery, giardiasis), liver disease, lung disease, opportunistic infections (e.g., AIDS related), malaria, pregnancy complications, and toxoplasmosis. polynucleotides or polypeptides, or agonists or antagonists of the invention, can be used to treat or detect any of these symptoms or diseases.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention of the present invention could either be by administering an effective amount of a polypeptide to the patient, or by removing cells from the patient, supplying the cells with a polynucleotide of the present invention, and returning the engineered cells to the patient (ex vivo therapy). Moreover, the polypeptide or polynucleotide of the present invention can be used as an antigen in a vaccine to raise an immune response against infectious disease.

Regeneration

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention can be used to differentiate, proliferate, and attract cells, leading to the regeneration of tissues. (See, Science 276:59-87 (1997).) The regeneration of tissues could be used to repair, replace, or protect tissue damaged by congenital defects, trauma (wounds, burns, incisions, or ulcers), age, disease (e.g. osteoporosis, osteocarthritis, periodontal disease, liver failure), surgery, including cosmetic plastic surgery, fibrosis, reperfusion injury, or systemic cytokine damage.

Tissues that could be regenerated using the present invention include organs (e.g., pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac), vasculature (including vascular and lymphatics), nervous, hematopoietic, and skeletal (bone, cartilage, tendon, and ligament) tissue. Preferably, regeneration occurs without or decreased scarring. Regeneration also may include angiogenesis.

Moreover, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, may increase regeneration of tissues difficult to heal. For example, increased tendon/ligament regeneration would quicken recovery time after damage. Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention could also be used prophylactically in an effort to avoid damage. Specific diseases that could be treated include of tendinitis, carpal tunnel syndrome, and other tendon or ligament defects. A further example of tissue regeneration of non-healing wounds includes pressure ulcers, ulcers associatedwith vascular insufficiency, surgical, and traumatic wounds.

Similarly, nerve and brain tissue could also be regenerated by using polynucleotides or polypeptides, as well as agonists or antagonists of the present invention, to proliferate and differentiate nerve cells. Diseases that could be treated using this method include central and peripheral nervous system diseases, neuropathies, or mechanical and traumatic disorders (e.g., spinal cord disorders, head trauma, cerebrovascular disease, and stoke). Specifically, diseases associated with peripheral nerve injuries, peripheral neuropathy (e.g., resulting from chemotherapy or other medical therapies), localized neuropathies, and central nervous system diseases

(e.g., Alzheimer's disease, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome), could all be treated using the polynucleotides or polypeptides, as well as agonists or antagonists of the present invention.

Chemotaxis

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may have chemotaxis activity. A chemotaxic molecule attracts or mobilizes cells (e.g., monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells) to a particular site in the body, such as inflammation, infection, or site of hyperproliferation. The mobilized cells can then fight off and/or heal the particular trauma or abnormality.

Polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may increase chemotaxic activity of particular cells. These chemotactic molecules can then be used to treat inflammation, infection, hyperproliferative disorders, or any immune system disorder by increasing the number of cells targeted to a particular location in the body. For example, chemotaxic molecules can be used to treat wounds and other trauma to tissues by attracting immune cells to the injured location. Chemotactic molecules of the present invention can also attract fibroblasts, which can be used to treat wounds.

It is also contemplated that polynucleotides or polypeptides, as well as agonists or antagonists of the present invention may inhibit chemotactic activity. These molecules could also be used to treat disorders. Thus, polynucleotides or polypeptides, as well as agonists or antagonists of the present invention could be used as an inhibitor of chemotaxis.

Binding Activity

A polypeptide of the present invention may be used to screen for molecules that bind to the polypeptide or for molecules to which the polypeptide binds. The binding of the polypeptide and the molecule may activate (agonist), increase, inhibit

(antagonist), or decrease activity of the polypeptide or the molecule bound. Examples of such molecules include antibodies, oligonucleotides, proteins (e.g., receptors),or small molecules.

Preferably, the molecule is closely related to the natural ligand of the polypeptide, e.g., a fragment of the ligand, or a natural substrate, a ligand, a structural or functional mimetic. (See, Coligan et al., Current Protocols in Immunology 1(2):Chapter 5 (1991).) Similarly, the molecule can be closely related to the natural receptor to which the polypeptide binds, or at least, a fragment of the receptor capable of being bound by the polypeptide (e.g., active site). In either case, the molecule can be rationally designed using known techniques.

Preferably, the screening for these molecules involves producing appropriate cells which express the polypeptide. Preferred cells include cells from mammals, yeast, Drosophila, or *E. coli*. Cells expressing the polypeptide (or cell membrane containing the expressed polypeptide) are then preferably contacted with a test compound potentially containing the molecule to observe binding, stimulation, or inhibition of activity of either the polypeptide or the molecule.

The assay may simply test binding of a candidate compound to the polypeptide, wherein binding is detected by a label, or in an assay involving competition with a labeled competitor. Further, the assay may test whether the candidate compound results in a signal generated by binding to the polypeptide.

Alternatively, the assay can be carried out using cell-free preparations, polypeptide/molecule affixed to a solid support, chemical libraries, or natural product mixtures. The assay may also simply comprise the steps of mixing a candidate compound with a solution containing a polypeptide, measuring polypeptide/molecule activity or binding, and comparing the polypeptide/molecule activity or binding to a standard.

Preferably, an ELISA assay can measure polypeptide level or activity in a sample (e.g., biological sample) using a monoclonal or polyclonal antibody. The antibody can measure polypeptide level or activity by either binding, directly or indirectly, to the polypeptide or by competing with the polypeptide for a substrate.

Additionally, the receptor to which the polypeptide of the present invention binds can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting (Coligan, et al., Current Protocols in Immun., 1(2), Chapter 5, (1991)). For example, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the polypeptides, for example, NIH3T3 cells which are known to contain multiple receptors for the FGF family proteins, and SC-3 cells, and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the polypeptides. Transfected cells which are grown on glass slides are exposed to the polypeptide of the present invention, after they have been labelled. The polypeptides can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase.

Following fixation and incubation, the slides are subjected to auto-radiographic analysis. Positive pools are identified and sub-pools are prepared and re-transfected using an iterative sub-pooling and re-screening process, eventually yielding a single clones that encodes the putative receptor.

As an alternative approach for receptor identification, the labeled polypeptides can be photoaffinity linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE analysis and exposed to X-ray film. The labeled complex containing the receptors of the polypeptides can be excised, resolved into peptide fragments, and subjected to protein microsequencing. The amino acid sequence obtained from microsequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the genes encoding the putative receptors.

Moreover, the techniques of gene-shuffling, motif-shuffling, exon-shuffling, and/or codon-shuffling (collectively referred to as "DNA shuffling") may be employed to modulate the activities of the polypeptide of the present invention thereby effectively generating agonists and antagonists of the polypeptide of the present invention. *See generally*, U.S. Patent Nos. 5,605,793, 5,811,238, 5,830,721, 5,834,252, and 5,837,458, and Patten, P. A., *et al., Curr. Opinion Biotechnol.* 8:724-

33 (1997); Harayama, S. *Trends Biotechnol.* 16(2):76-82 (1998); Hansson, L. O., *et al.*, *J. Mol. Biol.* 287:265-76 (1999); and Lorenzo, M. M. and Blasco, R. *Biotechniques* 24(2):308-13 (1998) (each of these patents and publications are hereby incorporated by reference). In one embodiment, alteration of polynucleotides and corresponding polypeptides may be achieved by DNA shuffling. DNA shuffling involves the assembly of two or more DNA segments into a desired molecule by homologous, or site-specific, recombination. In another embodiment, polynucleotides and corresponding polypeptides may be alterred by being subjected to random mutagenesis by error-prone PCR, random nucleotide insertion or other methods prior to recombination. In another embodiment, one or more components, motifs, sections, parts, domains, fragments, etc., of the polypeptide of the present invention may be recombined with one or more components, motifs, sections, parts, domains, fragments, etc. of one or more heterologous molecules. In preferred embodiments, the heterologous molecules are family members. In further preferred embodiments, the heterologous molecule is a growth factor such as, for example, platelet-derived growth factor (PDGF), insulin-like growth factor (IGF-I), transforming growth factor (TGF)-alpha, epidermal growth factor (EGF), fibroblast growth factor (FGF), TGF-beta, bone morphogenetic protein (BMP)-2, BMP-4, BMP-5, BMP-6, BMP-7, activins A and B, decapentaplegic(dpp), 60A, OP-2, dorsalin, growth differentiation factors (GDFs), nodal, MIS, inhibin-alpha, TGF-beta1, TGF-beta2, TGF-beta3, TGF-beta5, and glial-derived neurotrophic factor (GDNF).

Other preferred fragments are biologically active fragments of the polypeptide of the present invention. Biologically active fragments are those exhibiting activity similar, but not necessarily identical, to an activity of the polypeptide of the present invention. The biological activity of the fragments may include an improved desired activity, or a decreased undesirable activity.

Additionally, this invention provides a method of screening compounds to identify those which modulate the action of the polypeptide of the present invention. An example of such an assay comprises combining a mammalian fibroblast cell, a the polypeptide of the present invention, the compound to be screened and $^{3}[H]$

thymidine under cell culture conditions where the fibroblast cell would normally proliferate.. A control assay may be performed in the absence of the compound to be screened and compared to the amount of fibroblast proliferation in the presence of the compound to determine if the compound stimulates proliferation by determining the uptake of ^{3}[H] thymidine in each case. The amount of fibroblast cell proliferation is measured by liquid scintillation chromatography which measures the incorporation of ^{3}[H] thymidine. Both agonist and antagonist compounds may be identified by this procedure.

In another method, a mammalian cell or membrane preparation expressing a receptor for a polypeptide of the present invention is incubated with a labeled polypeptide of the present invention in the presence of the compound. The ability of the compound to enhance or block this interaction could then be measured. Alternatively, the response of a known second messenger system following interaction of a compound to be screened and the receptor is measured and the ability of the compound to bind to the receptor and elicit a second messenger response is measured to determine if the compound is a potential agonist or antagonist. Such second messenger systems include but are not limited to, cAMP guanylate cyclase, ion channels or phosphoinositide hydrolysis.

All of these above assays can be used as diagnostic or prognostic markers. The molecules discovered using these assays can be used to treat disease or to bring about a particular result in a patient (e.g., blood vessel growth) by activating or inhibiting the polypeptide/molecule. Moreover, the assays can discover agents which may inhibit or enhance the production of the polypeptides of the invention from suitably manipulated cells or tissues.

Therefore, the invention includes a method of identifying compounds which bind to a polypeptide of the invention comprising the steps of: (a) incubating a candidate binding compound with a polypeptide of the present invention; and (b) determining if binding has occurred. Moreover, the invention includes a method of identifying agonists/antagonists comprising the steps of: (a) incubating a candidate compound with a polypeptide of the present invention, (b) assaying a biological

activity, and (b) determining if a biological activity of the polypeptide has been altered.

Targeted Delivery

In another embodiment, the invention provides a method of delivering compositions to targeted cells expressing a receptor for a polypeptide of the invention, or cells expressing a cell bound form of a polypeptide of the invention.

As discussed herein, polypeptides or antibodies of the invention may be associated with heterologous polypeptides, heterologous nucleic acids, toxins, or prodrugs via hydrophobic, hydrophilic, ionic and/or covalent interactions. In one embodiment, the invention provides a method for the specific delivery of compositions of the invention to cells by administering polypeptides of the invention (including antibodies) that are associated with heterologous polypeptides or nucleic acids. In one example, the invention provides a method for delivering a therapeutic protein into the targeted cell. In another example, the invention provides a method for delivering a single stranded nucleic acid (e.g., antisense or ribozymes) or double stranded nucleic acid (e.g., DNA that can integrate into the cell's genome or replicate episomally and that can be transcribed) into the targeted cell.

In another embodiment, the invention provides a method for the specific destruction of cells (e.g., the destruction of tumor cells) by administering polypeptides of the invention (e.g., polypeptides of the invention or antibodies of the invention) in association with toxins or cytotoxic prodrugs.

By "toxin" is meant compounds that bind and activate endogenous cytotoxic effector systems, radioisotopes, holotoxins, modified toxins, catalytic subunits of toxins, or any molecules or enzymes not normally present in or on the surface of a cell that under defined conditions cause the cell's death. Toxins that may be used according to the methods of the invention include, but are not limited to, radioisotopes known in the art, compounds such as, for example, antibodies (or complement fixing containing portions thereof) that bind an inherent or induced endogenous cytotoxic effector system, thymidine kinase, endonuclease, RNAse, alpha

toxin, ricin, abrin, *Pseudomonas* exotoxin A, diphtheria toxin, saporin, momordin, gelonin, pokeweed antiviral protein, alpha-sarcin and cholera toxin. By "cytotoxic prodrug" is meant a non-toxic compound that is converted by an enzyme, normally present in the cell, into a cytotoxic compound. Cytotoxic prodrugs that may be used according to the methods of the invention include, but are not limited to, glutamyl derivatives of benzoic acid mustard alkylating agent, phosphate derivatives of etoposide or mitomycin C, cytosine arabinoside, daunorubisin, and phenoxyacetamide derivatives of doxorubicin.

Drug Screening

Further contemplated is the use of the polypeptides of the present invention, or the polynucleotides encoding these polypeptides, to screen for molecules which modify the activities of the polypeptides of the present invention. Such a method would include contacting the polypeptide of the present invention with a selected compound(s) suspected of having antagonist or agonist activity, and assaying the activity of these polypeptides following binding.

This invention is particularly useful for screening therapeutic compounds by using the polypeptides of the present invention, or binding fragments thereof, in any of a variety of drug screening techniques. The polypeptide or fragment employed in such a test may be affixed to a solid support, expressed on a cell surface, free in solution, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. One may measure, for example, the formulation of complexes between the agent being tested and a polypeptide of the present invention.

Thus, the present invention provides methods of screening for drugs or any other agents which affect activities mediated by the polypeptides of the present invention. These methods comprise contacting such an agent with a polypeptide of the present invention or a fragment thereof and assaying for the presence of a

complex between the agent and the polypeptide or a fragment thereof, by methods well known in the art. In such a competitive binding assay, the agents to screen are typically labeled. Following incubation, free agent is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of a particular agent to bind to the polypeptides of the present invention.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to the polypeptides of the present invention, and is described in great detail in European Patent Application 84/03564, published on September 13, 1984, which is incorporated herein by reference herein. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. The peptide test compounds are reacted with polypeptides of the present invention and washed. Bound polypeptides are then detected by methods well known in the art. Purified polypeptides are coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies may be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding polypeptides of the present invention specifically compete with a test compound for binding to the polypeptides or fragments thereof. In this manner, the antibodies are used to detect the presence of any peptide which shares one or more antigenic epitopes with a polypeptide of the invention.

Antisense And Ribozyme (Antagonists)

In specific embodiments, antagonists according to the present invention are nucleic acids corresponding to the sequences contained in SEQ ID NO:X, or the complementary strand thereof, and/or to nucleotide sequences contained in the cDNA contained in the related cDNA clone identified in Table 1. In one embodiment, antisense sequence is generated internally, by the organism, in another embodiment, the antisense sequence is separately administered (see, for example, O'Connor, J.,

Neurochem. 56:560 (1991). Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Antisense technology can be used to control gene expression through antisense DNA or RNA, or through triple-helix formation. Antisense techniques are discussed for example, in Okano, J., Neurochem. 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression, CRC Press, Boca Raton, FL (1988). Triple helix formation is discussed in, for instance, Lee et al., Nucleic Acids Research 6:3073 (1979); Cooney et al., Science 241:456 (1988); and Dervan et al., Science 251:1300 (1991). The methods are based on binding of a polynucleotide to a complementary DNA or RNA.

For example, the use of c-myc and c-myb antisense RNA constructs to inhibit the growth of the non-lymphocytic leukemia cell line HL-60 and other cell lines was previously described. (Wickstrom et al. (1988); Anfossi et al. (1989)). These experiments were performed in vitro by incubating cells with the oligoribonucleotide. A similar procedure for in vivo use is described in WO 91/15580. Briefly, a pair of oligonucleotides for a given antisense RNA is produced as follows: A sequence complimentary to the first 15 bases of the open reading frame is flanked by an EcoR1 site on the 5 end and a HindIII site on the 3 end. Next, the pair of oligonucleotides is heated at 90°C for one minute and then annealed in 2X ligation buffer (20mM TRIS HCl pH 7.5, 10mM MgCl2, 10MM dithiothreitol (DTT) and 0.2 mM ATP) and then ligated to the EcoR1/Hind III site of the retroviral vector PMV7 (WO 91/15580).

For example, the 5' coding portion of a polynucleotide that encodes the polypeptide of the present invention may be used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription thereby preventing transcription and the production of the receptor. The antisense RNA oligonucleotide hybridizes to the mRNA in vivo and blocks translation of the mRNA molecule into receptor polypeptide.

In one embodiment, the antisense nucleic acid of the invention is produced intracellularly by transcription from an exogenous sequence. For example, a vector or a portion thereof, is transcribed, producing an antisense nucleic acid (RNA) of the

invention. Such a vector would contain a sequence encoding the antisense nucleic acid. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors can be constructed by recombinant DNA technology methods standard in the art. Vectors can be plasmid, viral, or others known in the art, used for replication and expression in vertebrate cells. Expression of the sequence encoding the polypeptide of the present invnetion or fragments thereof, can be by any promoter known in the art to act in vertebrate, preferably human cells. Such promoters can be inducible or constitutive. Such promoters include, but are not limited to, the SV40 early promoter region (Bernoist and Chambon, Nature 29:304-310 (1981), the promoter contained in the 3' long terminal repeat of Rous sarcoma virus (Yamamoto et al., Cell 22:787-797 (1980), the herpes thymidine promoter (Wagner et al., Proc. Natl. Acad. Sci. U.S.A. 78:1441-1445 (1981), the regulatory sequences of the metallothionein gene (Brinster, et al., Nature 296:39-42 (1982)), etc.

The antisense nucleic acids of the invention comprise a sequence complementary to at least a portion of an RNA transcript of a gene of the present invention. However, absolute complementarity, although preferred, is not required. A sequence "complementary to at least a portion of an RNA," referred to herein, means a sequence having sufficient complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the antisense nucleic acid. Generally, the larger the hybridizing nucleic acid, the more base mismatches with a RNA it may contain and still form a stable duplex (or triplex as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures to determine the melting point of the hybridized complex.

Oligonucleotides that are complementary to the 5' end of the message, e.g., the 5' untranslated sequence up to and including the AUG initiation codon, should work most efficiently at inhibiting translation. However, sequences complementary to the

3' untranslated sequences of mRNAs have been shown to be effective at inhibiting translation of mRNAs as well. See generally, Wagner, R., 1994, Nature 372:333-335. Thus, oligonucleotides complementary to either the 5'- or 3'- non- translated, non-coding regions of polynucleotide sequences described herein could be used in an antisense approach to inhibit translation of endogenous mRNA. Oligonucleotides complementary to the 5' untranslated region of the mRNA should include the complement of the AUG start codon. Antisense oligonucleotides complementary to mRNA coding regions are less efficient inhibitors of translation but could be used in accordance with the invention. Whether designed to hybridize to the 5'-, 3'- or coding region of mRNA of the present invention, antisense nucleic acids should be at least six nucleotides in length, and are preferably oligonucleotides ranging from 6 to about 50 nucleotides in length. In specific aspects the oligonucleotide is at least 10 nucleotides, at least 17 nucleotides, at least 25 nucleotides or at least 50 nucleotides.

The polynucleotides of the invention can be DNA or RNA or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotide can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotide may include other appended groups such as peptides (e.g., for targeting host cell receptors in vivo), or agents facilitating transport across the cell membrane (see, e.g., Letsinger et al., 1989, Proc. Natl. Acad. Sci. U.S.A. 86:6553-6556; Lemaitre et al., 1987, Proc. Natl. Acad. Sci. 84:648-652; PCT Publication No. WO88/09810, published December 15, 1988) or the blood-brain barrier (see, e.g., PCT Publication No. WO89/10134, published April 25, 1988), hybridization-triggered cleavage agents. (See, e.g., Krol et al., 1988, BioTechniques 6:958-976) or intercalating agents. (See, e.g., Zon, 1988, Pharm. Res. 5:539-549). To this end, the oligonucleotide may be conjugated to another molecule, e.g., a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent, etc.

The antisense oligonucleotide may comprise at least one modified base moiety which is selected from the group including, but not limited to, 5-fluorouracil,

5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xantine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine.

The antisense oligonucleotide may also comprise at least one modified sugar moiety selected from the group including, but not limited to, arabinose, 2-fluoroarabinose, xylulose, and hexose.

In yet another embodiment, the antisense oligonucleotide comprises at least one modified phosphate backbone selected from the group including, but not limited to, a phosphorothioate, a phosphorodithioate, a phosphoramidothioate, a phosphoramidate, a phosphordiamidate, a methylphosphonate, an alkyl phosphotriester, and a formacetal or analog thereof.

In yet another embodiment, the antisense oligonucleotide is an a-anomeric oligonucleotide. An a-anomeric oligonucleotide forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual b-units, the strands run parallel to each other (Gautier et al., 1987, Nucl. Acids Res. 15:6625-6641). The oligonucleotide is a 2'-0-methylribonucleotide (Inoue et al., 1987, Nucl. Acids Res. 15:6131-6148), or a chimeric RNA-DNA analogue (Inoue et al., 1987, FEBS Lett. 215:327-330).

Polynucleotides of the invention may be synthesized by standard methods known in the art, e.g. by use of an automated DNA synthesizer (such as are

commercially available from Biosearch, Applied Biosystems, etc.). As examples, phosphorothioate oligonucleotides may be synthesized by the method of Stein et al. (1988, Nucl. Acids Res. 16:3209), methylphosphonate oligonucleotides can be prepared by use of controlled pore glass polymer supports (Sarin et al., 1988, Proc. Natl. Acad. Sci. U.S.A. 85:7448-7451), etc.

While antisense nucleotides complementary to the coding region sequence could be used, those complementary to the transcribed untranslated region are most preferred.

Potential antagonists according to the invention also include catalytic RNA, or a ribozyme (See, e.g., PCT International Publication WO 90/11364, published October 4, 1990; Sarver et al, Science 247:1222-1225 (1990). While ribozymes that cleave mRNA at site specific recognition sequences can be used to destroy mRNAs, the use of hammerhead ribozymes is preferred. Hammerhead ribozymes cleave mRNAs at locations dictated by flanking regions that form complementary base pairs with the target mRNA. The sole requirement is that the target mRNA have the following sequence of two bases: 5'-UG-3'. The construction and production of hammerhead ribozymes is well known in the art and is described more fully in Haseloff and Gerlach, Nature 334:585-591 (1988). There are numerous potential hammerhead ribozyme cleavage sites within the nucleotide sequence of SEQ ID NO:X. Preferably, the ribozyme is engineered so that the cleavage recognition site is located near the 5' end of the mRNA; i.e., to increase efficiency and minimize the intracellular accumulation of non-functional mRNA transcripts.

As in the antisense approach, the ribozymes of the invention can be composed of modified oligonucleotides (e.g. for improved stability, targeting, etc.) and should be delivered to cells which express in vivo. DNA constructs encoding the ribozyme may be introduced into the cell in the same manner as described above for the introduction of antisense encoding DNA. A preferred method of delivery involves using a DNA construct "encoding" the ribozyme under the control of a strong constitutive promoter, such as, for example, pol III or pol II promoter, so that transfected cells will produce sufficient quantities of the ribozyme to destroy

endogenous messages and inhibit translation. Since ribozymes unlike antisense molecules, are catalytic, a lower intracellular concentration is required for efficiency.

Antagonist/agonist compounds may be employed to inhibit the cell growth and proliferation effects of the polypeptides of the present invention on neoplastic cells and tissues, i.e. stimulation of angiogenesis of tumors, and, therefore, retard or prevent abnormal cellular growth and proliferation, for example, in tumor formation or growth.

The antagonist/agonist may also be employed to prevent hyper-vascular diseases, and prevent the proliferation of epithelial lens cells after extracapsular cataract surgery. Prevention of the mitogenic activity of the polypeptides of the present invention may also be desirous in cases such as restenosis after balloon angioplasty.

The antagonist/agonist may also be employed to prevent the growth of scar tissue during wound healing.

The antagonist/agonist may also be employed to treat the diseases described herein.

Thus, the invention provides a method of treating disorders or diseases, including but not limited to the disorders or diseases listed throughout this application, associated with overexpression of a polynucleotide of the present invention by administering to a patient (a) an antisense molecule directed to the polynucleotide of the present invention, and/or (b) a ribozyme directed to the polynucleotide of the present invention.

Other Activities

A polypeptide, polynucleotide, agonist, or antagonist of the present invention, as a result of the ability to stimulate vascular endothelial cell growth, may be employed in treatment for stimulating re-vascularization of ischemic tissues due to various disease conditions such as thrombosis, arteriosclerosis, and other cardiovascular conditions. The polypeptide, polynucleotide, agonist, or antagonist of

the present invention may also be employed to stimulate angiogenesis and limb regeneration, as discussed above.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for treating wounds due to injuries, burns, post-operative tissue repair, and ulcers since they are mitogenic to various cells of different origins, such as fibroblast cells and skeletal muscle cells, and therefore, facilitate the repair or replacement of damaged or diseased tissue.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed stimulate neuronal growth and to treat and prevent neuronal damage which occurs in certain neuronal disorders or neuro-degenerative conditions such as Alzheimer's disease, Parkinson's disease, and AIDS-related complex. A polypeptide, polynucleotide, agonist, or antagonist of the present invention may have the ability to stimulate chondrocyte growth, therefore, they may be employed to enhance bone and periodontal regeneration and aid in tissue transplants or bone grafts.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may be also be employed to prevent skin aging due to sunburn by stimulating keratinocyte growth.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for preventing hair loss, since FGF family members activate hair-forming cells and promotes melanocyte growth. Along the same lines, a polypeptide, polynucleotide, agonist, or antagonist of the present invention may be employed to stimulate growth and differentiation of hematopoietic cells and bone marrow cells when used in combination with other cytokines.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed to maintain organs before transplantation or for supporting cell culture of primary tissues. A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be employed for inducing tissue of mesodermal origin to differentiate in early embryos.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also increase or decrease the differentiation or proliferation of embryonic stem cells, besides, as discussed above, hematopoietic lineage.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be used to modulate mammalian characteristics, such as body height, weight, hair color, eye color, skin, percentage of adipose tissue, pigmentation, size, and shape (e.g., cosmetic surgery). Similarly, a polypeptide, polynucleotide, agonist, or antagonist of the present invention may be used to modulate mammalian metabolism affecting catabolism, anabolism, processing, utilization, and storage of energy.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may be used to change a mammal's mental state or physical state by influencing biorhythms, caricadic rhythms, depression (including depressive disorders), tendency for violence, tolerance for pain, reproductive capabilities (preferably by Activin or Inhibin-like activity), hormonal or endocrine levels, appetite, libido, memory, stress, or other cognitive qualities.

A polypeptide, polynucleotide, agonist, or antagonist of the present invention may also be used as a food additive or preservative, such as to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional components.

The above-recited applications have uses in a wide variety of hosts. Such hosts include, but are not limited to, human, murine, rabbit, goat, guinea pig, camel, horse, mouse, rat, hamster, pig, micro-pig, chicken, goat, cow, sheep, dog, cat, non-human primate, and human. In specific embodiments, the host is a mouse, rabbit, goat, guinea pig, chicken, rat, hamster, pig, sheep, dog or cat. In preferred embodiments, the host is a mammal. In most preferred embodiments, the host is a human.

<u>Other Preferred Embodiments</u>

Other preferred embodiments of the claimed invention include an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 50 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

Also preferred is a nucleic acid molecule wherein said sequence of contiguous nucleotides is included in the nucleotide sequence of SEQ ID NO:X in the range of positions identified as "Start" and "End" in columns 7 and 8 as defined for SEQ ID NO:X in Table 1.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 150 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least about 500 contiguous nucleotides in the nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the nucleotide sequence of SEQ ID NO:X in the range of positions identified as "Start" and "End" in columns 7 and 8 as defined for SEQ ID NO:X in Table 1.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in the related cDNA clone contained in the deposit.

Also preferred is an isolated nucleic acid molecule which hybridizes under stringent hybridization conditions to a nucleic acid molecule comprising a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto, and/or the cDNA in

the related cDNA clone contained in the deposit, wherein said nucleic acid molecule which hybridizes does not hybridize under stringent hybridization conditions to a nucleic acid molecule having a nucleotide sequence consisting of only A residues or of only T residues.

Also preferred is a composition of matter comprising a DNA molecule which comprises a cDNA clone contained in the deposit.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in the nucleotide sequence of the cDNA in the related cDNA clone contained in the deposit.

Also preferred is an isolated nucleic acid molecule, wherein said sequence of at least 50 contiguous nucleotides is included in the nucleotide sequence of an open reading frame sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 150 contiguous nucleotides in the nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to sequence of at least 500 contiguous nucleotides in the nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to the complete nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

A further preferred embodiment is a method for detecting in a biological sample a nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the

complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit; which method comprises a step of comparing a nucleotide sequence of at least one nucleic acid molecule in said sample with a sequence selected from said group and determining whether the sequence of said nucleic acid molecule in said sample is at least 95% identical to said selected sequence.

Also preferred is the above method wherein said step of comparing sequences comprises determining the extent of nucleic acid hybridization between nucleic acid molecules in said sample and a nucleic acid molecule comprising said sequence selected from said group. Similarly, also preferred is the above method wherein said step of comparing sequences is performed by comparing the nucleotide sequence determined from a nucleic acid molecule in said sample with said sequence selected from said group. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

A further preferred embodiment is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting nucleic acid molecules in said sample, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample which comprises a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a nucleotide sequence of SEQ ID NO:X; or the cDNA in the related cDNA clone identified in Table 1 which encodes a protein, wherein the method comprises a step of detecting in a biological sample

obtained from said subject nucleic acid molecules, if any, comprising a nucleotide sequence that is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence of the cDNA in the related cDNA clone contained in the deposit.

Also preferred is the above method for diagnosing a pathological condition which comprises a step of detecting nucleic acid molecules comprising a nucleotide sequence in a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from said group.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a panel of at least two nucleotide sequences, wherein at least one sequence in said panel is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the related cDNA clone contained in the deposit. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is a composition of matter comprising isolated nucleic acid molecules wherein the nucleotide sequences of said nucleic acid molecules comprise a DNA microarray or "chip" of at least 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 15, 20, 25, 30, 40, 50, 100, 150, 200, 250, 300, 500, 1000, 2000, 3000 or 4000 nucleotide sequences, wherein at least one sequence in said DNA microarray or "chip" is at least 95% identical to a sequence of at least 50 contiguous nucleotides in a sequence selected from the group consisting of: a nucleotide sequence of SEQ ID NO:X or the complementary strand thereto; and a nucleotide sequence encoded by the cDNA in the cDNA clone referenced in Table 1. The nucleic acid molecules can comprise DNA molecules or RNA molecules.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the

polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the complete amino acid sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and/or a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is an isolated polypeptide comprising an amino acid sequence at least 90% identical to a sequence of at least about 10 contiguous amino acids in the complete amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Also preferred is a polypeptide wherein said sequence of contiguous amino acids is included in the amino acid sequence of a portion of said polypeptide encoded by the cDNA clone referenced in Table 1; a polypeptide encoded by SEQ ID NO:X; and/or the polypeptide sequence of SEQ ID NO:Y.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 30 contiguous amino acids in the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence of at least about 100 contiguous amino acids in the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Also preferred is an isolated polypeptide comprising an amino acid sequence at least 95% identical to the amino acid sequence of a polypeptide encoded by the cDNA clone referenced in Table 1.

Further preferred is an isolated antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone contained in the deposit.

Further preferred is a method for detecting in a biological sample a polypeptide comprising an amino acid sequence which is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1; which method comprises a step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group and determining whether the sequence of said polypeptide molecule in said sample is at least 90% identical to said sequence of at least 10 contiguous amino acids.

Also preferred is the above method wherein said step of comparing an amino acid sequence of at least one polypeptide molecule in said sample with a sequence selected from said group comprises determining the extent of specific binding of polypeptides in said sample to an antibody which binds specifically to a polypeptide comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: a polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X;

and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is the above method wherein said step of comparing sequences is performed by comparing the amino acid sequence determined from a polypeptide molecule in said sample with said sequence selected from said group.

Also preferred is a method for identifying the species, tissue or cell type of a biological sample which method comprises a step of detecting polypeptide molecules in said sample, if any, comprising an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is the above method for identifying the species, tissue or cell type of a biological sample, which method comprises a step of detecting polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the above group.

Also preferred is a method for diagnosing in a subject a pathological condition associated with abnormal structure or expression of a nucleic acid sequence identified in Table 1 encoding a polypeptide, which method comprises a step of detecting in a biological sample obtained from said subject polypeptide molecules comprising an amino acid sequence in a panel of at least two amino acid sequences, wherein at least one sequence in said panel is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

In any of these methods, the step of detecting said polypeptide molecules includes using an antibody.

Also preferred is an isolated nucleic acid molecule comprising a nucleotide sequence which is at least 95% identical to a nucleotide sequence encoding a polypeptide wherein said polypeptide comprises an amino acid sequence that is at least 90% identical to a sequence of at least 10 contiguous amino acids in a sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Also preferred is an isolated nucleic acid molecule, wherein said nucleotide sequence encoding a polypeptide has been optimized for expression of said polypeptide in a prokaryotic host.

Also preferred is an isolated nucleic acid molecule, wherein said polypeptide comprises an amino acid sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1.

Further preferred is a method of making a recombinant vector comprising inserting any of the above isolated nucleic acid molecule into a vector. Also preferred is the recombinant vector produced by this method. Also preferred is a method of making a recombinant host cell comprising introducing the vector into a host cell, as well as the recombinant host cell produced by this method.

Also preferred is a method of making an isolated polypeptide comprising culturing this recombinant host cell under conditions such that said polypeptide is expressed and recovering said polypeptide. Also preferred is this method of making an isolated polypeptide, wherein said recombinant host cell is a eukaryotic cell and said polypeptide is a human protein comprising an amino acid sequence selected from the group consisting of: polypeptide sequence of SEQ ID NO:Y; a polypeptide encoded by SEQ ID NO:X; and a polypeptide encoded by the cDNA in the related cDNA clone referenced in Table 1. The isolated polypeptide produced by this method is also preferred.

Also preferred is a method of treatment of an individual in need of an increased level of a protein activity, which method comprises administering to such

an individual a Therapeutic comprising an amount of an isolated polypeptide, polynucleotide, immunogenic fragment or analogue thereof, binding agent, antibody, or antigen binding fragment of the claimed invention effective to increase the level of said protein activity in said individual.

Also preferred is a method of treatment of an individual in need of a decreased level of a protein activity, which method comprised administering to such an individual a Therapeutic comprising an amount of an isolated polypeptide, polynucleotide, immunogenic fragment or analogue thereof, binding agent, antibody, or antigen binding fragment of the claimed invention effective to decrease the level of said protein activity in said individual.

Having generally described the invention, the same will be more readily understood by reference to the following examples, which are provided by way of illustration and are not intended as limiting.

Examples

Example 1: Isolation of a Selected cDNA Clone From the Deposited Sample

Each deposited cDNA clone is contained in a plasmid vector. Table 5 identifies the vectors used to construct the cDNA library from which each clone was isolated. In many cases, the vector used to construct the library is a phage vector from which a plasmid has been excised. The following correlates the related plasmid for each phage vector used in constructing the cDNA library. For example, where a particular clone is identified in Table 5 as being isolated in the vector "Lambda Zap," the corresponding deposited clone is in "pBluescript."

Vector Used to Construct Library	Corresponding Deposited Plasmid
Lambda Zap	pBluescript (pBS)
Uni-Zap XR	pBluescript (pBS)
Zap Express	pBK
lafmid BA	plafmid BA
pSport1	pSport1
pCMVSport 2.0	pCMVSport 2.0
pCMVSport 3.0	pCMVSport 3.0
pCR®2.1	pCR®2.1

Vectors Lambda Zap (U.S. Patent Nos. 5,128,256 and 5,286,636), Uni-Zap XR (U.S. Patent Nos. 5,128, 256 and 5,286,636), Zap Express (U.S. Patent Nos. 5,128,256 and 5,286,636), pBluescript (pBS) (Short, J. M. et al., Nucleic Acids Res. 16:7583-7600 (1988); Alting-Mees, M. A. and Short, J. M., Nucleic Acids Res. 17:9494 (1989)) and pBK (Alting-Mees, M. A. et al., Strategies 5:58-61 (1992)) are commercially available from Stratagene Cloning Systems, Inc., 11011 N. Torrey Pines Road, La Jolla, CA, 92037. pBS contains an ampicillin resistance gene and pBK contains a neomycin resistance gene. Both can be transformed into E. coli strain XL-1 Blue, also available from Stratagene. pBS comes in 4 forms SK+, SK-, KS+ and KS. The S and K refers to the orientation of the polylinker to the T7 and T3

primer sequences which flank the polylinker region ("S" is for SacI and "K" is for KpnI which are the first sites on each respective end of the linker). "+" or "-" refer to the orientation of the f1 origin of replication ("ori"), such that in one orientation, single stranded rescue initiated from the f1 ori generates sense strand DNA and in the other, antisense.

Vectors pSport1, pCMVSport 2.0 and pCMVSport 3.0, were obtained from Life Technologies, Inc., P. O. Box 6009, Gaithersburg, MD 20897. All Sport vectors contain an ampicillin resistance gene and may be transformed into E. coli strain DH10B, also available from Life Technologies. (See, for instance, Gruber, C. E., et al., Focus 15:59 (1993).) Vector lafmid BA (Bento Soares, Columbia University, NY) contains an ampicillin resistance gene and can be transformed into E. coli strain XL-1 Blue. Vector pCR®2.1, which is available from Invitrogen, 1600 Faraday Avenue, Carlsbad, CA 92008, contains an ampicillin resistance gene and may be transformed into E. coli strain DH10B, available from Life Technologies. (See, for instance, Clark, J. M., Nuc. Acids Res. 16:9677-9686 (1988) and Mead, D. et al., Bio/Technology 9: (1991).) Preferably, a polynucleotide of the present invention does not comprise the phage vector sequences identified for the particular clone in Table 5, as well as the corresponding plasmid vector sequences designated above.

The deposited material in the sample assigned the ATCC Deposit Number cited by reference to Table 2 and 5 for any given cDNA clone also may contain one or more additional plasmids, each comprising a cDNA clone different from that given clone. Thus, deposits sharing the same ATCC Deposit Number contain at least a plasmid for each cDNA clone referenced in Table 1.

TABLE 5

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HUKA HUKB HUKC HUKD HUKE HUKF HUKG	Human Uterine Cancer	Lambda ZAP II	LP01
HCNA HCNB	Human Colon	Lambda Zap II	LP01
HFFA	Human Fetal Brain, random primed	Lambda Zap II	LP01
HTWA	Resting T-Cell	Lambda ZAP II	LP01
HBQA	Early Stage Human Brain, random primed	Lambda ZAP II	LP01
HLMB HLMF HLMG HLMH HLMI HLMJ HLMM HLMN	breast lymph node CDNA library	Lambda ZAP II	LP01
HCQA HCQB	human colon cancer	Lamda ZAP II	LP01
HMEA HMEC HMED HMEE HMEF HMEG HMEI HMEJ HMEK HMEL	Human Microvascular Endothelial Cells, fract. A	Lambda ZAP II	LP01
HUSA HUSC	Human Umbilical Vein Endothelial Cells, fract. A	Lambda ZAP II	LP01
HLQA HLQB	Hepatocellular Tumor	Lambda ZAP II	LP01
HHGA HHGB HHGC HHGD	Hemangiopericytoma	Lambda ZAP II	LP01
HSDM	Human Striatum Depression, re-rescue	Lambda ZAP II	LP01
HUSH	H Umbilical Vein Endothelial Cells, frac A, re-excision	Lambda ZAP II	LP01
HSGS	Salivary gland, subtracted	Lambda ZAP II	LP01
HFXA HFXB HFXC HFXD HFXE HFXF HFXG HFXH	Brain frontal cortex	Lambda ZAP II	LP01
HPQA HPQB HPQC	PERM TF274	Lambda ZAP II	LP01
HFXJ HFXK	Brain Frontal Cortex, re-excision	Lambda ZAP II	LP01
HCWA HCWB HCWC HCWD HCWE HCWF HCWG HCWH HCWI HCWJ HCWK	CD34 positive cells (Cord Blood)	ZAP Express	LP02
HCUA HCUB HCUC	CD34 depleted Buffy Coat (Cord Blood)	ZAP Express	LP02
HRSM	A-14 cell line	ZAP Express	LP02
HRSA	A1-CELL LINE	ZAP Express	LP02
HCUD HCUE HCUF HCUG HCUH HCUI	CD34 depleted Buffy Coat (Cord Blood), re-excision	ZAP Express	LP02
HBXE HBXF HBXG	H. Whole Brain #2, re-excision	ZAP Express	LP02
HRLM	L8 cell line	ZAP Express	LP02
HBXA HBXB HBXC HBXD	Human Whole Brain #2 - Oligo dT > 1.5Kb	ZAP Express	LP02
HUDA HUDB HUDC	Testes	ZAP Express	LP02
HHTM HHTN HHTO	H. hypothalamus, frac A;re-excision	ZAP Express	LP02
HHTL	H. hypothalamus, frac A	ZAP Express	LP02
HASA HASD	Human Adult Spleen	Uni-ZAP XR	LP03
HFKC HFKD HFKE HFKF HFKG	Human Fetal Kidney	Uni-ZAP XR	LP03
HE8A HE8B HE8C HE8D HE8E HE8F HE8M HE8N	Human 8 Week Whole Embryo	Uni-ZAP XR	LP03
HGBA HGBD HGBE HGBF HGBG HGBH HGBI	Human Gall Bladder	Uni-ZAP XR	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HLHA HLHB HLHC HLHD HLHE HLHF HLHG HLHH HLHQ	Human Fetal Lung III	Uni-ZAP XR	LP03
HPMA HPMB HPMC HPMD HPME HPMF HPMG HPMH	Human Placenta	Uni-ZAP XR	LP03
HPRA HPRB HPRC HPRD	Human Prostate	Uni-ZAP XR	LP03
HSIA HSIC HSID HSIE	Human Adult Small Intestine	Uni-ZAP XR	LP03
HTEA HTEB HTEC HTED HTEE HTEF HTEG HTEH HTEI HTEJ HTEK	Human Testes	Uni-ZAP XR	LP03
HTPA HTPB HTPC HTPD HTPE	Human Pancreas Tumor	Uni-ZAP XR	LP03
HTTA HTTB HTTC HTTD HTTE HTTF	Human Testes Tumor	Uni-ZAP XR	LP03
HAPA HAPB HAPC HAPM	Human Adult Pulmonary	Uni-ZAP XR	LP03
HETA HETB HETC HETD HETE HETF HETG HETH HETI	Human Endometrial Tumor	Uni-ZAP XR	LP03
HHFB HHFC HHFD HHFE HHFF HHFG HHFH HHFI	Human Fetal Heart	Uni-ZAP XR	LP03
HHPB HHPC HHPD HHPE HHPF HHPG HHPH	Human Hippocampus	Uni-ZAP XR	LP03
HCE1 HCE2 HCE3 HCE4 HCE5 HCEB HCEC HCED HCEE HCEF HCEG	Human Cerebellum	Uni-ZAP XR	LP03
HUVB HUVC HUVD HUVE	Human Umbilical Vein. Endo. remake	Uni-ZAP XR	LP03
HSTA HSTB HSTC HSTD	Human Skin Tumor	Uni-ZAP XR	LP03
HTAA HTAB HTAC HTAD HTAE	Human Activated T-Cells	Uni-ZAP XR	LP03
HFEA HFEB HFEC	Human Fetal Epithelium (Skin)	Uni-ZAP XR	LP03
HJPA HJPB HJPC HJPD	HUMAN JURKAT MEMBRANE BOUND POLYSOMES	Uni-ZAP XR	LP03
HESA	Human epithelioid sarcoma	Uni-Zap XR	LP03
HLTA HLTB HLTC HLTD HLTE HLTF	Human T-Cell Lymphoma	Uni-ZAP XR	LP03
HFTA HFTB HFTC HFTD	Human Fetal Dura Mater	Uni-ZAP XR	LP03
HRDA HRDB HRDC HRDD HRDE HRDF	Human Rhabdomyosarcoma	Uni-ZAP XR	LP03
HCAA HCAB HCAC	Cem cells cyclohexamide treated	Uni-ZAP XR	LP03
HRGA HRGB HRGC HRGD	Raji Cells, cyclohexamide treated	Uni-ZAP XR	LP03
HSUA HSUB HSUC HSUM	Supt Cells. cyclohexamide treated	Uni-ZAP XR	LP03
HT4A HT4C HT4D	Activated T-Cells, 12 hrs.	Uni-ZAP XR	LP03
HE9A HE9B HE9C HE9D HE9E HE9F HE9G HE9H HE9M HE9N	Nine Week Old Early Stage Human	Uni-ZAP XR	LP03
HATA HATB HATC HATD HATE	Human Adrenal Gland Tumor	Uni-ZAP XR	LP03
HT5A	Activated T-Cells, 24 hrs.	Uni-ZAP XR	LP03
HFGA HFGM	Human Fetal Brain	Uni-ZAP XR	LP03
HNEA HNEB HNEC HNED HNEE	Human Neutrophil	Uni-ZAP XR	LP03
HBGB HBGD	Human Primary Breast Cancer	Uni-ZAP XR	LP03
HBNA HBNB	Human Normal Breast	Uni-ZAP XR	LP03
HCAS	Cem Cells, cyclohexamide treated, subtra	Uni-ZAP XR	LP03
HHPS	Human Hippocampus, subtracted	pBS	LP03
HKCS HKCU	Human Colon Cancer, subtracted	pBS	LP03
HRGS	Raji cells, cyclohexamide treated,	pBS	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
	subtracted		
HSUT	Supt cells, cyclohexamide treated, differentially expressed	pBS	LP03
HT4S	Activated T-Cells, 12 hrs, subtracted	Uni-ZAP XR	LP03
HCDA HCDB HCDC HCDD HCDE	Human Chondrosarcoma	Uni-ZAP XR	LP03
HOAA HOAB HOAC	Human Osteosarcoma	Uni-ZAP XR	LP03
HTLA HTLB HTLC HTLD HTLE HTLF	Human adult testis, large inserts	Uni-ZAP XR	LP03
HLMA HLMC HLMD	Breast Lymph node cDNA library	Uni-ZAP XR	LP03
H6EA H6EB H6EC	HL-60, PMA 4H	Uni-ZAP XR	LP03
HTXA HTXB HTXC HTXD HTXE HTXF HTXG HTXH	Activated T-Cell (12hs)/Thiouridine labelledEco	Uni-ZAP XR	LP03
HNFA HNFB HNFC HNFD HNFE HNFF HNFG HNFH HNFJ	Human Neutrophil, Activated	Uni-ZAP XR	LP03
HTOB HTOC	HUMAN TONSILS, FRACTION 2	Uni-ZAP XR	LP03
HMGB	Human OB MG63 control fraction I	Uni-ZAP XR	LP03
HOPB	Human OB HOS control fraction I	Uni-ZAP XR	LP03
HORB	Human OB HOS treated (10 nM E2) fraction I	Uni-ZAP XR	LP03
HSVA HSVB HSVC	Human Chronic Synovitis	Uni-ZAP XR	LP03
HROA	HUMAN STOMACH	Uni-ZAP XR	LP03
HBJA HBJB HBJC HBJD HBJE HBJF HBJG HBJH HBJI HBJJ HBJK	HUMAN B CELL LYMPHOMA	Uni-ZAP XR	LP03
HCRA HCRB HCRC	human corpus colosum	Uni-ZAP XR	LP03
HODA HODB HODC HODD	human ovarian cancer	Uni-ZAP XR	LP03
HDSA	Dermatofibrosarcoma Protuberance	Uni-ZAP XR	LP03
HMWA HMWB HMWC HMWD HMWE HMWF HMWG HMWH HMWI HMWJ	Bone Marrow Cell Line (RS4;11)	Uni-ZAP XR	LP03
HSOA	stomach cancer (human)	Uni-ZAP XR	LP03
HERA	SKIN	Uni-ZAP XR	LP03
HMDA	Brain-medulloblastoma	Uni-ZAP XR	LP03
HGLA HGLB HGLD	Glioblastoma	Uni-ZAP XR	LP03
HEAA	H. Atrophic Endometrium	Uni-ZAP XR	LP03
HBCA HBCB	H. Lymph node breast Cancer	Uni-ZAP XR	LP03
HPWT	Human Prostate BPH, re-excision	Uni-ZAP XR	LP03
HFVG HFVH HFVI	Fetal Liver, subtraction II	pBS	LP03
HNFI	Human Neutrophils, Activated, re-excision	pBS	LP03
HBMB HBMC HBMD	Human Bone Marrow, re-excision	pBS	LP03
HKML HKMM HKMN	H. Kidney Medulla, re-excision	pBS	LP03
HKIX HKIY	H. Kidney Cortex, subtracted	pBS	LP03
HADT	H. Amygdala Depression, subtracted	pBS	LP03
H6AS	Hl-60, untreated, subtracted	Uni-ZAP XR	LP03
H6ES	HL-60, PMA 4H, subtracted	Uni-ZAP XR	LP03
H6BS	HL-60, RA 4h, Subtracted	Uni-ZAP XR	LP03
H6CS	HL-60, PMA 1d, subtracted	Uni-ZAP XR	LP03

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HTXJ HTXK	Activated T-cell(12h)/Thiouridine-re-excision	Uni-ZAP XR	LP03
HMSA HMSB HMSC HMSD HMSE HMSF HMSG HMSH HMSI HMSJ HMSK	Monocyte activated	Uni-ZAP XR	LP03
HAGA HAGB HAGC HAGD HAGE HAGF	Human Amygdala	Uni-ZAP XR	LP03
HSRA HSRB HSRE	STROMAL -OSTEOCLASTOMA	Uni-ZAP XR	LP03
HSRD HSRF HSRG HSRH	Human Osteoclastoma Stromal Cells - unamplified	Uni-ZAP XR	LP03
HSQA HSQB HSQC HSQD HSQE HSQF HSQG	Stromal cell TF274	Uni-ZAP XR	LP03
HSKA HSKB HSKC HSKD HSKE HSKF HSKZ	Smooth muscle, serum treated	Uni-ZAP XR	LP03
HSLA HSLB HSLC HSLD HSLE HSLF HSLG	Smooth muscle,control	Uni-ZAP XR	LP03
HSDA HSDD HSDE HSDF HSDG HSDH	Spinal cord	Uni-ZAP XR	LP03
HPWS	Prostate-BPH subtracted II	pBS	LP03
HSKW HSKX HSKY	Smooth Muscle- HASTE normalized	pBS	LP03
HFPB HFPC HFPD	H. Frontal cortex,epileptic;re-excision	Uni-ZAP XR	LP03
HSDI HSDJ HSDK	Spinal Cord, re-excision	Uni-ZAP XR	LP03
HSKN HSKO	Smooth Muscle Serum Treated, Norm	pBS	LP03
HSKG HSKH HSKI	Smooth muscle, serum induced,re-exc	pBS	LP03
HFCA HFCB HFCC HFCD HFCE HFCF	Human Fetal Brain	Uni-ZAP XR	LP04
HPTA HPTB HPTD	Human Pituitary	Uni-ZAP XR	LP04
HTHB HTHC HTHD	Human Thymus	Uni-ZAP XR	LP04
HE6B HE6C HE6D HE6E HE6F HE6G HE6S	Human Whole Six Week Old Embryo	Uni-ZAP XR	LP04
HSSA HSSB HSSC HSSD HSSE HSSF HSSG HSSH HSSI HSSJ HSSK	Human Synovial Sarcoma	Uni-ZAP XR	LP04
HE7T	7 Week Old Early Stage Human, subtracted	Uni-ZAP XR	LP04
HEPA HEPB HEPC	Human Epididymus	Uni-ZAP XR	LP04
HSNA HSNB HSNC HSNM HSNN	Human Synovium	Uni-ZAP XR	LP04
HPFB HPFC HPFD HPFE	Human Prostate Cancer, Stage C fraction	Uni-ZAP XR	LP04
HE2A HE2D HE2E HE2H HE2I HE2M HE2N HE2O	12 Week Old Early Stage Human	Uni-ZAP XR	LP04
HE2B HE2C HE2F HE2G HE2P HE2Q	12 Week Old Early Stage Human, II	Uni-ZAP XR	LP04
HPTS HPTT HPTU	Human Pituitary, subtracted	Uni-ZAP XR	LP04
HAUA HAUB HAUC	Amniotic Cells - TNF induced	Uni-ZAP XR	LP04
HAQA HAQB HAQC HAQD	Amniotic Cells - Primary Culture	Uni-ZAP XR	LP04
HWTA HWTB HWTC	wilm's tumor	Uni-ZAP XR	LP04
HBSD	Bone Cancer, re-excision	Uni-ZAP XR	LP04
HSGB	Salivary gland, re-excision	Uni-ZAP XR	LP04
HSJA HSJB HSJC	Smooth muscle-ILb induced	Uni-ZAP XR	LP04
HSXA HSXB HSXC HSXD	Human Substantia Nigra	Uni-ZAP XR	LP04
HSHA HSHB HSHC	Smooth muscle, IL1b induced	Uni-ZAP XR	LP04

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HOUA HOUB HOUC HOUD HOUE	Adipocytes	Uni-ZAP XR	LP04
HPWA HPWB HPWC HPWD HPWE	Prostate BPH	Uni-ZAP XR	LP04
HELA HELB HELC HELD HELE HELF HELG HELH	Endothelial cells-control	Uni-ZAP XR	LP04
HEMA HEMB HEMC HEMD HEME HEMF HEMG HEMH	Endothelial-induced	Uni-ZAP XR	LP04
HBIA HBIB HBIC	Human Brain, Striatum	Uni-ZAP XR	LP04
HHSA HHSB HHSC HHSD HHSE	Human Hypothalmus.Schizophrenia	Uni-ZAP XR	LP04
HNGA HNGB HNGC HNGD HNGE HNGF HNGG HNGH HNGI HNGJ	neutrophils control	Uni-ZAP XR	LP04
HNHA HNHB HNHC HNHD HNHE HNHF HNHG HNHH HNHI HNHJ	Neutrophils IL-1 and LPS induced	Uni-ZAP XR	LP04
HSDB HSDC	STRIATUM DEPRESSION	Uni-ZAP XR	LP04
HHPT	Hypothalamus	Uni-ZAP XR	LP04
HSAT HSAU HSAV HSAW HSAX HSAY HSAZ	Anergic T-cell	Uni-ZAP XR	LP04
HBMS HBMT HBMU HBMV HBMW HBMX	Bone marrow	Uni-ZAP XR	LP04
HOEA HOEB HOEC HOED HOEE HOEF HOEJ	Osteoblasts	Uni-ZAP XR	LP04
HAIA HAIB HAIC HAID HAIE HAIF	Epithelial-TNFa and INF induced	Uni-ZAP XR	LP04
HTGA HTGB HTGC HTGD	Apoptotic T-cell	Uni-ZAP XR	LP04
HMCA HMCB HMCC HMCD HMCE	Macrophage-oxLDL	Uni-ZAP XR	LP04
HMAA HMAB HMAC HMAD HMAE HMAF HMAG	Macrophage (GM-CSF treated)	Uni-ZAP XR	LP04
HPHA	Normal Prostate	Uni-ZAP XR	LP04
HPIA HPIB HPIC	LNCAP prostate cell line	Uni-ZAP XR	LP04
HPJA HPJB HPJC	PC3 Prostate cell line	Uni-ZAP XR	LP04
HOSE HOSF HOSG	Human Osteoclastoma, re-excision	Uni-ZAP XR	LP04
HTGE HTGF	Apoptotic T-cell, re-excision	Uni-ZAP XR	LP04
HMAJ HMAK	H Macrophage (GM-CSF treated), re-excision	Uni-ZAP XR	LP04
HACB HACC HACD	Human Adipose Tissue, re-excision	Uni-ZAP XR	LP04
HFPA	H. Frontal Cortex, Epileptic	Uni-ZAP XR	LP04
HFAA HFAB HFAC HFAD HFAE	Alzheimers, spongy change	Uni-ZAP XR	LP04
HFAM	Frontal Lobe, Dementia	Uni-ZAP XR	LP04
HMIA HMIB HMIC	Human Manic Depression Tissue	Uni-ZAP XR	LP04
HTSA HTSE HTSF HTSG HTSH	Human Thymus	pBS	LP05
HPBA HPBB HPBC HPBD HPBE	Human Pineal Gland	pBS	LP05
HSAA HSAB HSAC	HSA 172 Cells	pBS	LP05
HSBA HSBB HSBC HSBM	HSC172 cells	pBS	LP05
HJAA HJAB HJAC HJAD	Jurkat T-cell G1 phase	pBS	LP05
HJBA HJBB HJBC HJBD	Jurkat T-Cell, S phase	pBS	LP05
HAFA HAFB	Aorta endothelial cells + TNF-a	pBS	LP05
HAWA HAWB HAWC	Human White Adipose	pBS	LP05
HTNA HTNB	Human Thyroid	pBS	LP05
HONA	Normal Ovary, Premenopausal	pBS	LP05

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HARA HARB	Human Adult Retina	pBS	LP05
HLJA HLJB	Human Lung	pCMVSport 1	LP06
HOFM HOFN HOFO	H. Ovarian Tumor. II, OV5232	pCMVSport 2.0	LP07
HOGA HOGB HOGC	OV 10-3-95	pCMVSport 2.0	LP07
HCGL	CD34+cells. II	pCMVSport 2.0	LP07
HDLA	Hodgkin's Lymphoma I	pCMVSport 2.0	LP07
HDTA HDTB HDTC HDTD HDTE	Hodgkin's Lymphoma II	pCMVSport 2.0	LP07
HKAA HKAB HKAC HKAD HKAE HKAF HKAG HKAH	Keratinocyte	pCMVSport2.0	LP07
HCIM	CAPFINDER, Crohn's Disease, lib 2	pCMVSport 2.0	LP07
HKAL	Keratinocyte, lib 2	pCMVSport2.0	LP07
HKAT	Keratinocyte, lib 3	pCMVSport2.0	LP07
HNDA	Nasal polyps	pCMVSport2.0	LP07
HDRA	H. Primary Dendritic Cells,lib 3	pCMVSport2.0	LP07
HOHA HOHB HOHC	Human Osteoblasts II	pCMVSport2.0	LP07
HLDA HLDB HLDC	Liver, Hepatoma	pCMVSport3.0	LP08
HLDN HLDO HLDP	Human Liver, normal	pCMVSport3.0	LP08
HMTA	pBMC stimulated w/ poly I/C	pCMVSport3.0	LP08
HNTA	NTERA2, control	pCMVSport3.0	LP08
HDPA HDPB HDPC HDPD HDPF HDPG HDPH HDPI HDPJ HDPK	Primary Dendritic Cells, lib 1	pCMVSport3.0	LP08
HDPM HDPN HDPO HDPP	Primary Dendritic cells,frac 2	pCMVSport3.0	LP08
HMUA HMUB HMUC	Myoloid Progenitor Cell Line	pCMVSport3.0	LP08
HHEA HHEB HHEC HHED	T Cell helper I	pCMVSport3.0	LP08
HHEM HHEN HHEO HHEP	T cell helper II	pCMVSport3.0	LP08
HEQA HEQB HEQC	Human endometrial stromal cells	pCMVSport3.0	LP08
HJMA HJMB	Human endometrial stromal cells-treated with progesterone	pCMVSport3.0	LP08
HSWA HSWB HSWC	Human endometrial stromal cells-treated with estradiol	pCMVSport3.0	LP08
HSYA HSYB HSYC	Human Thymus Stromal Cells	pCMVSport3.0	LP08
HLWA HLWB HLWC	Human Placenta	pCMVSport3.0	LP08
HRAA HRAB HRAC	Rejected Kidney, lib 4	pCMVSport3.0	LP08
HMTM	PCR, pBMC I/C treated	PCRII	LP09
HMJA	H. Meniingima, M6	pSport 1	LP10
HMKA HMKB HMKC HMKD HMKE	H. Meningima, M1	pSport 1	LP10
HUSG HUSI	Human umbilical vein endothelial cells, IL-4 induced	pSport 1	LP10
HUSX HUSY	Human Umbilical Vein Endothelial Cells, uninduced	pSport 1	LP10
HOFA	Ovarian Tumor I, OV5232	pSport 1	LP10
HCFA HCFB HCFC HCFD	T-Cell PHA 16 hrs	pSport 1	LP10
HCFL HCFM HCFN HCFO	T-Cell PHA 24 hrs	pSport 1	LP10
HADA HADC HADD HADE HADF HADG	Human Adipose	pSport 1	LP10
HOVA HOVB HOVC	Human Ovary	pSport 1	LP10

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HTWB HTWC HTWD HTWE HTWF	Resting T-Cell Library,II	pSport 1	LP10
HMMA	Spleen metastic melanoma	pSport 1	LP10
HLYA HLYB HLYC HLYD HLYE	Spleen, Chronic lymphocytic leukemia	pSport 1	LP10
HCGA	CD34+ cell, I	pSport 1	LP10
HEOM HEON	Human Eosinophils	pSport 1	LP10
HTDA	Human Tonsil, Lib 3	pSport 1	LP10
HSPA	Salivary Gland, Lib 2	pSport 1	LP10
HCHA HCHB HCHC	Breast Cancer cell line, MDA 36	pSport 1	LP10
HCHM HCHN	Breast Cancer Cell line, angiogenic	pSport 1	LP10
HCIA	Crohn's Disease	pSport 1	LP10
HDAA HDAB HDAC	HEL cell line	pSport 1	LP10
HABA	Human Astrocyte	pSport 1	LP10
HUFA HUFB HUFC	Ulcerative Colitis	pSport 1	LP10
HNTM	NTERA2 + retinoic acid, 14 days	pSport 1	LP10
HDQA	Primary Dendritic cells,CapFinder2, frac 1	pSport 1	LP10
HDQM	Primary Dendritic Cells, CapFinder, frac 2	pSport 1	LP10
HLDX	Human Liver, normal,CapFinder	pSport 1	LP10
HULA HULB HULC	Human Dermal Endothelial Cells,untreated	pSport1	LP10
HUMA	Human Dermal Endothelial cells,treated	pSport1	LP10
HCJA	Human Stromal Endometrial fibroblasts, untreated	pSport1	LP10
HCJM	Human Stromal endometrial fibroblasts, treated w/ estradiol	pSport1	LP10
HEDA	Human Stromal endometrial fibroblasts, treated with progesterone	pSport1	LP10
HFNA	Human ovary tumor cell OV350721	pSport1	LP10
HKGA HKGB HKGC HKGD	Merkel Cells	pSport1	LP10
HISA HISB HISC	Pancreas Islet Cell Tumor	pSport1	LP10
HLSA	Skin, burned	pSport1	LP10
HBZA	Prostate,BPH, Lib 2	pSport 1	LP10
HBZS	Prostate BPH,Lib 2, subtracted	pSport 1	LP10
HFIA HFIB HFIC	Synovial Fibroblasts (control)	pSport 1	LP10
HFIH HFII HFIJ	Synovial hypoxia	pSport 1	LP10
HFIT HFIU HFIV	Synovial IL-1/TNF stimulated	pSport 1	LP10
HGCA	Messangial cell, frac 1	pSport1	LP10
HMVA HMVB HMVC	Bone Marrow Stromal Cell, untreated	pSport1	LP10
HFIX HFIY HFIZ	Synovial Fibroblasts (Il1/TNF), subt	pSport1	LP10
HFOX HFOY HFOZ	Synovial hypoxia-RSF subtracted	pSport1	LP10
HMQA HMQB HMQC HMQD	Human Activated Monocytes	Uni-ZAP XR	LP11
HLIA HLIB HLIC	Human Liver	pCMVSport 1	LP012
HHBA HHBB HHBC HHBD HHBE	Human Heart	pCMVSport 1	LP012
HBBA HBBB	Human Brain	pCMVSport 1	LP012
HLJA HLJB HLJC HLJD HLJE	Human Lung	pCMVSport 1	LP012

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HOGA HOGB HOGC	Ovarian Tumor	pCMVSport 2.0	LP012
HTJM	Human Tonsils. Lib 2	pCMVSport 2.0	LP012
HAMF HAMG	KMH2	pCMVSport 3.0	LP012
HAJA HAJB HAJC	L428	pCMVSport 3.0	LP012
HWBA HWBB HWBC HWBD HWBE	Dendritic cells, pooled	pCMVSport 3.0	LP012
HWAA HWAB HWAC HWAD HWAE	Human Bone Marrow. treated	pCMVSport 3.0	LP012
HYAA HYAB HYAC	B Cell lymphoma	pCMVSport 3.0	LP012
HWHG HWHH HWHI	Healing groin wound. 6.5 hours post incision	pCMVSport 3.0	LP012
HWHP HWHQ HWHR	Healing groin wound: 7.5 hours post incision	pCMVSport 3.0	LP012
HARM	Healing groin wound - zero hr post-incision (control)	pCMVSport 3.0	LP012
HBIM	Olfactory epithelium: nasalcavity	pCMVSport 3.0	LP012
HWDA	Healing Abdomen wound: 70&90 min post incision	pCMVSport 3.0	LP012
HWEA	Healing Abdomen Wound;15 days post incision	pCMVSport 3.0	LP012
HWJA	Healing Abdomen Wound;21&29 days	pCMVSport 3.0	LP012
HNAL	Human Tongue, frac 2	pSport1	LP012
HMJA	H. Meniingima, M6	pSport1	LP012
HMKA HMKB HMKC HMKD HMKE	H. Meningima, M1	pSport1	LP012
HOFA	Ovarian Tumor I. OV5232	pSport1	LP012
HCFA HCFB HCFC HCFD	T-Cell PHA 16 hrs	pSport1	LP012
HCFL HCFM HCFN HCFO	T-Cell PHA 24 hrs	pSport1	LP012
HMMA HMMB HMMC	Spleen metastic melanoma	pSport1	LP012
HTDA	Human Tonsil. Lib 3	pSport1	LP012
HDBA	Human Fetal Thymus	pSport1	LP012
HDUA	Pericardium	pSport1	LP012
HBZA	Prostate.BPH, Lib 2	pSport1	LP012
HWCA	Larynx tumor	pSport1	LP012
HWKA	Normal lung	pSport1	LP012
HSMB	Bone marrow stroma,treated	pSport1	LP012
HBHM	Normal trachea	pSport1	LP012
HLFC	Human Larynx	pSport1	LP012
HLRB	Siebben Polyposis	pSport1	LP012
HNIA	Mammary Gland	pSport1	LP012
HNJB	Palate carcinoma	pSport1	LP012
HNKA	Palate normal	pSport1	LP012
HMZA	Pharynx carcinoma	pSport1	LP012
HABG	Cheek Carcinoma	pSport1	LP012
HMZM	Pharynx Carcinoma	pSport1	LP012
HDRM	Larynx Carcinoma	pSport1	LP012
HVAA	Pancreas normal PCA4 No	pSport1	LP012
HICA	Tongue carcinoma	pSport1	LP012
HUKA HUKB HUKC HUKD HUKE	Human Uterine Cancer	Lambda ZAP II	LP013
HFFA	Human Fetal Brain, random primed	Lambda ZAP II	LP013
HTUA	Activated T-cell labeled with 4-thioluri	Lambda ZAP II	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HBQA	Early Stage Human Brain, random primed	Lambda ZAP II	LP013
HMEB	Human microvascular Endothelial cells, fract. B	Lambda ZAP II	LP013
HUSH	Human Umbilical Vein Endothelial cells, fract. A, re-excision	Lambda ZAP II	LP013
HLQC HLQD	Hepatocellular tumor, re-excision	Lambda ZAP II	LP013
HTWJ HTWK HTWL	Resting T-cell, re-excision	Lambda ZAP II	LP013
HF6S	Human Whole 6 week Old Embryo (II), subt	pBluescript	LP013
HHPS	Human Hippocampus, subtracted	pBluescript	LP013
HL1S	LNCAP, differential expression	pBluescript	LP013
HLHS HLHT	Early Stage Human Lung, Subtracted	pBluescript	LP013
HSUS	Supt cells, cyclohexamide treated, subtracted	pBluescript	LP013
HSUT	Supt cells, cyclohexamide treated, differentially expressed	pBluescript	LP013
HSDS	H. Striatum Depression, subtracted	pBluescript	LP013
HPTZ	Human Pituitary, Subtracted VII	pBluescript	LP013
HSDX	H. Striatum Depression, subt II	pBluescript	LP013
HSDZ	H. Striatum Depression, subt	pBluescript	LP013
HPBA HPBB HPBC HPBD HPBE	Human Pineal Gland	pBluescript SK-	LP013
HRTA	Colorectal Tumor	pBluescript SK-	LP013
HSBA HSBB HSBC HSBM	HSC172 cells	pBluescript SK-	LP013
HJAA HJAB HJAC HJAD	Jurkat T-cell G1 phase	pBluescript SK-	LP013
HJBA HJBB HJBC HJBD	Jurkat T-cell, S1 phase	pBluescript SK-	LP013
HTNA HTNB	Human Thyroid	pBluescript SK-	LP013
HAHA HAHB	Human Adult Heart	Uni-ZAP XR	LP013
HE6A	Whole 6 week Old Embryo	Uni-ZAP XR	LP013
HFCA HFCB HFCC HFCD HFCE	Human Fetal Brain	Uni-ZAP XR	LP013
HFKC HFKD HFKE HFKF HFKG	Human Fetal Kidney	Uni-ZAP XR	LP013
HGBA HGBD HGBE HGBF HGBG	Human Gall Bladder	Uni-ZAP XR	LP013
HPRA HPRB HPRC HPRD	Human Prostate	Uni-ZAP XR	LP013
HTEA HTEB HTEC HTED HTEE	Human Testes	Uni-ZAP XR	LP013
HTTA HTTB HTTC HTTD HTTE	Human Testes Tumor	Uni-ZAP XR	LP013
HYBA HYBB	Human Fetal Bone	Uni-ZAP XR	LP013
HFLA	Human Fetal Liver	Uni-ZAP XR	LP013
HHFB HHFC HHFD HHFE HHFF	Human Fetal Heart	Uni-ZAP XR	LP013
HUVB HUVC HUVD HUVE	Human Umbilical Vein, End. remake	Uni-ZAP XR	LP013
HTHB HTHC HTHD	Human Thymus	Uni-ZAP XR	LP013
HSTA HSTB HSTC HSTD	Human Skin Tumor	Uni-ZAP XR	LP013
HTAA HTAB HTAC HTAD HTAE	Human Activated T-cells	Uni-ZAP XR	LP013
HFEA HFEB HFEC	Human Fetal Epithelium (skin)	Uni-ZAP XR	LP013
HJPA HJPB HJPC HJPD	Human Jurkat Membrane Bound Polysomes	Uni-ZAP XR	LP013
HESA	Human Epithelioid Sarcoma	Uni-ZAP XR	LP013
HALS	Human Adult Liver, Subtracted	Uni-ZAP XR	LP013
HFTA HFTB HFTC HFTD	Human Fetal Dura Mater	Uni-ZAP XR	LP013
HCAA HCAB HCAC	Cem cells, cyclohexamide treated	Uni-ZAP XR	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HRGA HRGB HRGC HRGD	Raji Cells, cyclohexamide treated	Uni-ZAP XR	LP013
HE9A HE9B HE9C HE9D HE9E	Nine Week Old Early Stage Human	Uni-ZAP XR	LP013
HSFA	Human Fibrosarcoma	Uni-ZAP XR	LP013
HATA HATB HATC HATD HATE	Human Adrenal Gland Tumor	Uni-ZAP XR	LP013
HTRA	Human Trachea Tumor	Uni-ZAP XR	LP013
HE2A HE2D HE2E HE2H HE2I	12 Week Old Early Stage Human	Uni-ZAP XR	LP013
HE2B HE2C HE2F HE2G HE2P	12 Week Old Early Stage Human, II	Uni-ZAP XR	LP013
HNEA HNEB HNEC HNED HNEE	Human Neutrophil	Uni-ZAP XR	LP013
HBGA	Human Primary Breast Cancer	Uni-ZAP XR	LP013
HPTS HPTT HPTU	Human Pituitary, subtracted	Uni-ZAP XR	LP013
HMQA HMQB HMQC HMQD	Human Activated Monocytes	Uni-ZAP XR	LP013
HOAA HOAB HOAC	Human Osteosarcoma	Uni-ZAP XR	LP013
HTOA HTOD HTOE HTOF HTOG	human tonsils	Uni-ZAP XR	LP013
HMGB	Human OB MG63 control fraction I	Uni-ZAP XR	LP013
HOPB	Human OB HOS control fraction I	Uni-ZAP XR	LP013
HOQB	Human OB HOS treated (1 nM E2) fraction I	Uni-ZAP XR	LP013
HAUA HAUB HAUC	Amniotic Cells - TNF induced	Uni-ZAP XR	LP013
HAQA HAQB HAQC HAQD	Amniotic Cells - Primary Culture	Uni-ZAP XR	LP013
HROA HROC	HUMAN STOMACH	Uni-ZAP XR	LP013
HBJA HBJB HBJC HBJD HBJE	HUMAN B CELL LYMPHOMA	Uni-ZAP XR	LP013
HODA HODB HODC HODD	human ovarian cancer	Uni-ZAP XR	LP013
HCPA	Corpus Callosum	Uni-ZAP XR	LP013
HSOA	stomach cancer (human)	Uni-ZAP XR	LP013
HERA	SKIN	Uni-ZAP XR	LP013
HMDA	Brain-medulloblastoma	Uni-ZAP XR	LP013
HGLA HGLB HGLD	Glioblastoma	Uni-ZAP XR	LP013
HWTA HWTB HWTC	wilm's tumor	Uni-ZAP XR	LP013
HEAA	H. Atrophic Endometrium	Uni-ZAP XR	LP013
HAPN HAPO HAPP HAPQ HAPR	Human Adult Pulmonary;re-excision	Uni-ZAP XR	LP013
HLTG HLTH	Human T-cell lymphoma;re-excision	Uni-ZAP XR	LP013
HAHC HAHD HAHE	Human Adult Heart;re-excision	Uni-ZAP XR	LP013
HAGA HAGB HAGC HAGD HAGE	Human Amygdala	Uni-ZAP XR	LP013
HSJA HSJB HSJC	Smooth muscle-ILb induced	Uni-ZAP XR	LP013
HSHA HSHB HSHC	Smooth muscle, IL1b induced	Uni-ZAP XR	LP013
HPWA HPWB HPWC HPWD HPWE	Prostate BPH	Uni-ZAP XR	LP013
HPIA HPIB HPIC	LNCAP prostate cell line	Uni-ZAP XR	LP013
HPJA HPJB HPJC	PC3 Prostate cell line	Uni-ZAP XR	LP013
HBTA	Bone Marrow Stroma, TNF&LPS ind	Uni-ZAP XR	LP013
HMCF HMCG HMCH HMCI HMCJ	Macrophage-oxLDL; re-excision	Uni-ZAP XR	LP013
HAGG HAGH HAGI	Human Amygdala;re-excision	Uni-ZAP XR	LP013
HACA	H. Adipose Tissue	Uni-ZAP XR	LP013
HKFB	K562 + PMA (36 hrs),re-excision	ZAP Express	LP013
HCWT HCWU HCWV	CD34 positive cells (cord blood),re-ex	ZAP Express	LP013
HBWA	Whole brain	ZAP Express	LP013
HBXA HBXB HBXC HBXD	Human Whole Brain #2 - Oligo dT > 1.5Kb	ZAP Express	LP013

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HAVM	Temporal cortex-Alzheizmer	pT-Adv	LP014
HAVT	Hippocampus. Alzheimer Subtracted	pT-Adv	LP014
HHAS	CHME Cell Line	Uni-ZAP XR	LP014
HAJR	Larynx normal	pSport 1	LP014
HWLE HWLF HWLG HWLH	Colon Normal	pSport 1	LP014
HCRM HCRN HCRO	Colon Carcinoma	pSport 1	LP014
HWLI HWLJ HWLK	Colon Normal	pSport 1	LP014
HW[illegible] HWLR HWLS HWLT	Colon Tumor	pSport 1	LP014
HBFM	Gastrocnemius Muscle	pSport 1	LP014
HBOD HBOE	Quadriceps Muscle	pSport 1	LP014
HBKD HBKE	Soleus Muscle	pSport 1	LP014
HCCM	Pancreatic Langerhans	pSport 1	LP014
HWGA	Larynx carcinoma	pSport 1	LP014
HWGM HWGN	Larynx carcinoma	pSport 1	LP014
HWLA HWLB HWLC	Normal colon	pSport 1	LP014
HWLM HWLN	Colon Tumor	pSport 1	LP014
HVAM HVAN HVAO	Pancreas Tumor	pSport 1	LP014
HWGQ	Larynx carcinoma	pSport 1	LP014
HAQM HAQN	Salivary Gland	pSport 1	LP014
HASM	Stomach; normal	pSport 1	LP014
HBCM	Uterus; normal	pSport 1	LP014
HCDM	Testis; normal	pSport 1	LP014
HDJM	Brain; normal	pSport 1	LP014
HEFM	Adrenal Gland,normal	pSport 1	LP014
HBAA	Rectum normal	pSport 1	LP014
HFDM	Rectum tumour	pSport 1	LP014
HGAM	Colon, normal	pSport 1	LP014
HHMM	Colon, tumour	pSport 1	LP014
HCLB HCLC	Human Lung Cancer	Lambda Zap II	LP015
HRLA	L1 Cell line	ZAP Express	LP015
HHAM	Hypothalamus, Alzheimer's	pCMVSport 3.0	LP015
HKBA	Ku 812F Basophils Line	pSport 1	LP015
HS2S	Saos2, Dexamethosome Treated	pSport 1	LP016
HA5A	Lung Carcinoma A549 TNFalpha activated	pSport 1	LP016
HTFM	TF-1 Cell Line GM-CSF Treated	pSport 1	LP016
HYAS	Thyroid Tumour	pSport 1	LP016
HUTS	Larynx Normal	pSport 1	LP016
HXOA	Larynx Tumor	pSport 1	LP016
HEAH	Ea.hy.926 cell line	pSport 1	LP016
HINA	Adenocarcinoma Human	pSport 1	LP016
HRMA	Lung Mesothelium	pSport 1	LP016
HLCL	Human Pre-Differentiated Adipocytes	Uni-Zap XR	LP017
HS2A	Saos2 Cells	pSport 1	LP020
HS2I	Saos2 Cells: Vitamin D3 Treated	pSport 1	LP020
HUCM	CHME Cell Line, untreated	pSport 1	LP020
HEPN	Aryepiglottis Normal	pSport 1	LP020

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HPSN	Sinus Piniformis Tumour	pSport 1	LP020
HNSA	Stomach Normal	pSport 1	LP020
HNSM	Stomach Tumour	pSport 1	LP020
HNLA	Liver Normal Met5No	pSport 1	LP020
HUTA	Liver Tumour Met 5 Tu	pSport 1	LP020
HOCN	Colon Normal	pSport 1	LP020
HOCT	Colon Tumor	pSport 1	LP020
HTNT	Tongue Tumour	pSport 1	LP020
HLXN	Larynx Normal	pSport 1	LP020
HLXT	Larynx Tumour	pSport 1	LP020
HTYN	Thymus	pSport 1	LP020
HPLN	Placenta	pSport 1	LP020
HTNG	Tongue Normal	pSport 1	LP020
HZAA	Thyroid Normal (SDCA2 No)	pSport 1	LP020
HWES	Thyroid Thyroiditis	pSport 1	LP020
HFHD	Ficolled Human Stromal Cells, 5Fu treated	pTrip1Ex2	LP021
HFHM,HFHN	Ficolled Human Stromal Cells, Untreated	pTrip1Ex2	LP021
HPCI	Hep G2 Cells, lambda library	lambda Zap-CMV XR	LP021
HBCA,HBCB,HBCC	H. Lymph node breast Cancer	Uni-ZAP XR	LP021
HCOK	Chondrocytes	pSPORT1	LP022
HDCA, HDCB, HDCC	Dendritic Cells From CD34 Cells	pSPORT1	LP022
HDMA, HDMB	CD40 activated monocyte dendritic cells	pSPORT1	LP022
HDDM, HDDN, HDDO	LPS activated derived dendritic cells	pSPORT1	LP022
HPCR	Hep G2 Cells, PCR library	lambda Zap-CMV XR	LP022
HAAA, HAAB, HAAC	Lung, Cancer (4005313A3): Invasive Poorly Differentiated Lung Adenocarcinoma	pSPORT1	LP022
HIPA, HIPB, HIPC	Lung, Cancer (4005163 B7): Invasive, Poorly Diff. Adenocarcinoma, Metastatic	pSPORT1	LP022
HOOH, HOOI	Ovary, Cancer: (4004562 B6) Papillary Serous Cystic Neoplasm, Low Malignant Pot	pSPORT1	LP022
HIDA	Lung, Normal: (4005313 B1)	pSPORT1	LP022
HUJA,HUJB,HUJC,HUJD,HUJE	B-Cells	pCMVSport 3.0	LP022
HNOA,HNOB,HNOC,HNOD	Ovary, Normal: (9805C040R)	pSPORT1	LP022
HNLM	Lung, Normal: (4005313 B1)	pSPORT1	LP022
HSCL	Stromal Cells	pSPORT1	LP022
HAAX	Lung, Cancer: (4005313 A3) Invasive Poorly-differentiated Metastatic lung adenocarcinoma	pSPORT1	LP022
HUUA,HUUB,HUUC,HUUD	B-cells (unstimulated)	pTrip1Ex2	LP022
HWWA,HWWB,HWWC,HWWD,HWWE,HWWF,HWWG	B-cells (stimulated)	pSPORT1	LP022
HCCC	Colon, Cancer: (9808C064R)	pCMVSport 3.0	LP023
HPDO HPDP HPDQ HPDR HPD	Ovary, Cancer (9809C332): Poorly differentiated adenocarcinoma	pSport 1	LP023

Libraries owned by Catalog	Catalog Description	Vector	ATCC Deposit
HPCO HPCP HPCQ HPCT	Ovary, Cancer (15395A1F): Grade II Papillary Carcinoma	pSport 1	LP023
HOCM HOCO HOCP HOCQ	Ovary, Cancer: (15799A1F) Poorly differentiated carcinoma	pSport 1	LP023
HCBM HCBN HCBO	Breast, Cancer: (4004943 A5)	pSport 1	LP023
HNBT HNBU HNBV	Breast, Normal: (4005522B2)	pSport 1	LP023
HBCP HBCQ	Breast, Cancer: (4005522 A2)	pSport 1	LP023
HBCJ	Breast, Cancer: (9806C012R)	pSport 1	LP023
HSAM HSAN	Stromal cells 3.88	pSport 1	LP023
HVCA HVCB HVCC HVCD	Ovary, Cancer: (4004332 A2)	pSport 1	LP023
HSCK HSEN HSEO	Stromal cells (HBM3.18)	pSport 1	LP023
HSCP HSCQ	stromal cell clone 2.5	pSport 1	LP023
HUXA	Breast Cancer: (4005385 A2)	pSport 1	LP023
HCOM HCON HCOO HCOP HCOQ	Ovary, Cancer (4004650 A3): Well-Differentiated Micropapillary Serous Carcinoma	pSport 1	LP023
HBNM	Breast, Cancer: (9802C020E)	pSport 1	LP023
HVVA HVVB HVVC HVVD HVVE	Human Bone Marrow, treated	pSport 1	LP023

Two approaches can be used to isolate a particular clone from the deposited sample of plasmid DNAs cited for that clone in Table 5. First, a plasmid is directly isolated by screening the clones using a polynucleotide probe corresponding to the nucleotide sequence of SEQ ID NO:X.

Particularly, a specific polynucleotide with 30-40 nucleotides is synthesized using an Applied Biosystems DNA synthesizer according to the sequence reported. The oligonucleotide is labeled, for instance, with ^{32}P-γ-ATP using T4 polynucleotide kinase and purified according to routine methods. (E.g., Maniatis et al., Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Press, Cold Spring, NY (1982).) The plasmid mixture is transformed into a suitable host, as indicated above (such as XL-1 Blue (Stratagene)) using techniques known to those of skill in the art, such as those provided by the vector supplier or in related publications or patents cited above. The transformants are plated on 1.5% agar plates (containing the appropriate selection agent, e.g., ampicillin) to a density of about 150 transformants (colonies) per plate. These plates are screened using Nylon membranes according to routine methods for bacterial colony screening (e.g., Sambrook et al., Molecular Cloning: A Laboratory Manual, 2nd Edit., (1989), Cold Spring Harbor Laboratory Press, pages 1.93 to 1.104), or other techniques known to those of skill in the art.

Alternatively, two primers of 17-20 nucleotides derived from both ends of the nucleotide sequence of SEQ ID NO:X are synthesized and used to amplify the desired cDNA using the deposited cDNA plasmid as a template. The polymerase chain reaction is carried out under routine conditions, for instance, in 25 μl of reaction mixture with 0.5 ug of the above cDNA template. A convenient reaction mixture is 1.5-5 mM $MgCl_2$, 0.01% (w/v) gelatin, 20 μM each of dATP, dCTP, dGTP, dTTP, 25 pmol of each primer and 0.25 Unit of Taq polymerase. Thirty five cycles of PCR (denaturation at 94°C for 1 min; annealing at 55°C for 1 min; elongation at 72°C for 1 min) are performed with a Perkin-Elmer Cetus automated thermal cycler. The amplified product is analyzed by agarose gel electrophoresis and the DNA band with expected molecular weight is excised and purified. The PCR product is verified to be the selected sequence by subcloning and sequencing the DNA product.

Several methods are available for the identification of the 5' or 3' non-coding portions of a gene which may not be present in the deposited clone. These methods include but are not

limited to, filter probing, clone enrichment using specific probes, and protocols similar or identical to 5' and 3' "RACE" protocols which are well known in the art. For instance, a method similar to 5' RACE is available for generating the missing 5' end of a desired full-length transcript. (Fromont-Racine et al., Nucleic Acids Res. 21(7):1683-1684 (1993).)

Briefly, a specific RNA oligonucleotide is ligated to the 5' ends of a population of RNA presumably containing full-length gene RNA transcripts. A primer set containing a primer specific to the ligated RNA oligonucleotide and a primer specific to a known sequence of the gene of interest is used to PCR amplify the 5' portion of the desired full-length gene. This amplified product may then be sequenced and used to generate the full length gene.

This above method starts with total RNA isolated from the desired source, although poly-A+ RNA can be used. The RNA preparation can then be treated with phosphatase if necessary to eliminate 5' phosphate groups on degraded or damaged RNA which may interfere with the later RNA ligase step. The phosphatase should then be inactivated and the RNA treated with tobacco acid pyrophosphatase in order to remove the cap structure present at the 5' ends of messenger RNAs. This reaction leaves a 5' phosphate group at the 5' end of the cap cleaved RNA which can then be ligated to an RNA oligonucleotide using T4 RNA ligase.

This modified RNA preparation is used as a template for first strand cDNA synthesis using a gene specific oligonucleotide. The first strand synthesis reaction is used as a template for PCR amplification of the desired 5' end using a primer specific to the ligated RNA oligonucleotide and a primer specific to the known sequence of the gene of interest. The resultant product is then sequenced and analyzed to confirm that the 5' end sequence belongs to the desired gene.

Example 2: Isolation of Genomic Clones Corresponding to a Polynucleotide

A human genomic P1 library (Genomic Systems, Inc.) is screened by PCR using primers selected for the sequence corresponding to SEQ ID NO:X, according to the method described in Example 1. (See also, Sambrook.)

Example 3: Tissue specific expression analysis

The Human Genome Sciences, Inc. (HGS) database is derived from sequencing tissue specific cDNA libraries. Libraries generated from a particular tissue are selected and the specific tissue expression pattern of EST groups or assembled contigs within these libraries is determined by comparison of the expression patterns of those groups or contigs within the entire database. ESTs which show tissue specific expression are selected.

The original clone from which the specific EST sequence was generated, is obtained from the catalogued library of clones and the insert amplified by PCR using methods known in the art. The PCR product is denatured then transferred in 96 well format to a nylon membrane (Schleicher and Scheull) generating an array filter of tissue specific clones. Housekeeping genes, maize genes, and known tissue specific genes are included on the filters. These targets can be used in signal normalization and to validate assay sensitivity. Additional targets are included to monitor probe length and specificity of hybridization.

Radioactively labeled hybridization probes are generated by first strand cDNA synthesis per the manufacturer's instructions (Life Technologies) from mRNA/RNA samples prepared from the specific tissue being analyzed. The hybridization probes are purified by gel exclusion chromatography, quantitated, and hybridized with the array filters in hybridization bottles at 65°C overnight. The filters are washed under stringent conditions and signals are captured using a Fuji phosphorimager.

Data is extracted using AIS software and following background subtraction, signal normalization is performed. This includes a normalization of filter-wide expression levels between different experimental runs. Genes that are differentially expressed in the tissue of interest are identified and the full length sequence of these clones is generated.

Example 4: Chromosomal Mapping of the Polynucleotides

An oligonucleotide primer set is designed according to the sequence at the 5' end of SEQ ID NO:X. This primer preferably spans about 100 nucleotides. This primer set is then used in a polymerase chain reaction under the following set of conditions : 30 seconds, 95°C; 1 minute, 56°C; 1 minute, 70°C. This cycle is repeated 32 times followed by one 5 minute

cycle at 70°C. Human, mouse, and hamster DNA is used as template in addition to a somatic cell hybrid panel containing individual chromosomes or chromosome fragments (Bios, Inc). The reactions is analyzed on either 8% polyacrylamide gels or 3.5 % agarose gels. Chromosome mapping is determined by the presence of an approximately 100 bp PCR fragment in the particular somatic cell hybrid.

Example 5: Bacterial Expression of a Polypeptide

A polynucleotide encoding a polypeptide of the present invention is amplified using PCR oligonucleotide primers corresponding to the 5' and 3' ends of the DNA sequence, as outlined in Example 1, to synthesize insertion fragments. The primers used to amplify the cDNA insert should preferably contain restriction sites, such as BamHI and XbaI, at the 5' end of the primers in order to clone the amplified product into the expression vector. For example, BamHI and XbaI correspond to the restriction enzyme sites on the bacterial expression vector pQE-9. (Qiagen, Inc., Chatsworth, CA). This plasmid vector encodes antibiotic resistance (Amp^r), a bacterial origin of replication (ori), an IPTG-regulatable promoter/operator (P/O), a ribosome binding site (RBS), a 6-histidine tag (6-His), and restriction enzyme cloning sites.

The pQE-9 vector is digested with BamHI and XbaI and the amplified fragment is ligated into the pQE-9 vector maintaining the reading frame initiated at the bacterial RBS. The ligation mixture is then used to transform the E. coli strain M15/rep4 (Qiagen, Inc.) which contains multiple copies of the plasmid pREP4, which expresses the lacI repressor and also confers kanamycin resistance (Kan^r). Transformants are identified by their ability to grow on LB plates and ampicillin/kanamycin resistant colonies are selected. Plasmid DNA is isolated and confirmed by restriction analysis.

Clones containing the desired constructs are grown overnight (O/N) in liquid culture in LB media supplemented with both Amp (100 ug/ml) and Kan (25 ug/ml). The O/N culture is used to inoculate a large culture at a ratio of 1:100 to 1:250. The cells are grown to an optical density 600 ($O.D.^{600}$) of between 0.4 and 0.6. IPTG (Isopropyl-B-D-thiogalacto pyranoside) is then added to a final concentration of 1 mM. IPTG induces by inactivating the lacI repressor, clearing the P/O leading to increased gene expression.

Cells are grown for an extra 3 to 4 hours. Cells are then harvested by centrifugation (20 mins at 6000Xg). The cell pellet is solubilized in the chaotropic agent 6 Molar Guanidine HCl by stirring for 3-4 hours at 4°C. The cell debris is removed by centrifugation, and the supernatant containing the polypeptide is loaded onto a nickel-nitrilo-tri-acetic acid ("Ni-NTA") affinity resin column (available from QIAGEN, Inc., *supra*). Proteins with a 6 x His tag bind to the Ni-NTA resin with high affinity and can be purified in a simple one-step procedure (for details see: The QIAexpressionist (1995) QIAGEN, Inc., *supra*).

Briefly, the supernatant is loaded onto the column in 6 M guanidine-HCl, pH 8, the column is first washed with 10 volumes of 6 M guanidine-HCl, pH 8, then washed with 10 volumes of 6 M guanidine-HCl pH 6, and finally the polypeptide is eluted with 6 M guanidine-HCl, pH 5.

The purified protein is then renatured by dialyzing it against phosphate-buffered saline (PBS) or 50 mM Na-acetate, pH 6 buffer plus 200 mM NaCl. Alternatively, the protein can be successfully refolded while immobilized on the Ni-NTA column. The recommended conditions are as follows: renature using a linear 6M-1M urea gradient in 500 mM NaCl, 20% glycerol, 20 mM Tris/HCl pH 7.4, containing protease inhibitors. The renaturation should be performed over a period of 1.5 hours or more. After renaturation the proteins are eluted by the addition of 250 mM immidazole. Immidazole is removed by a final dialyzing step against PBS or 50 mM sodium acetate pH 6 buffer plus 200 mM NaCl. The purified protein is stored at 4° C or frozen at -80° C.

In addition to the above expression vector, the present invention further includes an expression vector comprising phage operator and promoter elements operatively linked to a polynucleotide of the present invention, called pHE4a. (ATCC Accession Number 209645, deposited on February 25, 1998.) This vector contains: 1) a neomycinphosphotransferase gene as a selection marker, 2) an E. coli origin of replication, 3) a T5 phage promoter sequence, 4) two lac operator sequences, 5) a Shine-Delgarno sequence, and 6) the lactose operon repressor gene (lacIq). The origin of replication (oriC) is derived from pUC19 (LTI, Gaithersburg, MD). The promoter sequence and operator sequences are made synthetically.

DNA can be inserted into the pHEa by restricting the vector with NdeI and XbaI, BamHI, XhoI, or Asp718, running the restricted product on a gel, and isolating the larger fragment (the stuffer fragment should be about 310 base pairs). The DNA insert is generated according to the PCR protocol described in Example 1, using PCR primers having restriction

sites for NdeI (5' primer) and XbaI, BamHI, XhoI, or Asp718 (3' primer). The PCR insert is gel purified and restricted with compatible enzymes. The insert and vector are ligated according to standard protocols.

The engineered vector could easily be substituted in the above protocol to express protein in a bacterial system.

Example 6: Purification of a Polypeptide from an Inclusion Body

The following alternative method can be used to purify a polypeptide expressed in *E coli* when it is present in the form of inclusion bodies. Unless otherwise specified, all of the following steps are conducted at 4-10°C.

Upon completion of the production phase of the *E. coli* fermentation, the cell culture is cooled to 4-10°C and the cells harvested by continuous centrifugation at 15,000 rpm (Heraeus Sepatech). On the basis of the expected yield of protein per unit weight of cell paste and the amount of purified protein required, an appropriate amount of cell paste, by weight, is suspended in a buffer solution containing 100 mM Tris, 50 mM EDTA, pH 7.4. The cells are dispersed to a homogeneous suspension using a high shear mixer.

The cells are then lysed by passing the solution through a microfluidizer (Microfuidics, Corp. or APV Gaulin, Inc.) twice at 4000-6000 psi. The homogenate is then mixed with NaCl solution to a final concentration of 0.5 M NaCl, followed by centrifugation at 7000 xg for 15 min. The resultant pellet is washed again using 0.5M NaCl, 100 mM Tris, 50 mM EDTA, pH 7.4.

The resulting washed inclusion bodies are solubilized with 1.5 M guanidine hydrochloride (GuHCl) for 2-4 hours. After 7000 xg centrifugation for 15 min., the pellet is discarded and the polypeptide containing supernatant is incubated at 4°C overnight to allow further GuHCl extraction.

Following high speed centrifugation (30,000 xg) to remove insoluble particles, the GuHCl solubilized protein is refolded by quickly mixing the GuHCl extract with 20 volumes of buffer containing 50 mM sodium, pH 4.5, 150 mM NaCl, 2 mM EDTA by vigorous stirring. The refolded diluted protein solution is kept at 4°C without mixing for 12 hours prior to further purification steps.

To clarify the refolded polypeptide solution, a previously prepared tangential filtration unit equipped with 0.16 µm membrane filter with appropriate surface area (e.g., Filtron), equilibrated with 40 mM sodium acetate, pH 6.0 is employed. The filtered sample is loaded onto a cation exchange resin (e.g., Poros HS-50, Perseptive Biosystems). The column is washed with 40 mM sodium acetate, pH 6.0 and eluted with 250 mM, 500 mM, 1000 mM, and 1500 mM NaCl in the same buffer, in a stepwise manner. The absorbance at 280 nm of the effluent is continuously monitored. Fractions are collected and further analyzed by SDS-PAGE.

Fractions containing the polypeptide are then pooled and mixed with 4 volumes of water. The diluted sample is then loaded onto a previously prepared set of tandem columns of strong anion (Poros HQ-50, Perseptive Biosystems) and weak anion (Poros CM-20, Perseptive Biosystems) exchange resins. The columns are equilibrated with 40 mM sodium acetate, pH 6.0. Both columns are washed with 40 mM sodium acetate, pH 6.0, 200 mM NaCl. The CM-20 column is then eluted using a 10 column volume linear gradient ranging from 0.2 M NaCl, 50 mM sodium acetate, pH 6.0 to 1.0 M NaCl, 50 mM sodium acetate, pH 6.5. Fractions are collected under constant A_{280} monitoring of the effluent. Fractions containing the polypeptide (determined, for instance, by 16% SDS-PAGE) are then pooled.

The resultant polypeptide should exhibit greater than 95% purity after the above refolding and purification steps. No major contaminant bands should be observed from Commassie blue stained 16% SDS-PAGE gel when 5 µg of purified protein is loaded. The purified protein can also be tested for endotoxin/LPS contamination, and typically the LPS content is less than 0.1 ng/ml according to LAL assays.

Example 7: Cloning and Expression of a Polypeptide in a Baculovirus Expression System

In this example, the plasmid shuttle vector pA2 is used to insert a polynucleotide into a baculovirus to express a polypeptide. This expression vector contains the strong polyhedrin promoter of the *Autographa californica* nuclear polyhedrosis virus (AcMNPV) followed by convenient restriction sites such as BamHI, Xba I and Asp718. The polyadenylation site of the simian virus 40 ("SV40") is used for efficient polyadenylation. For easy selection of recombinant virus, the plasmid contains the beta-galactosidase gene from *E. coli* under control of a weak Drosophila promoter in the same orientation, followed by the

polyadenylation signal of the polyhedrin gene. The inserted genes are flanked on both sides by viral sequences for cell-mediated homologous recombination with wild-type viral DNA to generate a viable virus that express the cloned polynucleotide.

Many other baculovirus vectors can be used in place of the vector above, such as pAc373, pVL941, and pAcIM1, as one skilled in the art would readily appreciate, as long as the construct provides appropriately located signals for transcription, translation, secretion and the like, including a signal peptide and an in-frame AUG as required. Such vectors are described, for instance, in Luckow et al., Virology 170:31-39 (1989).

Specifically, the cDNA sequence contained in the deposited clone, including the AUG initiation codon, is amplified using the PCR protocol described in Example 1. If a naturally occurring signal sequence is used to produce the polypeptide of the present invention, the pA2 vector does not need a second signal peptide. Alternatively, the vector can be modified (pA2 GP) to include a baculovirus leader sequence, using the standard methods described in Summers et al., "A Manual of Methods for Baculovirus Vectors and Insect Cell Culture Procedures," Texas Agricultural Experimental Station Bulletin No. 1555 (1987).

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The plasmid is digested with the corresponding restriction enzymes and optionally, can be dephosphorylated using calf intestinal phosphatase, using routine procedures known in the art. The DNA is then isolated from a 1% agarose gel using a commercially available kit ("Geneclean" BIO 101 Inc., La Jolla, Ca.).

The fragment and the dephosphorylated plasmid are ligated together with T4 DNA ligase. *E. coli* HB101 or other suitable *E. coli* hosts such as XL-1 Blue (Stratagene Cloning Systems, La Jolla, CA) cells are transformed with the ligation mixture and spread on culture plates. Bacteria containing the plasmid are identified by digesting DNA from individual colonies and analyzing the digestion product by gel electrophoresis. The sequence of the cloned fragment is confirmed by DNA sequencing.

Five μg of a plasmid containing the polynucleotide is co-transfected with 1.0 μg of a commercially available linearized baculovirus DNA ("BaculoGold™ baculovirus DNA", Pharmingen, San Diego, CA), using the lipofection method described by Felgner et al., Proc.

Natl. Acad. Sci. USA 84:7413-7417 (1987). One μg of BaculoGold™ virus DNA and 5 μg of the plasmid are mixed in a sterile well of a microtiter plate containing 50 μl of serum-free Grace's medium (Life Technologies Inc., Gaithersburg, MD). Afterwards, 10 μl Lipofectin plus 90 μl Grace's medium are added, mixed and incubated for 15 minutes at room temperature. Then the transfection mixture is added drop-wise to Sf9 insect cells (ATCC CRL 1711) seeded in a 35 mm tissue culture plate with 1 ml Grace's medium without serum. The plate is then incubated for 5 hours at 27° C. The transfection solution is then removed from the plate and 1 ml of Grace's insect medium supplemented with 10% fetal calf serum is added. Cultivation is then continued at 27° C for four days.

After four days the supernatant is collected and a plaque assay is performed, as described by Summers and Smith, *supra*. An agarose gel with "Blue Gal" (Life Technologies Inc., Gaithersburg) is used to allow easy identification and isolation of gal-expressing clones, which produce blue-stained plaques. (A detailed description of a "plaque assay" of this type can also be found in the user's guide for insect cell culture and baculovirology distributed by Life Technologies Inc., Gaithersburg, page 9-10.) After appropriate incubation, blue stained plaques are picked with the tip of a micropipettor (e.g., Eppendorf). The agar containing the recombinant viruses is then resuspended in a microcentrifuge tube containing 200 μl of Grace's medium and the suspension containing the recombinant baculovirus is used to infect Sf9 cells seeded in 35 mm dishes. Four days later the supernatants of these culture dishes are harvested and then they are stored at 4° C.

To verify the expression of the polypeptide, Sf9 cells are grown in Grace's medium supplemented with 10% heat-inactivated FBS. The cells are infected with the recombinant baculovirus containing the polynucleotide at a multiplicity of infection ("MOI") of about 2. If radiolabeled proteins are desired, 6 hours later the medium is removed and is replaced with SF900 II medium minus methionine and cysteine (available from Life Technologies Inc., Rockville, MD). After 42 hours, 5 μCi of ^{35}S-methionine and 5 μCi ^{35}S-cysteine (available from Amersham) are added. The cells are further incubated for 16 hours and then are harvested by centrifugation. The proteins in the supernatant as well as the intracellular proteins are analyzed by SDS-PAGE followed by autoradiography (if radiolabeled).

Microsequencing of the amino acid sequence of the amino terminus of purified protein may be used to determine the amino terminal sequence of the produced protein.

Example 8: Expression of a Polypeptide in Mammalian Cells

The polypeptide of the present invention can be expressed in a mammalian cell. A typical mammalian expression vector contains a promoter element, which mediates the initiation of transcription of mRNA, a protein coding sequence, and signals required for the termination of transcription and polyadenylation of the transcript. Additional elements include enhancers, Kozak sequences and intervening sequences flanked by donor and acceptor sites for RNA splicing. Highly efficient transcription is achieved with the early and late promoters from SV40, the long terminal repeats (LTRs) from Retroviruses, e.g., RSV, HTLVI, HIVI and the early promoter of the cytomegalovirus (CMV). However, cellular elements can also be used (e.g., the human actin promoter).

Suitable expression vectors for use in practicing the present invention include, for example, vectors such as pSVL and pMSG (Pharmacia, Uppsala, Sweden), pRSVcat (ATCC 37152), pSV2dhfr (ATCC 37146), pBC12MI (ATCC 67109), pCMVSport 2.0, and pCMVSport 3.0. Mammalian host cells that could be used include, human Hela, 293, H9 and Jurkat cells, mouse NIH3T3 and C127 cells, Cos 1, Cos 7 and CV1, quail QC1-3 cells, mouse L cells and Chinese hamster ovary (CHO) cells.

Alternatively, the polypeptide can be expressed in stable cell lines containing the polynucleotide integrated into a chromosome. The co-transfection with a selectable marker such as DHFR, gpt, neomycin, hygromycin allows the identification and isolation of the transfected cells.

The transfected gene can also be amplified to express large amounts of the encoded protein. The DHFR (dihydrofolate reductase) marker is useful in developing cell lines that carry several hundred or even several thousand copies of the gene of interest. (See, e.g., Alt, F. W., et al., J. Biol. Chem. 253:1357-1370 (1978); Hamlin, J. L. and Ma, C., Biochem. et Biophys. Acta, 1097:107-143 (1990); Page, M. J. and Sydenham, M. A., Biotechnology 9:64-68 (1991).) Another useful selection marker is the enzyme glutamine synthase (GS) (Murphy et al., Biochem J. 227:277-279 (1991); Bebbington et al., Bio/Technology 10:169-175 (1992). Using these markers, the mammalian cells are grown in selective medium and the cells with the highest resistance are selected. These cell lines contain the amplified gene(s) integrated into a chromosome. Chinese hamster ovary (CHO) and NSO cells are often used for the production of proteins.

Derivatives of the plasmid pSV2-dhfr (ATCC Accession No. 37146), the expression vectors pC4 (ATCC Accession No. 209646) and pC6 (ATCC Accession No.209647) contain the strong promoter (LTR) of the Rous Sarcoma Virus (Cullen et al., Molecular and Cellular Biology, 438-447 (March, 1985)) plus a fragment of the CMV-enhancer (Boshart et al., Cell 41:521-530 (1985).) Multiple cloning sites, e.g., with the restriction enzyme cleavage sites BamHI, XbaI and Asp718, facilitate the cloning of the gene of interest. The vectors also contain the 3' intron, the polyadenylation and termination signal of the rat preproinsulin gene, and the mouse DHFR gene under control of the SV40 early promoter.

Specifically, the plasmid pC6, for example, is digested with appropriate restriction enzymes and then dephosphorylated using calf intestinal phosphates by procedures known in the art. The vector is then isolated from a 1% agarose gel.

A polynucleotide of the present invention is amplified according to the protocol outlined in Example 1. If a naturally occurring signal sequence is used to produce the polypeptide of the present invention, the vector does not need a second signal peptide. Alternatively, if a naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

The amplified fragment is isolated from a 1% agarose gel using a commercially available kit ("Geneclean," BIO 101 Inc., La Jolla, Ca.). The fragment then is digested with appropriate restriction enzymes and again purified on a 1% agarose gel.

The amplified fragment is then digested with the same restriction enzyme and purified on a 1% agarose gel. The isolated fragment and the dephosphorylated vector are then ligated with T4 DNA ligase. *E. coli* HB101 or XL-1 Blue cells are then transformed and bacteria are identified that contain the fragment inserted into plasmid pC6 using, for instance, restriction enzyme analysis.

Chinese hamster ovary cells lacking an active DHFR gene is used for transfection. Five μg of the expression plasmid pC6 or pC4 is cotransfected with 0.5 μg of the plasmid pSVneo using lipofectin (Felgner et al., *supra*). The plasmid pSV2-neo contains a dominant selectable marker, the *neo* gene from Tn5 encoding an enzyme that confers resistance to a group of antibiotics including G418. The cells are seeded in alpha minus MEM supplemented with 1 mg/ml G418. After 2 days, the cells are trypsinized and seeded in hybridoma cloning plates (Greiner, Germany) in alpha minus MEM supplemented with 10, 25, or 50 ng/ml of metothrexate plus 1 mg/ml G418. After about 10-14 days single clones

are trypsinized and then seeded in 6-well petri dishes or 10 ml flasks using different concentrations of methotrexate (50 nM, 100 nM, 200 nM, 400 nM, 800 nM). Clones growing at the highest concentrations of methotrexate are then transferred to new 6-well plates containing even higher concentrations of methotrexate (1 μM, 2 μM, 5 μM, 10 mM, 20 mM). The same procedure is repeated until clones are obtained which grow at a concentration of 100 - 200 μM. Expression of the desired gene product is analyzed, for instance, by SDS-PAGE and Western blot or by reversed phase HPLC analysis.

Example 9: Protein Fusions

The polypeptides of the present invention are preferably fused to other proteins. These fusion proteins can be used for a variety of applications. For example, fusion of the present polypeptides to His-tag, HA-tag, protein A, IgG domains, and maltose binding protein facilitates purification. (See Example 5; see also EP A 394,827; Traunecker, et al., Nature 331:84-86 (1988).) Similarly, fusion to IgG-1, IgG-3, and albumin increases the halflife time in vivo. Nuclear localization signals fused to the polypeptides of the present invention can target the protein to a specific subcellular localization, while covalent heterodimer or homodimers can increase or decrease the activity of a fusion protein. Fusion proteins can also create chimeric molecules having more than one function. Finally, fusion proteins can increase solubility and/or stability of the fused protein compared to the non-fused protein. All of the types of fusion proteins described above can be made by modifying the following protocol, which outlines the fusion of a polypeptide to an IgG molecule, or the protocol described in Example 5.

Briefly, the human Fc portion of the IgG molecule can be PCR amplified, using primers that span the 5' and 3' ends of the sequence described below. These primers also should have convenient restriction enzyme sites that will facilitate cloning into an expression vector, preferably a mammalian expression vector.

For example, if pC4 (Accession No. 209646) is used, the human Fc portion can be ligated into the BamHI cloning site. Note that the 3' BamHI site should be destroyed. Next, the vector containing the human Fc portion is re-restricted with BamHI, linearizing the vector, and a polynucleotide of the present invention, isolated by the PCR protocol described in Example 1, is ligated into this BamHI site. Note that the polynucleotide is cloned without

a stop codon, otherwise a fusion protein will not be produced.

If the naturally occurring signal sequence is used to produce the polypeptide of the present invention, pC4 does not need a second signal peptide. Alternatively, if the naturally occurring signal sequence is not used, the vector can be modified to include a heterologous signal sequence. (See, e.g., WO 96/34891.)

Human IgG Fc region:
GGGATCCGGAGCCCAAATCTTCTGACAAAACTCACACATGCCCACCGTGCCCAG
CACCTGAATTCGAGGGTGCACCGTCAGTCTTCCTCTTCCCCCCAAAACCCAAGGA
CACCCTCATGATCTCCCGGACTCCTGAGGTCACATGCGTGGTGGTGGACGTAAGC
CACGAAGACCCTGAGGTCAAGTTCAACTGGTACGTGGACGGCGTGGAGGTGCAT
AATGCCAAGACAAAGCCGCGGGAGGAGCAGTACAACAGCACGTACCGTGTGGTC
AGCGTCCTCACCGTCCTGCACCAGGACTGGCTGAATGGCAAGGAGTACAAGTGC
AAGGTCTCCAACAAAGCCCTCCCAACCCCCATCGAGAAAACCATCTCCAAAGCC
AAAGGGCAGCCCCGAGAACCACAGGTGTACACCCTGCCCCCATCCCGGGATGAG
CTGACCAAGAACCAGGTCAGCCTGACCTGCCTGGTCAAAGGCTTCTATCCAAGC
GACATCGCCGTGGAGTGGGAGAGCAATGGGCAGCCGGAGAACAACTACAAGAC
CACGCCTCCCGTGCTGGACTCCGACGGCTCCTTCTTCCTCTACAGCAAGCTCACC
GTGGACAAGAGCAGGTGGCAGCAGGGGAACGTCTTCTCATGCTCCGTGATGCAT
GAGGCTCTGCACAACCACTACACGCAGAAGAGCCTCTCCCTGTCTCCGGGTAAAT
GAGTGCGACGGCCGCGACTCTAGAGGAT (SEQ ID NO:1685)

Example 10: Production of an Antibody from a Polypeptide

a) Hybridoma Technology

The antibodies of the present invention can be prepared by a variety of methods. (See, Current Protocols, Chapter 2.) As one example of such methods, cells expressing polypeptide of the present invention are administered to an animal to induce the production of sera containing polyclonal antibodies. In a preferred method, a preparation of polypeptide of the present invention is prepared and purified to render it substantially free of natural contaminants. Such a preparation is then introduced into an animal in order to produce polyclonal antisera of greater specific activity.

Monoclonal antibodies specific for polypeptide of the present invention are prepared using hybridoma technology. (Kohler et al., Nature 256:495 (1975); Kohler et al., Eur. J. Immunol. 6:511 (1976); Kohler et al., Eur. J. Immunol. 6:292 (1976); Hammerling et al., in: Monoclonal Antibodies and T-Cell Hybridomas, Elsevier, N.Y., pp. 563-681 (1981)). In general, an animal (preferably a mouse) is immunized with polypeptide of the present invention or, more preferably, with a secreted polypeptide of the present invention-expressing cell. Such polypeptide-expressing cells are cultured in any suitable tissue culture medium, preferably in Earle's modified Eagle's medium supplemented with 10% fetal bovine serum (inactivated at about 56°C), and supplemented with about 10 g/l of nonessential amino acids, about 1,000 U/ml of penicillin, and about 100 µg/ml of streptomycin.

The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the ATCC. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands et al. (Gastroenterology 80:225-232 (1981)). The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the polypeptide of the present invention.

Alternatively, additional antibodies capable of binding to polypeptide of the present invention can be produced in a two-step procedure using anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, protein specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the polypeptide of the present invention-specific antibody can be blocked by polypeptide of the present invention. Such antibodies comprise anti-idiotypic antibodies to the polypeptide of the present invention-specific antibody and are used to immunize an animal to induce formation of further polypeptide of the present invention-specific antibodies.

For in vivo use of antibodies in humans, an antibody is "humanized". Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric and humanized

antibodies are known in the art and are discussed herein. (See, for review, Morrison, Science 229:1202 (1985); Oi et al., BioTechniques 4:214 (1986); Cabilly et al., U.S. Patent No. 4,816,567; Taniguchi et al., EP 171496; Morrison et al., EP 173494; Neuberger et al., WO 8601533; Robinson et al., WO 8702671; Boulianne et al., Nature 312:643 (1984); Neuberger et al., Nature 314:268 (1985).)

b) Isolation Of Antibody Fragments Directed Against Polypeptide of the Present Invention From A Library Of scFvs

Naturally occurring V-genes isolated from human PBLs are constructed into a library of antibody fragments which contain reactivities against polypeptide of the present invention to which the donor may or may not have been exposed (see e.g., U.S. Patent 5,885,793 incorporated herein by reference in its entirety).

Rescue of the Library. A library of scFvs is constructed from the RNA of human PBLs as described in PCT publication WO 92/01047. To rescue phage displaying antibody fragments, approximately 109 E. coli harboring the phagemid are used to inoculate 50 ml of 2xTY containing 1% glucose and 100 μg/ml of ampicillin (2xTY-AMP-GLU) and grown to an O.D. of 0.8 with shaking. Five ml of this culture is used to innoculate 50 ml of 2xTY-AMP-GLU, 2 x 108 TU of delta gene 3 helper (M13 delta gene III, see PCT publication WO 92/01047) are added and the culture incubated at 37°C for 45 minutes without shaking and then at 37°C for 45 minutes with shaking. The culture is centrifuged at 4000 r.p.m. for 10 min. and the pellet resuspended in 2 liters of 2xTY containing 100 μg/ml ampicillin and 50 ug/ml kanamycin and grown overnight. Phage are prepared as described in PCT publication WO 92/01047.

M13 delta gene III is prepared as follows: M13 delta gene III helper phage does not encode gene III protein, hence the phage(mid) displaying antibody fragments have a greater avidity of binding to antigen. Infectious M13 delta gene III particles are made by growing the helper phage in cells harboring a pUC19 derivative supplying the wild type gene III protein during phage morphogenesis. The culture is incubated for 1 hour at 37° C without shaking and then for a further hour at 37°C with shaking. Cells are spun down (IEC-Centra 8,400 r.p.m. for 10 min), resuspended in 300 ml 2xTY broth containing 100 μg ampicillin/ml and 25 μg kanamycin/ml (2xTY-AMP-KAN) and grown overnight, shaking at 37°C. Phage particles are purified and concentrated from the culture medium by two PEG-precipitations

(Sambrook et al., 1990), resuspended in 2 ml PBS and passed through a 0.45 μm filter (Minisart NML; Sartorius) to give a final concentration of approximately 1013 transducing units/ml (ampicillin-resistant clones).

Panning of the Library. Immunotubes (Nunc) are coated overnight in PBS with 4 ml of either 100 μg/ml or 10 μg/ml of a polypeptide of the present invention. Tubes are blocked with 2% Marvel-PBS for 2 hours at 37°C and then washed 3 times in PBS. Approximately 1013 TU of phage is applied to the tube and incubated for 30 minutes at room temperature tumbling on an over and under turntable and then left to stand for another 1.5 hours. Tubes are washed 10 times with PBS 0.1% Tween-20 and 10 times with PBS. Phage are eluted by adding 1 ml of 100 mM triethylamine and rotating 15 minutes on an under and over turntable after which the solution is immediately neutralized with 0.5 ml of 1.0M Tris-HCl, pH 7.4. Phage are then used to infect 10 ml of mid-log E. coli TG1 by incubating eluted phage with bacteria for 30 minutes at 37°C. The E. coli are then plated on TYE plates containing 1% glucose and 100 μg/ml ampicillin. The resulting bacterial library is then rescued with delta gene 3 helper phage as described above to prepare phage for a subsequent round of selection. This process is then repeated for a total of 4 rounds of affinity purification with tube-washing increased to 20 times with PBS, 0.1% Tween-20 and 20 times with PBS for rounds 3 and 4.

Characterization of Binders. Eluted phage from the 3rd and 4th rounds of selection are used to infect E. coli HB 2151 and soluble scFv is produced (Marks, et al., 1991) from single colonies for assay. ELISAs are performed with microtitre plates coated with either 10 pg/ml of the polypeptide of the present invention in 50 mM bicarbonate pH 9.6. Clones positive in ELISA are further characterized by PCR fingerprinting (see, e.g., PCT publication WO 92/01047) and then by sequencing. These ELISA positive clones may also be further characterized by techniques known in the art, such as, for example, epitope mapping, binding affinity, receptor signal transduction, ability to block or competitively inhibit antibody/antigen binding, and competitive agonistic or antagonistic activity.

Example 11: Method of Determining Alterations in a Gene Corresponding to a Polynucleotide

RNA isolated from entire families or individual patients presenting with a phenotype of interest (such as a disease) is be isolated. cDNA is then generated from these RNA samples using protocols known in the art. (See, Sambrook.) The cDNA is then used as a template for PCR, employing primers surrounding regions of interest in SEQ ID NO:X; and/or the nucleotide sequence of the related cDNA in the cDNA clone contained in a deposited library. Suggested PCR conditions consist of 35 cycles at 95 degrees C for 30 seconds; 60-120 seconds at 52-58 degrees C; and 60-120 seconds at 70 degrees C, using buffer solutions described in Sidransky et al., Science 252:706 (1991).

PCR products are then sequenced using primers labeled at their 5' end with T4 polynucleotide kinase, employing SequiTherm Polymerase. (Epicentre Technologies). The intron-exon borders of selected exons is also determined and genomic PCR products analyzed to confirm the results. PCR products harboring suspected mutations is then cloned and sequenced to validate the results of the direct sequencing.

PCR products is cloned into T-tailed vectors as described in Holton et al., Nucleic Acids Research, 19:1156 (1991) and sequenced with T7 polymerase (United States Biochemical). Affected individuals are identified by mutations not present in unaffected individuals.

Genomic rearrangements are also observed as a method of determining alterations in a gene corresponding to a polynucleotide. Genomic clones isolated according to Example 2 are nick-translated with digoxigenindeoxy-uridine 5'-triphosphate (Boehringer Manheim), and FISH performed as described in Johnson et al., Methods Cell Biol. 35:73-99 (1991). Hybridization with the labeled probe is carried out using a vast excess of human cot-1 DNA for specific hybridization to the corresponding genomic locus.

Chromosomes are counterstained with 4,6-diamino-2-phenylidole and propidium iodide, producing a combination of C- and R-bands. Aligned images for precise mapping are obtained using a triple-band filter set (Chroma Technology, Brattleboro, VT) in combination with a cooled charge-coupled device camera (Photometrics, Tucson, AZ) and variable excitation wavelength filters. (Johnson et al., Genet. Anal. Tech. Appl., 8:75 (1991).) Image collection, analysis and chromosomal fractional length measurements are performed using the ISee Graphical Program System. (Inovision Corporation, Durham, NC.) Chromosome alterations of the genomic region hybridized by the probe are identified as insertions, deletions, and translocations. These alterations are used as a diagnostic marker for an

associated disease.

Example 12: Method of Detecting Abnormal Levels of a Polypeptide in a Biological Sample

A polypeptide of the present invention can be detected in a biological sample, and if an increased or decreased level of the polypeptide is detected, this polypeptide is a marker for a particular phenotype. Methods of detection are numerous, and thus, it is understood that one skilled in the art can modify the following assay to fit their particular needs.

For example, antibody-sandwich ELISAs are used to detect polypeptides in a sample, preferably a biological sample. Wells of a microtiter plate are coated with specific antibodies, at a final concentration of 0.2 to 10 ug/ml. The antibodies are either monoclonal or polyclonal and are produced by the method described in Example 10. The wells are blocked so that non-specific binding of the polypeptide to the well is reduced.

The coated wells are then incubated for > 2 hours at RT with a sample containing the polypeptide. Preferably, serial dilutions of the sample should be used to validate results. The plates are then washed three times with deionized or distilled water to remove unbounded polypeptide.

Next, 50 ul of specific antibody-alkaline phosphatase conjugate, at a concentration of 25-400 ng, is added and incubated for 2 hours at room temperature. The plates are again washed three times with deionized or distilled water to remove unbounded conjugate.

Add 75 ul of 4-methylumbelliferyl phosphate (MUP) or p-nitrophenyl phosphate (NPP) substrate solution to each well and incubate 1 hour at room temperature. Measure the reaction by a microtiter plate reader. Prepare a standard curve, using serial dilutions of a control sample, and plot polypeptide concentration on the X-axis (log scale) and fluorescence or absorbance of the Y-axis (linear scale). Interpolate the concentration of the polypeptide in the sample using the standard curve.

Example 13: Formulation

The invention also provides methods of treatment and/or prevention of diseases or disorders (such as, for example, any one or more of the diseases or disorders disclosed

herein) by administration to a subject of an effective amount of a Therapeutic. By therapeutic is meant a polynucleotides or polypeptides of the invention (including fragments and variants), agonists or antagonists thereof, and/or antibodies thereto, in combination with a pharmaceutically acceptable carrier type (e.g., a sterile carrier).

The Therapeutic will be formulated and dosed in a fashion consistent with good medical practice, taking into account the clinical condition of the individual patient (especially the side effects of treatment with the Therapeutic alone), the site of delivery, the method of administration, the scheduling of administration, and other factors known to practitioners. The "effective amount" for purposes herein is thus determined by such considerations.

As a general proposition, the total pharmaceutically effective amount of the Therapeutic administered parenterally per dose will be in the range of about 1ug/kg/day to 10 mg/kg/day of patient body weight, although, as noted above, this will be subject to therapeutic discretion. More preferably, this dose is at least 0.01 mg/kg/day, and most preferably for humans between about 0.01 and 1 mg/kg/day for the hormone. If given continuously, the Therapeutic is typically administered at a dose rate of about 1 ug/kg/hour to about 50 ug/kg/hour, either by 1-4 injections per day or by continuous subcutaneous infusions, for example, using a mini-pump. An intravenous bag solution may also be employed. The length of treatment needed to observe changes and the interval following treatment for responses to occur appears to vary depending on the desired effect.

Therapeutics can be are administered orally, rectally, parenterally, intracistemally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), bucally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler, diluent, encapsulating material or formulation auxiliary of any. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics are administered orally, rectally, parenterally, intracistemally, intravaginally, intraperitoneally, topically (as by powders, ointments, gels, drops or transdermal patch), bucally, or as an oral or nasal spray. "Pharmaceutically acceptable carrier" refers to a non-toxic solid, semisolid or liquid filler,

diluent, encapsulating material or formulation auxiliary of any type. The term "parenteral" as used herein refers to modes of administration which include intravenous, intramuscular, intraperitoneal, intrasternal, subcutaneous and intraarticular injection and infusion.

Therapeutics of the invention are also suitably administered by sustained-release systems. Suitable examples of sustained-release Therapeutics include suitable polymeric materials (such as, for example, semi-permeable polymer matrices in the form of shaped articles, e.g., films, or mirocapsules), suitable hydrophobic materials (for example as an emulsion in an acceptable oil) or ion exchange resins, and sparingly soluble derivatives (such as, for example, a sparingly soluble salt).

Sustained-release matrices include polylactides (U.S. Pat. No. 3,773,919, EP 58,481), copolymers of L-glutamic acid and gamma-ethyl-L-glutamate (Sidman et al., Biopolymers 22:547-556 (1983)), poly (2- hydroxyethyl methacrylate) (Langer et al., J. Biomed. Mater. Res. 15:167-277 (1981), and Langer, Chem. Tech. 12:98-105 (1982)), ethylene vinyl acetate (Langer et al., Id.) or poly-D- (-)-3-hydroxybutyric acid (EP 133,988).

Sustained-release Therapeutics also include liposomally entrapped Therapeutics of the invention (*see* generally, Langer, *Science* 249:1527-1533 (1990); Treat et al., in *Liposomes in the Therapy of Infectious Disease and Cancer*, Lopez-Berestein and Fidler (eds.), Liss, New York, pp. 317 -327 and 353-365 (1989)). Liposomes containing the Therapeutic are prepared by methods known per se: DE 3,218,121; Epstein et al., Proc. Natl. Acad. Sci. (USA) 82:3688-3692 (1985); Hwang et al., Proc. Natl. Acad. Sci.(USA) 77:4030-4034 (1980); EP 52,322; EP 36,676; EP 88,046; EP 143,949; EP 142,641; Japanese Pat. Appl. 83-118008; U.S. Pat. Nos. 4,485,045 and 4,544,545; and EP 102,324. Ordinarily, the liposomes are of the small (about 200-800 Angstroms) unilamellar type in which the lipid content is greater than about 30 mol. percent cholesterol, the selected proportion being adjusted for the optimal Therapeutic.

In yet an additional embodiment, the Therapeutics of the invention are delivered by way of a pump (*see* Langer, *supra*; Sefton, CRC Crit. Ref. Biomed. Eng. 14:201 (1987); Buchwald et al., Surgery 88:507 (1980); Saudek et al., N. Engl. J. Med. 321:574 (1989)).

Other controlled release systems are discussed in the review by Langer (*Science* 249:1527-1533 (1990)).

For parenteral administration, in one embodiment, the Therapeutic is formulated generally by mixing it at the desired degree of purity, in a unit dosage injectable form

(solution, suspension, or emulsion), with a pharmaceutically acceptable carrier, i.e., one that is non-toxic to recipients at the dosages and concentrations employed and is compatible with other ingredients of the formulation. For example, the formulation preferably does not include oxidizing agents and other compounds that are known to be deleterious to the Therapeutic.

Generally, the formulations are prepared by contacting the Therapeutic uniformly and intimately with liquid carriers or finely divided solid carriers or both. Then, if necessary, the product is shaped into the desired formulation. Preferably the carrier is a parenteral carrier, more preferably a solution that is isotonic with the blood of the recipient. Examples of such carrier vehicles include water, saline, Ringer's solution, and dextrose solution. Non-aqueous vehicles such as fixed oils and ethyl oleate are also useful herein, as well as liposomes.

The carrier suitably contains minor amounts of additives such as substances that enhance isotonicity and chemical stability. Such materials are non-toxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate, succinate, acetic acid, and other organic acids or their salts; antioxidants such as ascorbic acid; low molecular weight (less than about ten residues) polypeptides, e.g., polyarginine or tripeptides; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids, such as glycine, glutamic acid, aspartic acid, or arginine; monosaccharides, disaccharides, and other carbohydrates including cellulose or its derivatives, glucose, manose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; counterions such as sodium; and/or nonionic surfactants such as polysorbates, poloxamers, or PEG.

The Therapeutic is typically formulated in such vehicles at a concentration of about 0.1 mg/ml to 100 mg/ml, preferably 1-10 mg/ml, at a pH of about 3 to 8. It will be understood that the use of certain of the foregoing excipients, carriers, or stabilizers will result in the formation of polypeptide salts.

Any pharmaceutical used for therapeutic administration can be sterile. Sterility is readily accomplished by filtration through sterile filtration membranes (e.g., 0.2 micron membranes). Therapeutics generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

Therapeutics ordinarily will be stored in unit or multi-dose containers, for example,

sealed ampoules or vials, as an aqueous solution or as a lyophilized formulation for reconstitution. As an example of a lyophilized formulation, 10-ml vials are filled with 5 ml of sterile-filtered 1% (w/v) aqueous Therapeutic solution, and the resulting mixture is lyophilized. The infusion solution is prepared by reconstituting the lyophilized Therapeutic using bacteriostatic Water-for-Injection.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the Therapeutics of the invention. Associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use or sale for human administration. In addition, the Therapeutics may be employed in conjunction with other therapeutic compounds.

The Therapeutics of the invention may be administered alone or in combination with adjuvants. Adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, alum, alum plus deoxycholate (ImmunoAg), MTP-PE (Biocine Corp.), QS21 (Genentech, Inc.), BCG, and MPL. In a specific embodiment, Therapeutics of the invention are administered in combination with alum. In another specific embodiment, Therapeutics of the invention are administered in combination with QS-21. Further adjuvants that may be administered with the Therapeutics of the invention include, but are not limited to, Monophosphoryl lipid immunomodulator, AdjuVax 100a, QS-21, QS-18, CRL1005, Aluminum salts, MF-59, and Virosomal adjuvant technology. Vaccines that may be administered with the Therapeutics of the invention include, but are not limited to, vaccines directed toward protection against MMR (measles, mumps, rubella), polio, varicella, tetanus/diptheria, hepatitis A, hepatitis B, haemophilus influenzae B, whooping cough, pneumonia, influenza, Lyme's Disease, rotavirus, cholera, yellow fever, Japanese encephalitis, poliomyelitis, rabies, typhoid fever, and pertussis. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

The Therapeutics of the invention may be administered alone or in combination with other therapeutic agents. Therapeutic agents that may be administered in combination with the Therapeutics of the invention, include but not limited to, other members of the TNF family, chemotherapeutic agents, antibiotics, steroidal and non-steroidal anti-inflammatories, conventional immunotherapeutic agents, cytokines and/or growth factors. Combinations may be administered either concomitantly, e.g., as an admixture, separately but simultaneously or concurrently; or sequentially. This includes presentations in which the combined agents are administered together as a therapeutic mixture, and also procedures in which the combined agents are administered separately but simultaneously, e.g., as through separate intravenous lines into the same individual. Administration "in combination" further includes the separate administration of one of the compounds or agents given first, followed by the second.

In one embodiment, the Therapeutics of the invention are administered in combination with members of the TNF family. TNF, TNF-related or TNF-like molecules that may be administered with the Therapeutics of the invention include, but are not limited to, soluble forms of TNF-alpha, lymphotoxin-alpha (LT-alpha, also known as TNF-beta), LT-beta (found in complex heterotrimer LT-alpha2-beta), OPGL, FasL, CD27L, CD30L, CD40L, 4-1BBL, DcR3, OX40L, TNF-gamma (International Publication No. WO 96/14328), AIM-I (International Publication No. WO 97/33899), endokine-alpha (International Publication No. WO 98/07880), TR6 (International Publication No. WO 98/30694), OPG, and neutrokine-alpha (International Publication No. WO 98/18921, OX40, and nerve growth factor (NGF), and soluble forms of Fas, CD30, CD27, CD40 and 4-IBB, TR2 (International Publication No. WO 96/34095), DR3 (International Publication No. WO 97/33904), DR4 (International Publication No. WO 98/32856), TR5 (International Publication No. WO 98/30693), TR6 (International Publication No. WO 98/30694), TR7 (International Publication No. WO 98/41629), TRANK, TR9 (International Publication No. WO 98/56892),TR10 (International Publication No. WO 98/54202), 312C2 (International Publication No. WO 98/06842), and TR12, and soluble forms CD154, CD70, and CD153.

In certain embodiments, Therapeutics of the invention are administered in combination with antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors. Nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, RETROVIR™ (zidovudine/AZT), VIDEX™

(didanosine/ddI), HIVID™ (zalcitabine/ddC), ZERIT™ (stavudine/d4T), EPIVIR™ (lamivudine/3TC), and COMBIVIR™ (zidovudine/lamivudine). Non-nucleoside reverse transcriptase inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, VIRAMUNE™ (nevirapine), RESCRIPTOR™ (delavirdine), and SUSTIVA™ (efavirenz). Protease inhibitors that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, CRIXIVAN™ (indinavir), NORVIR™ (ritonavir), INVIRASE™ (saquinavir), and VIRACEPT™ (nelfinavir). In a specific embodiment, antiretroviral agents, nucleoside reverse transcriptase inhibitors, non-nucleoside reverse transcriptase inhibitors, and/or protease inhibitors may be used in any combination with Therapeutics of the invention to treat AIDS and/or to prevent or treat HIV infection.

In other embodiments, Therapeutics of the invention may be administered in combination with anti-opportunistic infection agents. Anti-opportunistic agents that may be administered in combination with the Therapeutics of the invention, include, but are not limited to, TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, ATOVAQUONE™, ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, ETHAMBUTOL™, RIFABUTIN™, CLARITHROMYCIN™, AZITHROMYCIN™, GANCICLOVIR™, FOSCARNET™, CIDOFOVIR™, FLUCONAZOLE™, ITRACONAZOLE™, KETOCONAZOLE™, ACYCLOVIR™, FAMCICOLVIR™, PYRIMETHAMINE™, LEUCOVORIN™, NEUPOGEN™ (filgrastim/G-CSF), and LEUKINE™ (sargramostim/GM-CSF). In a specific embodiment, Therapeutics of the invention are used in any combination with TRIMETHOPRIM-SULFAMETHOXAZOLE™, DAPSONE™, PENTAMIDINE™, and/or ATOVAQUONE™ to prophylactically treat or prevent an opportunistic *Pneumocystis carinii* pneumonia infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ISONIAZID™, RIFAMPIN™, PYRAZINAMIDE™, and/or ETHAMBUTOL™ to prophylactically treat or prevent an opportunistic *Mycobacterium avium* complex infection. In another specific embodiment, Therapeutics of the invention are used in any combination with RIFABUTIN™, CLARITHROMYCIN™, and/or AZITHROMYCIN™ to prophylactically treat or prevent an opportunistic *Mycobacterium tuberculosis* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with GANCICLOVIR™,

FOSCARNET™, and/or CIDOFOVIR™ to prophylactically treat or prevent an opportunistic cytomegalovirus infection. In another specific embodiment, Therapeutics of the invention are used in any combination with FLUCONAZOLE™, ITRACONAZOLE™, and/or KETOCONAZOLE™ to prophylactically treat or prevent an opportunistic fungal infection. In another specific embodiment, Therapeutics of the invention are used in any combination with ACYCLOVIR™ and/or FAMCICOLVIR™ to prophylactically treat or prevent an opportunistic herpes simplex virus type I and/or type II infection. In another specific embodiment, Therapeutics of the invention are used in any combination with PYRIMETHAMINE™ and/or LEUCOVORIN™ to prophylactically treat or prevent an opportunistic *Toxoplasma gondii* infection. In another specific embodiment, Therapeutics of the invention are used in any combination with LEUCOVORIN™ and/or NEUPOGEN™ to prophylactically treat or prevent an opportunistic bacterial infection.

In a further embodiment, the Therapeutics of the invention are administered in combination with an antiviral agent. Antiviral agents that may be administered with the Therapeutics of the invention include, but are not limited to, acyclovir, ribavirin, amantadine, and remantidine.

In a further embodiment, the Therapeutics of the invention are administered in combination with an antibiotic agent. Antibiotic agents that may be administered with the Therapeutics of the invention include, but are not limited to, amoxicillin, beta-lactamases, aminoglycosides, beta-lactam (glycopeptide), beta-lactamases, Clindamycin, chloramphenicol, cephalosporins, ciprofloxacin, ciprofloxacin, erythromycin, fluoroquinolones, macrolides, metronidazole, penicillins, quinolones, rifampin, streptomycin, sulfonamide, tetracyclines, trimethoprim, trimethoprim-sulfamthoxazole, and vancomycin.

Conventional nonspecific immunosuppressive agents, that may be administered in combination with the Therapeutics of the invention include, but are not limited to, steroids, cyclosporine, cyclosporine analogs, cyclophosphamide methylprednisone, prednisone, azathioprine, FK-506, 15-deoxyspergualin, and other immunosuppressive agents that act by suppressing the function of responding T cells.

In specific embodiments, Therapeutics of the invention are administered in combination with immunosuppressants. Immunosuppressants preparations that may be administered with the Therapeutics of the invention include, but are not limited to, ORTHOCLONE™ (OKT3), SANDIMMUNE™/NEORAL™/SANGDYA™ (cyclosporin),

PROGRAF™ (tacrolimus), CELLCEPT™ (mycophenolate), Azathioprine, glucorticosteroids, and RAPAMUNE™ (sirolimus). In a specific embodiment, immunosuppressants may be used to prevent rejection of organ or bone marrow transplantation.

In an additional embodiment, Therapeutics of the invention are administered alone or in combination with one or more intravenous immune globulin preparations. Intravenous immune globulin preparations that may be administered with the Therapeutics of the invention include, but not limited to, GAMMAR™, IVEEGAM™, SANDOGLOBULIN™, GAMMAGARD S/D™, and GAMIMUNE™. In a specific embodiment, Therapeutics of the invention are administered in combination with intravenous immune globulin preparations in transplantation therapy (e.g., bone marrow transplant).

In an additional embodiment, the Therapeutics of the invention are administered alone or in combination with an anti-inflammatory agent. Anti-inflammatory agents that may be administered with the Therapeutics of the invention include, but are not limited to, glucocorticoids and the nonsteroidal anti-inflammatories, aminoarylcarboxylic acid derivatives, arylacetic acid derivatives, arylbutyric acid derivatives, arylcarboxylic acids, arylpropionic acid derivatives, pyrazoles, pyrazolones, salicylic acid derivatives, thiazinecarboxamides, e-acetamidocaproic acid, S-adenosylmethionine, 3-amino-4-hydroxybutyric acid, amixetrine, bendazac, benzydamine, bucolome, difenpiramide, ditazol, emorfazone, guaiazulene, nabumetone, nimesulide, orgotein, oxaceprol, paranyline, perisoxal, pifoxime, proquazone, proxazole, and tenidap.

In another embodiment, compostions of the invention are administered in combination with a chemotherapeutic agent. Chemotherapeutic agents that may be administered with the Therapeutics of the invention include, but are not limited to, antibiotic derivatives (e.g., doxorubicin, bleomycin, daunorubicin, and dactinomycin); antiestrogens (e.g., tamoxifen); antimetabolites (e.g., fluorouracil, 5-FU, methotrexate, floxuridine, interferon alpha-2b, glutamic acid, plicamycin, mercaptopurine, and 6-thioguanine); cytotoxic agents (e.g., carmustine, BCNU, lomustine, CCNU, cytosine arabinoside, cyclophosphamide, estramustine, hydroxyurea, procarbazine, mitomycin, busulfan, cis-platin, and vincristine sulfate); hormones (e.g., medroxyprogesterone, estramustine phosphate sodium, ethinyl estradiol, estradiol, megestrol acetate, methyltestosterone, diethylstilbestrol diphosphate, chlorotrianisene, and testolactone); nitrogen mustard derivatives (e.g., mephalen, chorambucil, mechlorethamine (nitrogen mustard) and thiotepa); steroids and

combinations (e.g., bethamethasone sodium phosphate); and others (e.g., dicarbazine, asparaginase, mitotane, vincristine sulfate, vinblastine sulfate, and etoposide).

In a specific embodiment, Therapeutics of the invention are administered in combination with CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone) or any combination of the components of CHOP. In another embodiment, Therapeutics of the invention are administered in combination with Rituximab. In a further embodiment, Therapeutics of the invention are administered with Rituxmab and CHOP, or Rituxmab and any combination of the components of CHOP.

In an additional embodiment, the Therapeutics of the invention are administered in combination with cytokines. Cytokines that may be administered with the Therapeutics of the invention include, but are not limited to, IL2, IL3, IL4, IL5, IL6, IL7, IL10, IL12, IL13, IL15, anti-CD40, CD40L, IFN-gamma and TNF-alpha. In another embodiment, Therapeutics of the invention may be administered with any interleukin, including, but not limited to, IL-1alpha, IL-1beta, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IL-16, IL-17, IL-18, IL-19, IL-20, and IL-21.

In an additional embodiment, the Therapeutics of the invention are administered in combination with angiogenic proteins. Angiogenic proteins that may be administered with the Therapeutics of the invention include, but are not limited to, Glioma Derived Growth Factor (GDGF), as disclosed in European Patent Number EP-399816; Platelet Derived Growth Factor-A (PDGF-A), as disclosed in European Patent Number EP-682110; Platelet Derived Growth Factor-B (PDGF-B), as disclosed in European Patent Number EP-282317; Placental Growth Factor (PIGF), as disclosed in International Publication Number WO 92/06194; Placental Growth Factor-2 (PIGF-2), as disclosed in Hauser et al., Gorwth Factors, 4:259-268 (1993); Vascular Endothelial Growth Factor (VEGF), as disclosed in International Publication Number WO 90/13649; Vascular Endothelial Growth Factor-A (VEGF-A), as disclosed in European Patent Number EP-506477; Vascular Endothelial Growth Factor-2 (VEGF-2), as disclosed in International Publication Number WO 96/39515; Vascular Endothelial Growth Factor B (VEGF-3); Vascular Endothelial Growth Factor B-186 (VEGF-B186), as disclosed in International Publication Number WO 96/26736; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/02543; Vascular Endothelial Growth Factor-D (VEGF-D), as disclosed in International Publication Number WO 98/07832; and Vascular Endothelial Growth Factor-E (VEGF-E), as

disclosed in German Patent Number DE19639601. The above mentioned references are incorporated herein by reference herein.

In an additional embodiment, the Therapeutics of the invention are administered in combination with hematopoietic growth factors. Hematopoietic growth factors that may be administered with the Therapeutics of the invention include, but are not limited to, LEUKINE™ (SARGRAMOSTIM™) and NEUPOGEN™ (FILGRASTIM™).

In an additional embodiment, the Therapeutics of the invention are administered in combination with Fibroblast Growth Factors. Fibroblast Growth Factors that may be administered with the Therapeutics of the invention include, but are not limited to, FGF-1, FGF-2, FGF-3, FGF-4, FGF-5, FGF-6, FGF-7, FGF-8, FGF-9, FGF-10, FGF-11, FGF-12, FGF-13, FGF-14, and FGF-15.

In additional embodiments, the Therapeutics of the invention are administered in combination with other therapeutic or prophylactic regimens, such as, for example, radiation therapy.

Example 14: Method of Treating Decreased Levels of the Polypeptide

The present invention relates to a method for treating an individual in need of an increased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an agonist of the invention (including polypeptides of the invention). Moreover, it will be appreciated that conditions caused by a decrease in the standard or normal expression level of a polypeptide of the present invention in an individual can be treated by administering the agonist or antagonist of the present invention. Thus, the invention also provides a method of treatment of an individual in need of an increased level of the polypeptide comprising administering to such an individual a Therapeutic comprising an amount of the agonist or antagonist to increase the activity level of the polypeptide in such an individual.

For example, a patient with decreased levels of a polypeptide receives a daily dose 0.1-100 ug/kg of the agonist or antagonist for six consecutive days. The exact details of the dosing scheme, based on administration and formulation, are provided in Example 13.

Example 15: Method of Treating Increased Levels of the Polypeptide

The present invention also relates to a method of treating an individual in need of a decreased level of a polypeptide of the invention in the body comprising administering to such an individual a composition comprising a therapeutically effective amount of an antagonist of the invention (including polypeptides and antibodies of the invention).

In one example, antisense technology is used to inhibit production of a polypeptide of the present invention. This technology is one example of a method of decreasing levels of a polypeptide, due to a variety of etiologies, such as cancer.

For example, a patient diagnosed with abnormally increased levels of a polypeptide is administered intravenously antisense polynucleotides at 0.5, 1.0, 1.5, 2.0 and 3.0 mg/kg day for 21 days. This treatment is repeated after a 7-day rest period if the treatment was well tolerated. The formulation of the antisense polynucleotide is provided in Example 13.

Example 16: Method of Treatment Using Gene Therapy-Ex Vivo

One method of gene therapy transplants fibroblasts, which are capable of expressing a polypeptide, onto a patient. Generally, fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in tissue-culture medium and separated into small pieces. Small chunks of the tissue are placed on a wet surface of a tissue culture flask, approximately ten pieces are placed in each flask. The flask is turned upside down, closed tight and left at room temperature over night. After 24 hours at room temperature, the flask is inverted and the chunks of tissue remain fixed to the bottom of the flask and fresh media (e.g., Ham's F12 media, with 10% FBS, penicillin and streptomycin) is added. The flasks are then incubated at 37 degree C for approximately one week.

At this time, fresh media is added and subsequently changed every several days. After an additional two weeks in culture, a monolayer of fibroblasts emerge. The monolayer is trypsinized and scaled into larger flasks.

pMV-7 (Kirschmeier, P.T. et al., DNA, 7:219-25 (1988)), flanked by the long terminal repeats of the Moloney murine sarcoma virus, is digested with EcoRI and HindIII and subsequently treated with calf intestinal phosphatase. The linear vector is fractionated on agarose gel and purified, using glass beads.

The cDNA encoding a polypeptide of the present invention can be amplified using

PCR primers which correspond to the 5' and 3' end sequences respectively as set forth in Example 1 using primers and having appropriate restriction sites and initiation/stop codons, if necessary. Preferably, the 5' primer contains an EcoRI site and the 3' primer includes a HindIII site. Equal quantities of the Moloney murine sarcoma virus linear backbone and the amplified EcoRI and HindIII fragment are added together, in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The ligation mixture is then used to transform bacteria HB101, which are then plated onto agar containing kanamycin for the purpose of confirming that the vector has the gene of interest properly inserted.

The amphotropic pA317 or GP+am12 packaging cells are grown in tissue culture to confluent density in Dulbecco's Modified Eagles Medium (DMEM) with 10% calf serum (CS), penicillin and streptomycin. The MSV vector containing the gene is then added to the media and the packaging cells transduced with the vector. The packaging cells now produce infectious viral particles containing the gene (the packaging cells are now referred to as producer cells).

Fresh media is added to the transduced producer cells, and subsequently, the media is harvested from a 10 cm plate of confluent producer cells. The spent media, containing the infectious viral particles, is filtered through a millipore filter to remove detached producer cells and this media is then used to infect fibroblast cells. Media is removed from a sub-confluent plate of fibroblasts and quickly replaced with the media from the producer cells. This media is removed and replaced with fresh media. If the titer of virus is high, then virtually all fibroblasts will be infected and no selection is required. If the titer is very low, then it is necessary to use a retroviral vector that has a selectable marker, such as neo or his. Once the fibroblasts have been efficiently infected, the fibroblasts are analyzed to determine whether protein is produced.

The engineered fibroblasts are then transplanted onto the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads.

Example 17: Gene Therapy Using Endogenous Genes Corresponding To Polynucleotides of the Invention

Another method of gene therapy according to the present invention involves operably

associating the endogenous polynucleotide sequence of the invention with a promoter via homologous recombination as described, for example, in U.S. Patent NO: 5,641,670, issued June 24, 1997; International Publication NO: WO 96/29411, published September 26, 1996; International Publication NO: WO 94/12650, published August 4, 1994; Koller et al., *Proc. Natl. Acad. Sci. USA*, 86:8932-8935 (1989); and Zijlstra et al., *Nature*, 342:435-438 (1989). This method involves the activation of a gene which is present in the target cells, but which is not expressed in the cells, or is expressed at a lower level than desired.

Polynucleotide constructs are made which contain a promoter and targeting sequences, which are homologous to the 5' non-coding sequence of endogenous polynucleotide sequence, flanking the promoter. The targeting sequence will be sufficiently near the 5' end of the polynucleotide sequence so the promoter will be operably linked to the endogenous sequence upon homologous recombination. The promoter and the targeting sequences can be amplified using PCR. Preferably, the amplified promoter contains distinct restriction enzyme sites on the 5' and 3' ends. Preferably, the 3' end of the first targeting sequence contains the same restriction enzyme site as the 5' end of the amplified promoter and the 5' end of the second targeting sequence contains the same restriction site as the 3' end of the amplified promoter.

The amplified promoter and the amplified targeting sequences are digested with the appropriate restriction enzymes and subsequently treated with calf intestinal phosphatase. The digested promoter and digested targeting sequences are added together in the presence of T4 DNA ligase. The resulting mixture is maintained under conditions appropriate for ligation of the two fragments. The construct is size fractionated on an agarose gel then purified by phenol extraction and ethanol precipitation.

In this Example, the polynucleotide constructs are administered as naked polynucleotides via electroporation. However, the polynucleotide constructs may also be administered with transfection-facilitating agents, such as liposomes, viral sequences, viral particles, precipitating agents, etc. Such methods of delivery are known in the art.

Once the cells are transfected, homologous recombination will take place which results in the promoter being operably linked to the endogenous polynucleotide sequence. This results in the expression of polynucleotide corresponding to the polynucleotide in the cell. Expression may be detected by immunological staining, or any other method known in the art.

Fibroblasts are obtained from a subject by skin biopsy. The resulting tissue is placed in DMEM + 10% fetal calf serum. Exponentially growing or early stationary phase fibroblasts are trypsinized and rinsed from the plastic surface with nutrient medium. An aliquot of the cell suspension is removed for counting, and the remaining cells are subjected to centrifugation. The supernatant is aspirated and the pellet is resuspended in 5 ml of electroporation buffer (20 mM HEPES pH 7.3, 137 mM NaCl, 5 mM KCl, 0.7 mM Na_2 HPO_4, 6 mM dextrose). The cells are recentrifuged, the supernatant aspirated, and the cells resuspended in electroporation buffer containing 1 mg/ml acetylated bovine serum albumin. The final cell suspension contains approximately $3X10^6$ cells/ml. Electroporation should be performed immediately following resuspension.

Plasmid DNA is prepared according to standard techniques. For example, to construct a plasmid for targeting to the locus corresponding to the polynucleotide of the invention, plasmid pUC18 (MBI Fermentas, Amherst, NY) is digested with HindIII. The CMV promoter is amplified by PCR with an XbaI site on the 5' end and a BamHI site on the 3'end. Two non-coding sequences are amplified via PCR: one non-coding sequence (fragment 1) is amplified with a HindIII site at the 5' end and an Xba site at the 3'end; the other non-coding sequence (fragment 2) is amplified with a BamHI site at the 5'end and a HindIII site at the 3'end. The CMV promoter and the fragments (1 and 2) are digested with the appropriate enzymes (CMV promoter - XbaI and BamHI; fragment 1 - XbaI; fragment 2 - BamHI) and ligated together. The resulting ligation product is digested with HindIII, and ligated with the HindIII-digested pUC18 plasmid.

Plasmid DNA is added to a sterile cuvette with a 0.4 cm electrode gap (Bio-Rad). The final DNA concentration is generally at least 120 µg/ml. 0.5 ml of the cell suspension (containing approximately $1.5.X10^6$ cells) is then added to the cuvette, and the cell suspension and DNA solutions are gently mixed. Electroporation is performed with a Gene-Pulser apparatus (Bio-Rad). Capacitance and voltage are set at 960 µF and 250-300 V, respectively. As voltage increases, cell survival decreases, but the percentage of surviving cells that stably incorporate the introduced DNA into their genome increases dramatically. Given these parameters, a pulse time of approximately 14-20 mSec should be observed.

Electroporated cells are maintained at room temperature for approximately 5 min, and the contents of the cuvette are then gently removed with a sterile transfer pipette. The cells are added directly to 10 ml of prewarmed nutrient media (DMEM with 15% calf serum) in a

10 cm dish and incubated at 37 degree C. The following day, the media is aspirated and replaced with 10 ml of fresh media and incubated for a further 16-24 hours.

The engineered fibroblasts are then injected into the host, either alone or after having been grown to confluence on cytodex 3 microcarrier beads. The fibroblasts now produce the protein product. The fibroblasts can then be introduced into a patient as described above.

Example 18: Method of Treatment Using Gene Therapy - In Vivo

Another aspect of the present invention is using *in vivo* gene therapy methods to treat disorders, diseases and conditions. The gene therapy method relates to the introduction of naked nucleic acid (DNA, RNA, and antisense DNA or RNA) sequences into an animal to increase or decrease the expression of the polypeptide. The polynucleotide of the present invention may be operatively linked to a promoter or any other genetic elements necessary for the expression of the polypeptide by the target tissue. Such gene therapy and delivery techniques and methods are known in the art, see, for example, WO90/11092, WO98/11779; U.S. Patent NO. 5693622, 5705151, 5580859; Tabata et al., Cardiovasc. Res. 35(3):470-479 (1997); Chao et al., Pharmacol. Res. 35(6):517-522 (1997); Wolff, Neuromuscul. Disord. 7(5):314-318 (1997); Schwartz et al., Gene Ther. 3(5):405-411 (1996); Tsurumi et al., Circulation 94(12):3281-3290 (1996) (incorporated herein by reference).

The polynucleotide constructs may be delivered by any method that delivers injectable materials to the cells of an animal, such as, injection into the interstitial space of tissues (heart, muscle, skin, lung, liver, intestine and the like). The polynucleotide constructs can be delivered in a pharmaceutically acceptable liquid or aqueous carrier.

The term "naked" polynucleotide, DNA or RNA, refers to sequences that are free from any delivery vehicle that acts to assist, promote, or facilitate entry into the cell, including viral sequences, viral particles, liposome formulations, lipofectin or precipitating agents and the like. However, the polynucleotides of the present invention may also be delivered in liposome formulations (such as those taught in Felgner P.L. et al. (1995) Ann. NY Acad. Sci. 772:126-139 and Abdallah B. et al. (1995) Biol. Cell 85(1):1-7) which can be prepared by methods well known to those skilled in the art.

The polynucleotide vector constructs used in the gene therapy method are preferably constructs that will not integrate into the host genome nor will they contain sequences that

allow for replication. Any strong promoter known to those skilled in the art can be used for driving the expression of DNA. Unlike other gene therapies techniques, one major advantage of introducing naked nucleic acid sequences into target cells is the transitory nature of the polynucleotide synthesis in the cells. Studies have shown that non-replicating DNA sequences can be introduced into cells to provide production of the desired polypeptide for periods of up to six months.

The polynucleotide construct can be delivered to the interstitial space of tissues within the an animal, including of muscle, skin, brain, lung, liver, spleen, bone marrow, thymus, heart, lymph, blood, bone, cartilage, pancreas, kidney, gall bladder, stomach, intestine, testis, ovary, uterus, rectum, nervous system, eye, gland, and connective tissue. Interstitial space of the tissues comprises the intercellular fluid, mucopolysaccharide matrix among the reticular fibers of organ tissues, elastic fibers in the walls of vessels or chambers, collagen fibers of fibrous tissues, or that same matrix within connective tissue ensheathing muscle cells or in the lacunae of bone. It is similarly the space occupied by the plasma of the circulation and the lymph fluid of the lymphatic channels. Delivery to the interstitial space of muscle tissue is preferred for the reasons discussed below. They may be conveniently delivered by injection into the tissues comprising these cells. They are preferably delivered to and expressed in persistent, non-dividing cells which are differentiated, although delivery and expression may be achieved in non-differentiated or less completely differentiated cells, such as, for example, stem cells of blood or skin fibroblasts. *In vivo* muscle cells are particularly competent in their ability to take up and express polynucleotides.

For the naked polynucleotide injection, an effective dosage amount of DNA or RNA will be in the range of from about 0.05 g/kg body weight to about 50 mg/kg body weight. Preferably the dosage will be from about 0.005 mg/kg to about 20 mg/kg and more preferably from about 0.05 mg/kg to about 5 mg/kg. Of course, as the artisan of ordinary skill will appreciate, this dosage will vary according to the tissue site of injection. The appropriate and effective dosage of nucleic acid sequence can readily be determined by those of ordinary skill in the art and may depend on the condition being treated and the route of administration. The preferred route of administration is by the parenteral route of injection into the interstitial space of tissues. However, other parenteral routes may also be used, such as, inhalation of an aerosol formulation particularly for delivery to lungs or bronchial tissues, throat or mucous membranes of the nose. In addition, naked polynucleotide constructs can be delivered to

arteries during angioplasty by the catheter used in the procedure.

The dose response effects of injected polynucleotide in muscle *in vivo* is determined as follows. Suitable template DNA for production of mRNA coding for polypeptide of the present invention is prepared in accordance with a standard recombinant DNA methodology. The template DNA, which may be either circular or linear, is either used as naked DNA or complexed with liposomes. The quadriceps muscles of mice are then injected with various amounts of the template DNA.

Five to six week old female and male Balb/C mice are anesthetized by intraperitoneal injection with 0.3 ml of 2.5% Avertin. A 1.5 cm incision is made on the anterior thigh, and the quadriceps muscle is directly visualized. The template DNA is injected in 0.1 ml of carrier in a 1 cc syringe through a 27 gauge needle over one minute, approximately 0.5 cm from the distal insertion site of the muscle into the knee and about 0.2 cm deep. A suture is placed over the injection site for future localization, and the skin is closed with stainless steel clips.

After an appropriate incubation time (e.g., 7 days) muscle extracts are prepared by excising the entire quadriceps. Every fifth 15 um cross-section of the individual quadriceps muscles is histochemically stained for protein expression. A time course for protein expression may be done in a similar fashion except that quadriceps from different mice are harvested at different times. Persistence of DNA in muscle following injection may be determined by Southern blot analysis after preparing total cellular DNA and HIRT supernatants from injected and control mice. The results of the above experimentation in mice can be use to extrapolate proper dosages and other treatment parameters in humans and other animals using naked DNA.

Example 19: Transgenic Animals

The polypeptides of the invention can also be expressed in transgenic animals. Animals of any species, including, but not limited to, mice, rats, rabbits, hamsters, guinea pigs, pigs, micro-pigs, goats, sheep, cows and non-human primates, *e.g.*, baboons, monkeys, and chimpanzees may be used to generate transgenic animals. In a specific embodiment, techniques described herein or otherwise known in the art, are used to express polypeptides of the invention in humans, as part of a gene therapy protocol.

Any technique known in the art may be used to introduce the transgene (i.e., polynucleotides of the invention) into animals to produce the founder lines of transgenic animals. Such techniques include, but are not limited to, pronuclear microinjection (Paterson et al., Appl. Microbiol. Biotechnol. 40:691-698 (1994); Carver et al., Biotechnology (NY) 11:1263-1270 (1993); Wright et al., Biotechnology (NY) 9:830-834 (1991); and Hoppe et al., U.S. Pat. No. 4,873,191 (1989)); retrovirus mediated gene transfer into germ lines (Van der Putten et al., Proc. Natl. Acad. Sci., USA 82:6148-6152 (1985)), blastocysts or embryos; gene targeting in embryonic stem cells (Thompson et al., Cell 56:313-321 (1989)); electroporation of cells or embryos (Lo, 1983, Mol Cell. Biol. 3:1803-1814 (1983)); introduction of the polynucleotides of the invention using a gene gun (see, e.g., Ulmer et al., Science 259:1745 (1993); introducing nucleic acid constructs into embryonic pleuripotent stem cells and transferring the stem cells back into the blastocyst; and sperm-mediated gene transfer (Lavitrano et al., Cell 57:717-723 (1989); etc. For a review of such techniques, see Gordon, "Transgenic Animals," Intl. Rev. Cytol. 115:171-229 (1989), which is incorporated by reference herein in its entirety.

Any technique known in the art may be used to produce transgenic clones containing polynucleotides of the invention, for example, nuclear transfer into enucleated oocytes of nuclei from cultured embryonic, fetal, or adult cells induced to quiescence (Campell et al., Nature 380:64-66 (1996); Wilmut et al., Nature 385:810-813 (1997)).

The present invention provides for transgenic animals that carry the transgene in all their cells, as well as animals which carry the transgene in some, but not all their cells, *i.e.,* mosaic animals or chimeric. The transgene may be integrated as a single transgene or as multiple copies such as in concatamers, *e.g.,* head-to-head tandems or head-to-tail tandems. The transgene may also be selectively introduced into and activated in a particular cell type by following, for example, the teaching of Lasko et al. (Lasko et al., Proc. Natl. Acad. Sci. USA 89:6232-6236 (1992)). The regulatory sequences required for such a cell-type specific activation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art. When it is desired that the polynucleotide transgene be integrated into the chromosomal site of the endogenous gene, gene targeting is preferred. Briefly, when such a technique is to be utilized, vectors containing some nucleotide sequences homologous to the endogenous gene are designed for the purpose of integrating, via homologous recombination with chromosomal sequences, into and disrupting the function of the nucleotide sequence of

the endogenous gene. The transgene may also be selectively introduced into a particular cell type, thus inactivating the endogenous gene in only that cell type, by following, for example, the teaching of Gu et al. (Gu et al., Science 265:103-106 (1994)). The regulatory sequences required for such a cell-type specific inactivation will depend upon the particular cell type of interest, and will be apparent to those of skill in the art.

Once transgenic animals have been generated, the expression of the recombinant gene may be assayed utilizing standard techniques. Initial screening may be accomplished by Southern blot analysis or PCR techniques to analyze animal tissues to verify that integration of the transgene has taken place. The level of mRNA expression of the transgene in the tissues of the transgenic animals may also be assessed using techniques which include, but are not limited to, Northern blot analysis of tissue samples obtained from the animal, *in situ* hybridization analysis, and reverse transcriptase-PCR (rt-PCR). Samples of transgenic gene-expressing tissue may also be evaluated immunocytochemically or immunohistochemically using antibodies specific for the transgene product.

Once the founder animals are produced, they may be bred, inbred, outbred, or crossbred to produce colonies of the particular animal. Examples of such breeding strategies include, but are not limited to: outbreeding of founder animals with more than one integration site in order to establish separate lines; inbreeding of separate lines in order to produce compound transgenics that express the transgene at higher levels because of the effects of additive expression of each transgene; crossing of heterozygous transgenic animals to produce animals homozygous for a given integration site in order to both augment expression and eliminate the need for screening of animals by DNA analysis; crossing of separate homozygous lines to produce compound heterozygous or homozygous lines; and breeding to place the transgene on a distinct background that is appropriate for an experimental model of interest.

Transgenic animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

Example 20: Knock-Out Animals

Endogenous gene expression can also be reduced by inactivating or "knocking out" the gene and/or its promoter using targeted homologous recombination. (*E.g.*, see Smithies et al., Nature 317:230-234 (1985); Thomas & Capecchi, Cell 51:503-512 (1987); Thompson et al., Cell 5:313-321 (1989); each of which is incorporated by reference herein in its entirety). For example, a mutant, non-functional polynucleotide of the invention (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous polynucleotide sequence (either the coding regions or regulatory regions of the gene) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express polypeptides of the invention *in vivo*. In another embodiment, techniques known in the art are used to generate knockouts in cells that contain, but do not express the gene of interest. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the targeted gene. Such approaches are particularly suited in research and agricultural fields where modifications to embryonic stem cells can be used to generate animal offspring with an inactive targeted gene (*e.g.*, see Thomas & Capecchi 1987 and Thompson 1989, *supra*). However this approach can be routinely adapted for use in humans provided the recombinant DNA constructs are directly administered or targeted to the required site *in vivo* using appropriate viral vectors that will be apparent to those of skill in the art.

In further embodiments of the invention, cells that are genetically engineered to express the polypeptides of the invention, or alternatively, that are genetically engineered not to express the polypeptides of the invention (e.g., knockouts) are administered to a patient *in vivo*. Such cells may be obtained from the patient (i.e., animal, including human) or an MHC compatible donor and can include, but are not limited to fibroblasts, bone marrow cells, blood cells (e.g., lymphocytes), adipocytes, muscle cells, endothelial cells etc. The cells are genetically engineered *in vitro* using recombinant DNA techniques to introduce the coding sequence of polypeptides of the invention into the cells, or alternatively, to disrupt the coding sequence and/or endogenous regulatory sequence associated with the polypeptides of the invention, e.g., by transduction (using viral vectors, and preferably vectors that integrate the transgene into the cell genome) or transfection procedures, including, but not limited to, the use of plasmids, cosmids, YACs, naked DNA, electroporation, liposomes, etc. The coding sequence of the polypeptides of the invention can be placed under the control of a strong constitutive or inducible promoter or promoter/enhancer to achieve expression, and

preferably secretion, of the polypeptides of the invention. The engineered cells which express and preferably secrete the polypeptides of the invention can be introduced into the patient systemically, e.g., in the circulation, or intraperitoneally.

Alternatively, the cells can be incorporated into a matrix and implanted in the body, e.g., genetically engineered fibroblasts can be implanted as part of a skin graft; genetically engineered endothelial cells can be implanted as part of a lymphatic or vascular graft. (See, for example, Anderson et al. U.S. Patent No. 5,399,349; and Mulligan & Wilson, U.S. Patent No. 5,460,959 each of which is incorporated by reference herein in its entirety).

When the cells to be administered are non-autologous or non-MHC compatible cells, they can be administered using well known techniques which prevent the development of a host immune response against the introduced cells. For example, the cells may be introduced in an encapsulated form which, while allowing for an exchange of components with the immediate extracellular environment, does not allow the introduced cells to be recognized by the host immune system.

Transgenic and "knock-out" animals of the invention have uses which include, but are not limited to, animal model systems useful in elaborating the biological function of polypeptides of the present invention, studying conditions and/or disorders associated with aberrant expression, and in screening for compounds effective in ameliorating such conditions and/or disorders.

Example 22: Assays Detecting Stimulation or Inhibition of B cell Proliferation and Differentiation

Generation of functional humoral immune responses requires both soluble and cognate signaling between B-lineage cells and their microenvironment. Signals may impart a positive stimulus that allows a B-lineage cell to continue its programmed development, or a negative stimulus that instructs the cell to arrest its current developmental pathway. To date, numerous stimulatory and inhibitory signals have been found to influence B cell responsiveness including IL-2, IL-4, IL-5, IL-6, IL-7, IL10, IL-13, IL-14 and IL-15. Interestingly, these signals are by themselves weak effectors but can, in combination with various co-stimulatory proteins, induce activation, proliferation, differentiation, homing, tolerance and death among B cell populations.

One of the best studied classes of B-cell co-stimulatory proteins is the TNF-superfamily. Within this family CD40, CD27, and CD30 along with their respective ligands CD154, CD70, and CD153 have been found to regulate a variety of immune responses. Assays which allow for the detection and/or observation of the proliferation and differentiation of these B-cell populations and their precursors are valuable tools in determining the effects various proteins may have on these B-cell populations in terms of proliferation and differentiation. Listed below are two assays designed to allow for the detection of the differentiation, proliferation, or inhibition of B-cell populations and their precursors.

In Vitro Assay- Agonists or antagonists of the invention can be assessed for its ability to induce activation, proliferation, differentiation or inhibition and/or death in B-cell populations and their precursors. The activity of the agonists or antagonists of the invention on purified human tonsillar B cells, measured qualitatively over the dose range from 0.1 to 10,000 ng/mL, is assessed in a standard B-lymphocyte co-stimulation assay in which purified tonsillar B cells are cultured in the presence of either formalin-fixed Staphylococcus aureus Cowan I (SAC) or immobilized anti-human IgM antibody as the priming agent. Second signals such as IL-2 and IL-15 synergize with SAC and IgM crosslinking to elicit B cell proliferation as measured by tritiated-thymidine incorporation. Novel synergizing agents can be readily identified using this assay. The assay involves isolating human tonsillar B cells by magnetic bead (MACS) depletion of CD3-positive cells. The resulting cell population is greater than 95% B cells as assessed by expression of CD45R(B220).

Various dilutions of each sample are placed into individual wells of a 96-well plate to which are added 10^5 B-cells suspended in culture medium (RPMI 1640 containing 10% FBS, 5 X 10^{-5}M 2ME, 100U/ml penicillin, 10ug/ml streptomycin, and 10^{-5} dilution of SAC) in a total volume of 150ul. Proliferation or inhibition is quantitated by a 20h pulse (1uCi/well) with 3H-thymidine (6.7 Ci/mM) beginning 72h post factor addition. The positive and negative controls are IL2 and medium respectively.

In Vivo Assay- BALB/c mice are injected (i.p.) twice per day with buffer only, or 2 mg/Kg of agonists or antagonists of the invention, or truncated forms thereof. Mice receive this treatment for 4 consecutive days, at which time they are sacrificed and various tissues and serum collected for analyses. Comparison of H&E sections from normal spleens and spleens treated with agonists or antagonists of the invention identify the results of the activity

of the agonists or antagonists on spleen cells, such as the diffusion of peri-arterial lymphatic sheaths, and/or significant increases in the nucleated cellularity of the red pulp regions, which may indicate the activation of the differentiation and proliferation of B-cell populations. Immunohistochemical studies using a B cell marker, anti-CD45R(B220), are used to determine whether any physiological changes to splenic cells, such as splenic disorganization, are due to increased B-cell representation within loosely defined B-cell zones that infiltrate established T-cell regions.

Flow cytometric analyses of the spleens from mice treated with agonist or antagonist is used to indicate whether the agonists or antagonists specifically increases the proportion of ThB+, CD45R(B220)dull B cells over that which is observed in control mice.
Likewise, a predicted consequence of increased mature B-cell representation in vivo is a relative increase in serum Ig titers. Accordingly, serum IgM and IgA levels are compared between buffer and agonists or antagonists-treated mice.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 23: T Cell Proliferation Assay

A CD3-induced proliferation assay is performed on PBMCs and is measured by the uptake of ^{3}H-thymidine. The assay is performed as follows. Ninety-six well plates are coated with 100 µl/well of mAb to CD3 (HIT3a, Pharmingen) or isotype-matched control mAb (B33.1) overnight at 4 degrees C (1 µg/ml in .05M bicarbonate buffer, pH 9.5), then washed three times with PBS. PBMC are isolated by F/H gradient centrifugation from human peripheral blood and added to quadruplicate wells (5 x 10^4/well) of mAb coated plates in RPMI containing 10% FCS and P/S in the presence of varying concentrations of agonists or antagonists of the invention (total volume 200 ul). Relevant protein buffer and medium alone are controls. After 48 hr. culture at 37 degrees C, plates are spun for 2 min. at 1000 rpm and 100 µl of supernatant is removed and stored –20 degrees C for measurement of IL-2 (or other cytokines) if effect on proliferation is observed. Wells are supplemented with 100 ul of medium containing 0.5 uCi of ^{3}H-thymidine and cultured at 37 degrees C for 18-24 hr. Wells are harvested and incorporation of ^{3}H-thymidine used as a measure of proliferation.

Anti-CD3 alone is the positive control for proliferation. IL-2 (100 U/ml) is also used as a control which enhances proliferation. Control antibody which does not induce proliferation of T cells is used as the negative controls for the effects of agonists or antagonists of the invention.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 24: Effect of Agonists or Antagonists of the Invention on the Expression of MHC Class II, Costimulatory and Adhesion Molecules and Cell Differentiation of Monocytes and Monocyte-Derived Human Dendritic Cells

Dendritic cells are generated by the expansion of proliferating precursors found in the peripheral blood: adherent PBMC or elutriated monocytic fractions are cultured for 7-10 days with GM-CSF (50 ng/ml) and IL-4 (20 ng/ml). These dendritic cells have the characteristic phenotype of immature cells (expression of CD1, CD80, CD86, CD40 and MHC class II antigens). Treatment with activating factors, such as TNF-α, causes a rapid change in surface phenotype (increased expression of MHC class I and II, costimulatory and adhesion molecules, downregulation of FCγRII, upregulation of CD83). These changes correlate with increased antigen-presenting capacity and with functional maturation of the dendritic cells.

FACS analysis of surface antigens is performed as follows. Cells are treated 1-3 days with increasing concentrations of agonist or antagonist of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degrees C. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Effect on the production of cytokines. Cytokines generated by dendritic cells, in particular IL-12, are important in the initiation of T-cell dependent immune responses. IL-12 strongly influences the development of Thl helper T-cell immune response, and induces cytotoxic T and NK cell function. An ELISA is used to measure the IL-12 release as follows. Dendritic cells (10^6/ml) are treated with increasing concentrations of agonists or antagonists of the

invention for 24 hours. LPS (100 ng/ml) is added to the cell culture as positive control. Supernatants from the cell cultures are then collected and analyzed for IL-12 content using commercial ELISA kit (e..g, R & D Systems (Minneapolis, MN)). The standard protocols provided with the kits are used.

Effect on the expression of MHC Class II, costimulatory and adhesion molecules. Three major families of cell surface antigens can be identified on monocytes: adhesion molecules, molecules involved in antigen presentation, and Fc receptor. Modulation of the expression of MHC class II antigens and other costimulatory molecules, such as B7 and ICAM-1, may result in changes in the antigen presenting capacity of monocytes and ability to induce T cell activation. Increase expression of Fc receptors may correlate with improved monocyte cytotoxic activity, cytokine release and phagocytosis.

FACS analysis is used to examine the surface antigens as follows. Monocytes are treated 1-5 days with increasing concentrations of agonists or antagonists of the invention or LPS (positive control), washed with PBS containing 1% BSA and 0.02 mM sodium azide, and then incubated with 1:20 dilution of appropriate FITC- or PE-labeled monoclonal antibodies for 30 minutes at 4 degreesC. After an additional wash, the labeled cells are analyzed by flow cytometry on a FACScan (Becton Dickinson).

Monocyte activation and/or increased survival. Assays for molecules that activate (or alternatively, inactivate) monocytes and/or increase monocyte survival (or alternatively, decrease monocyte survival) are known in the art and may routinely be applied to determine whether a molecule of the invention functions as an inhibitor or activator of monocytes. Agonists or antagonists of the invention can be screened using the three assays described below. For each of these assays, Peripheral blood mononuclear cells (PBMC) are purified from single donor leukopacks (American Red Cross, Baltimore, MD) by centrifugation through a Histopaque gradient (Sigma). Monocytes are isolated from PBMC by counterflow centrifugal elutriation.

Monocyte Survival Assay. Human peripheral blood monocytes progressively lose viability when cultured in absence of serum or other stimuli. Their death results from internally regulated process (apoptosis). Addition to the culture of activating factors, such as TNF-alpha

dramatically improves cell survival and prevents DNA fragmentation. Propidium iodide (PI) staining is used to measure apoptosis as follows. Monocytes are cultured for 48 hours in polypropylene tubes in serum-free medium (positive control), in the presence of 100 ng/ml TNF-alpha (negative control), and in the presence of varying concentrations of the compound to be tested. Cells are suspended at a concentration of 2×10^6/ml in PBS containing PI at a final concentration of 5 μg/ml, and then incubaed at room temperature for 5 minutes before FACScan analysis. PI uptake has been demonstrated to correlate with DNA fragmentation in this experimental paradigm.

Effect on cytokine release. An important function of monocytes/macrophages is their regulatory activity on other cellular populations of the immune system through the release of cytokines after stimulation. An ELISA to measure cytokine release is performed as follows. Human monocytes are incubated at a density of 5×10^5 cells/ml with increasing concentrations of agonists or antagonists of the invention and under the same conditions, but in the absence of agonists or antagonists. For IL-12 production, the cells are primed overnight with IFN (100 U/ml) in presence of agonist or antagonist of the invention. LPS (10 ng/ml) is then added. Conditioned media are collected after 24h and kept frozen until use. Measurement of TNF-alpha, IL-10, MCP-1 and IL-8 is then performed using a commercially available ELISA kit (e. g, R & D Systems (Minneapolis, MN)) and applying the standard protocols provided with the kit.

Oxidative burst. Purified monocytes are plated in 96-w plate at $2\text{-}1 \times 10^5$ cell/well. Increasing concentrations of agonists or antagonists of the invention are added to the wells in a total volume of 0.2 ml culture medium (RPMI 1640 + 10% FCS, glutamine and antibiotics). After 3 days incubation, the plates are centrifuged and the medium is removed from the wells. To the macrophage monolayers, 0.2 ml per well of phenol red solution (140 mM NaCl, 10 mM potassium phosphate buffer pH 7.0, 5.5 mM dextrose, 0.56 mM phenol red and 19 U/ml of HRPO) is added, together with the stimulant (200 nM PMA). The plates are incubated at 37°C for 2 hours and the reaction is stopped by adding 20 μl 1N NaOH per well. The absorbance is read at 610 nm. To calculate the amount of H_2O_2 produced by the macrophages, a standard curve of a H_2O_2 solution of known molarity is performed for each experiment.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 25: Biological Effects of Agonists or Antagonists of the Invention

Astrocyte and Neuronal Assays.

Agonists or antagonists of the invention, expressed in *Escherichia coli* and purified as described above, can be tested for activity in promoting the survival, neurite outgrowth, or phenotypic differentiation of cortical neuronal cells and for inducing the proliferation of glial fibrillary acidic protein immunopositive cells, astrocytes. The selection of cortical cells for the bioassay is based on the prevalent expression of FGF-1 and FGF-2 in cortical structures and on the previously reported enhancement of cortical neuronal survival resulting from FGF-2 treatment. A thymidine incorporation assay, for example, can be used to elucidate an agonist or antagonist of the invention's activity on these cells.

Moreover, previous reports describing the biological effects of FGF-2 (basic FGF) on cortical or hippocampal neurons *in vitro* have demonstrated increases in both neuron survival and neurite outgrowth (Walicke et al., "Fibroblast growth factor promotes survival of dissociated hippocampal neurons and enhances neurite extension." *Proc. Natl. Acad. Sci. USA 83*:3012-3016. (1986), assay herein incorporated by reference in its entirety). However, reports from experiments done on PC-12 cells suggest that these two responses are not necessarily synonymous and may depend on not only which FGF is being tested but also on which receptor(s) are expressed on the target cells. Using the primary cortical neuronal culture paradigm, the ability of an agonist or antagonist of the invention to induce neurite outgrowth can be compared to the response achieved with FGF-2 using, for example, a thymidine incorporation assay.

Fibroblast and endothelial cell assays.

Human lung fibroblasts are obtained from Clonetics (San Diego, CA) and maintained in growth media from Clonetics. Dermal microvascular endothelial cells are obtained from

Cell Applications (San Diego, CA). For proliferation assays, the human lung fibroblasts and dermal microvascular endothelial cells can be cultured at 5,000 cells/well in a 96-well plate for one day in growth medium. The cells are then incubated for one day in 0.1% BSA basal medium. After replacing the medium with fresh 0.1% BSA medium, the cells are incubated with the test proteins for 3 days. Alamar Blue (Alamar Biosciences, Sacramento, CA) is added to each well to a final concentration of 10%. The cells are incubated for 4 hr. Cell viability is measured by reading in a CytoFluor fluorescence reader. For the PGE_2 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or agonists or antagonists of the invention with or without IL-1α for 24 hours. The supernatants are collected and assayed for PGE_2 by EIA kit (Cayman, Ann Arbor, MI). For the IL-6 assays, the human lung fibroblasts are cultured at 5,000 cells/well in a 96-well plate for one day. After a medium change to 0.1% BSA basal medium, the cells are incubated with FGF-2 or with or without agonists or antagonists of the invention IL-1α for 24 hours. The supernatants are collected and assayed for IL-6 by ELISA kit (Endogen, Cambridge, MA).

Human lung fibroblasts are cultured with FGF-2 or agonists or antagonists of the invention for 3 days in basal medium before the addition of Alamar Blue to assess effects on growth of the fibroblasts. FGF-2 should show a stimulation at 10 - 2500 ng/ml which can be used to compare stimulation with agonists or antagonists of the invention.

Parkinson Models.

The loss of motor function in Parkinson's disease is attributed to a deficiency of striatal dopamine resulting from the degeneration of the nigrostriatal dopaminergic projection neurons. An animal model for Parkinson's that has been extensively characterized involves the systemic administration of 1-methyl-4 phenyl 1,2,3,6-tetrahydropyridine (MPTP). In the CNS, MPTP is taken-up by astrocytes and catabolized by monoamine oxidase B to 1-methyl-4-phenyl pyridine (MPP^+) and released. Subsequently, MPP^+ is actively accumulated in dopaminergic neurons by the high-affinity reuptake transporter for dopamine. MPP^+ is then concentrated in mitochondria by the electrochemical gradient and selectively inhibits nicotidamide adenine disphosphate: ubiquinone oxidoreductionase (complex I), thereby interfering with electron transport and eventually generating oxygen radicals.

It has been demonstrated in tissue culture paradigms that FGF-2 (basic FGF) has trophic activity towards nigral dopaminergic neurons (Ferrari et al., Dev. Biol. 1989). Recently, Dr. Unsicker's group has demonstrated that administering FGF-2 in gel foam implants in the striatum results in the near complete protection of nigral dopaminergic neurons from the toxicity associated with MPTP exposure (Otto and Unsicker, J. Neuroscience, 1990).

Based on the data with FGF-2, agonists or antagonists of the invention can be evaluated to determine whether it has an action similar to that of FGF-2 in enhancing dopaminergic neuronal survival *in vitro* and it can also be tested *in vivo* for protection of dopaminergic neurons in the striatum from the damage associated with MPTP treatment. The potential effect of an agonist or antagonist of the invention is first examined in vitro in a dopaminergic neuronal cell culture paradigm. The cultures are prepared by dissecting the midbrain floor plate from gestation day 14 Wistar rat embryos. The tissue is dissociated with trypsin and seeded at a density of 200,000 cells/cm^2 on polyorthinine-laminin coated glass coverslips. The cells are maintained in Dulbecco's Modified Eagle's medium and F12 medium containing hormonal supplements (N1). . The cultures are fixed with paraformaldehyde after 8 days in vitro and are processed for tyrosine hydroxylase, a specific marker for dopminergic neurons, immunohistochemical staining. Dissociated cell cultures are prepared from embryonic rats. The culture medium is changed every third day and the factors are also added at that time.

Since the dopaminergic neurons are isolated from animals at gestation day 14, a developmental time which is past the stage when the dopaminergic precursor cells are proliferating, an increase in the number of tyrosine hydroxylase immunopositive neurons would represent an increase in the number of dopaminergic neurons surviving *in vitro*. Therefore, if an agonist or antagonist of the invention acts to prolong the survival of dopaminergic neurons, it would suggest that the agonist or antagonist may be involved in Parkinson's Disease.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 26: The Effect of Agonists or Antagonists of the Invention on the Growth of Vascular Endothelial Cells

On day 1, human umbilical vein endothelial cells (HUVEC) are seeded at 2-5x10^4 cells/35 mm dish density in M199 medium containing 4% fetal bovine serum (FBS), 16 units/ml heparin, and 50 units/ml endothelial cell growth supplements (ECGS, Biotechnique, Inc.). On day 2, the medium is replaced with M199 containing 10% FBS, 8 units/ml heparin. An agonist or antagonist of the invention, and positive controls, such as VEGF and basic FGF (bFGF) are added, at varying concentrations. On days 4 and 6, the medium is replaced. On day 8, cell number is determined with a Coulter Counter.

An increase in the number of HUVEC cells indicates that the compound of the invention may proliferate vascular endothelial cells, while a decrease in the number of HUVEC cell indicates that the compound of the invention inhibits vascular endothelial cells.

The studies described in this example tested activity of a polypeptide of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), agonists, and/or antagonists of the invention.

Example 27: Rat Corneal Wound Healing Model

This animal model shows the effect of an agonist or antagonist of the invention on neovascularization. The experimental protocol includes:

a) Making a 1-1.5 mm long incision from the center of cornea into the stromal layer.

b) Inserting a spatula below the lip of the incision facing the outer corner of the eye.

c) Making a pocket (its base is 1-1.5 mm form the edge of the eye).

d) Positioning a pellet, containing 50ng- 5ug of an agonist or antagonist of the invention, within the pocket.

e) Treatment with an agonist or antagonist of the invention can also be applied topically to the corneal wounds in a dosage range of 20mg - 500mg (daily treatment for five days).

The studies described in this example tested activity of agonists or antagonists of the

invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 28: Diabetic Mouse and Glucocorticoid-Impaired Wound Healing Models

A. Diabetic db+/db+ Mouse Model.

To demonstrate that an agonist or antagonist of the invention accelerates the healing process, the genetically diabetic mouse model of wound healing is used. The full thickness wound healing model in the db+/db+ mouse is a well characterized, clinically relevant and reproducible model of impaired wound healing. Healing of the diabetic wound is dependent on formation of granulation tissue and re-epithelialization rather than contraction (Gartner, M.H. *et al., J. Surg. Res. 52*:389 (1992); Greenhalgh, D.G. *et al., Am. J. Pathol. 136*:1235 (1990)).

The diabetic animals have many of the characteristic features observed in Type II diabetes mellitus. Homozygous (db+/db+) mice are obese in comparison to their normal heterozygous (db+/+m) littermates. Mutant diabetic (db+/db+) mice have a single autosomal recessive mutation on chromosome 4 (db+) (Coleman *et al. Proc. Natl. Acad. Sci. USA 77*:283-293 (1982)). Animals show polyphagia, polydipsia and polyuria. Mutant diabetic mice (db+/db+) have elevated blood glucose, increased or normal insulin levels, and suppressed cell-mediated immunity (Mandel *et al., J. Immunol. 120*:1375 (1978); Debray-Sachs, M. *et al., Clin. Exp. Immunol. 51(1)*:1-7 (1983); Leiter *et al., Am. J. of Pathol. 114*:46-55 (1985)). Peripheral neuropathy, myocardial complications, and microvascular lesions, basement membrane thickening and glomerular filtration abnormalities have been described in these animals (Norido, F. *et al., Exp. Neurol. 83(2)*:221-232 (1984); Robertson *et al., Diabetes 29(1)*:60-67 (1980); Giacomelli *et al., Lab Invest. 40(4)*:460-473 (1979); Coleman, D.L., *Diabetes 31 (Suppl)*:1-6 (1982)). These homozygous diabetic mice develop hyperglycemia that is resistant to insulin analogous to human type II diabetes (Mandel *et al., J. Immunol. 120*:1375-1377 (1978)).

The characteristics observed in these animals suggests that healing in this model may be similar to the healing observed in human diabetes (Greenhalgh, *et al., Am. J. of Pathol. 136*:1235-1246 (1990)).

Genetically diabetic female C57BL/KsJ (db+/db+) mice and their non-diabetic

(db+/+m) heterozygous littermates are used in this study (Jackson Laboratories). The animals are purchased at 6 weeks of age and are 8 weeks old at the beginning of the study. Animals are individually housed and received food and water ad libitum. All manipulations are performed using aseptic techniques. The experiments are conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

Wounding protocol is performed according to previously reported methods (Tsuboi, R. and Rifkin, D.B., *J. Exp. Med. 172*:245-251 (1990)). Briefly, on the day of wounding, animals are anesthetized with an intraperitoneal injection of Avertin (0.01 mg/mL), 2,2,2-tribromoethanol and 2-methyl-2-butanol dissolved in deionized water. The dorsal region of the animal is shaved and the skin washed with 70% ethanol solution and iodine. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is then created using a Keyes tissue punch. Immediately following wounding, the surrounding skin is gently stretched to eliminate wound expansion. The wounds are left open for the duration of the experiment. Application of the treatment is given topically for 5 consecutive days commencing on the day of wounding. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of surgery and at two day intervals thereafter. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

An agonist or antagonist of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology and immunohistochemistry. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Three groups of 10 animals each (5 diabetic and 5 non-diabetic controls) are evaluated: 1) Vehicle placebo control, 2) untreated group, and 3) treated group.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and

obtaining the total square area of the wound. Contraction is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is $64mm^2$, the corresponding size of the dermal punch. Calculations are made using the following formula:

[Open area on day 8] - [Open area on day 1] / [Open area on day 1]

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using a Reichert-Jung microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic examination of the wounds are used to assess whether the healing process and the morphologic appearance of the repaired skin is altered by treatment with an agonist or antagonist of the invention. This assessment included verification of the presence of cell accumulation, inflammatory cells, capillaries, fibroblasts, re-epithelialization and epidermal maturity (Greenhalgh, D.G. *et al., Am. J. Pathol. 136:*1235 (1990)). A calibrated lens micrometer is used by a blinded observer.

Tissue sections are also stained immunohistochemically with a polyclonal rabbit anti-human keratin antibody using ABC Elite detection system. Human skin is used as a positive tissue control while non-immune IgG is used as a negative control. Keratinocyte growth is determined by evaluating the extent of reepithelialization of the wound using a calibrated lens micrometer.

Proliferating cell nuclear antigen/cyclin (PCNA) in skin specimens is demonstrated by using anti-PCNA antibody (1:50) with an ABC Elite detection system. Human colon cancer served as a positive tissue control and human brain tissue is used as a negative tissue control. Each specimen included a section with omission of the primary antibody and substitution with non-immune mouse IgG. Ranking of these sections is based on the extent of proliferation on a scale of 0-8, the lower side of the scale reflecting slight proliferation to the higher side reflecting intense proliferation.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

B. Steroid Impaired Rat Model

The inhibition of wound healing by steroids has been well documented in various *in vitro* and *in vivo* systems (Wahl, Glucocorticoids and Wound healing. In: Anti-Inflammatory Steroid Action: Basic and Clinical Aspects. 280-302 (1989); Wahl*et al., J. Immunol. 115*: 476-481 (1975); Werb *et al., J. Exp. Med. 147*:1684-1694 (1978)). Glucocorticoids retard wound healing by inhibiting angiogenesis, decreasing vascular permeability (Ebert *et al., An. Intern. Med. 37*:701-705 (1952)), fibroblast proliferation, and collagen synthesis (Beck *et al., Growth Factors. 5:* 295-304 (1991); Haynes *et al., J. Clin. Invest. 61:* 703-797 (1978)) and producing a transient reduction of circulating monocytes (Haynes et al., *J. Clin. Invest. 61:* 703-797 (1978); Wahl, "Glucocorticoids and wound healing", *In:* Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989)). The systemic administration of steroids to impaired wound healing is a well establish phenomenon in rats (Beck *et al., Growth Factors. 5:* 295-304 (1991); Haynes *et al., J. Clin. Invest. 61:* 703-797 (1978); Wahl, "Glucocorticoids and wound healing", *In*: Antiinflammatory Steroid Action: Basic and Clinical Aspects, Academic Press, New York, pp. 280-302 (1989); Pierce *et al., Proc. Natl. Acad. Sci. USA 86*: 2229-2233 (1989)).

To demonstrate that an agonist or antagonist of the invention can accelerate the healing process, the effects of multiple topical applications of the agonist or antagonist on full thickness excisional skin wounds in rats in which healing has been impaired by the systemic administration of methylprednisolone is assessed.

Young adult male Sprague Dawley rats weighing 250-300 g (Charles River Laboratories) are used in this example. The animals are purchased at 8 weeks of age and are 9 weeks old at the beginning of the study. The healing response of rats is impaired by the systemic administration of methylprednisolone (17mg/kg/rat intramuscularly) at the time of wounding. Animals are individually housed and received food and water *ad libitum*. All manipulations are performed using aseptic techniques. This study is conducted according to the rules and guidelines of Human Genome Sciences, Inc. Institutional Animal Care and Use Committee and the Guidelines for the Care and Use of Laboratory Animals.

The wounding protocol is followed according to section A, above. On the day of wounding, animals are anesthetized with an intramuscular injection of ketamine (50 mg/kg) and xylazine (5 mg/kg). The dorsal region of the animal is shaved and the skin washed with 70% ethanol and iodine solutions. The surgical area is dried with sterile gauze prior to wounding. An 8 mm full-thickness wound is created using a Keyes tissue punch. The

wounds are left open for the duration of the experiment. Applications of the testing materials are given topically once a day for 7 consecutive days commencing on the day of wounding and subsequent to methylprednisolone administration. Prior to treatment, wounds are gently cleansed with sterile saline and gauze sponges.

Wounds are visually examined and photographed at a fixed distance at the day of wounding and at the end of treatment. Wound closure is determined by daily measurement on days 1-5 and on day 8. Wounds are measured horizontally and vertically using a calibrated Jameson caliper. Wounds are considered healed if granulation tissue is no longer visible and the wound is covered by a continuous epithelium.

The agonist or antagonist of the invention is administered using at a range different doses, from 4mg to 500mg per wound per day for 8 days in vehicle. Vehicle control groups received 50mL of vehicle solution.

Animals are euthanized on day 8 with an intraperitoneal injection of sodium pentobarbital (300mg/kg). The wounds and surrounding skin are then harvested for histology. Tissue specimens are placed in 10% neutral buffered formalin in tissue cassettes between biopsy sponges for further processing.

Four groups of 10 animals each (5 with methylprednisolone and 5 without glucocorticoid) are evaluated: 1) Untreated group 2) Vehicle placebo control 3) treated groups.

Wound closure is analyzed by measuring the area in the vertical and horizontal axis and obtaining the total area of the wound. Closure is then estimated by establishing the differences between the initial wound area (day 0) and that of post treatment (day 8). The wound area on day 1 is $64mm^2$, the corresponding size of the dermal punch. Calculations are made using the following formula:

[Open area on day 8] - [Open area on day 1] / [Open area on day 1]

Specimens are fixed in 10% buffered formalin and paraffin embedded blocks are sectioned perpendicular to the wound surface (5mm) and cut using an Olympus microtome. Routine hematoxylin-eosin (H&E) staining is performed on cross-sections of bisected wounds. Histologic examination of the wounds allows assessment of whether the healing process and the morphologic appearance of the repaired skin is improved by treatment with an agonist or

antagonist of the invention. A calibrated lens micrometer is used by a blinded observer to determine the distance of the wound gap.

Experimental data are analyzed using an unpaired t test. A p value of < 0.05 is considered significant.

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 29: Lymphadema Animal Model

The purpose of this experimental approach is to create an appropriate and consistent lymphedema model for testing the therapeutic effects of an agonist or antagonist of the invention in lymphangiogenesis and re-establishment of the lymphatic circulatory system in the rat hind limb. Effectiveness is measured by swelling volume of the affected limb, quantification of the amount of lymphatic vasculature, total blood plasma protein, and histopathology. Acute lymphedema is observed for 7-10 days. Perhaps more importantly, the chronic progress of the edema is followed for up to 3-4 weeks.

Prior to beginning surgery, blood sample is drawn for protein concentration analysis. Male rats weighing approximately ~350g are dosed with Pentobarbital. Subsequently, the right legs are shaved from knee to hip. The shaved area is swabbed with gauze soaked in 70% EtOH. Blood is drawn for serum total protein testing. Circumference and volumetric measurements are made prior to injecting dye into paws after marking 2 measurement levels (0.5 cm above heel, at mid-pt of dorsal paw). The intradermal dorsum of both right and left paws are injected with 0.05 ml of 1% Evan's Blue. Circumference and volumetric measurements are then made following injection of dye into paws.

Using the knee joint as a landmark, a mid-leg inguinal incision is made circumferentially allowing the femoral vessels to be located. Forceps and hemostats are used to dissect and separate the skin flaps. After locating the femoral vessels, the lymphatic vessel that runs along side and underneath the vessel(s) is located. The main lymphatic vessels in this area are then electrically coagulated or suture ligated.

Using a microscope, muscles in back of the leg (near the semitendinosis and adductors) are bluntly dissected. The popliteal lymph node is then located. The 2 proximal

and 2 distal lymphatic vessels and distal blood supply of the popliteal node are then and ligated by suturing. The popliteal lymph node, and any accompanying adipose tissue, is then removed by cutting connective tissues.

Care is taken to control any mild bleeding resulting from this procedure. After lymphatics are occluded, the skin flaps are sealed by using liquid skin (Vetbond) (AJ Buck). The separated skin edges are sealed to the underlying muscle tissue while leaving a gap of ~0.5 cm around the leg. Skin also may be anchored by suturing to underlying muscle when necessary.

To avoid infection, animals are housed individually with mesh (no bedding). Recovering animals are checked daily through the optimal edematous peak, which typically occurred by day 5-7. The plateau edematous peak are then observed. To evaluate the intensity of the lymphedema, the circumference and volumes of 2 designated places on each paw before operation and daily for 7 days are measured. The effect plasma proteins on lymphedema is determined and whether protein analysis is a useful testing perimeter is also investigated. The weights of both control and edematous limbs are evaluated at 2 places. Analysis is performed in a blind manner.

Circumference Measurements: Under brief gas anesthetic to prevent limb movement, a cloth tape is used to measure limb circumference. Measurements are done at the ankle bone and dorsal paw by 2 different people then those 2 readings are averaged. Readings are taken from both control and edematous limbs.

Volumetric Measurements: On the day of surgery, animals are anesthetized with Pentobarbital and are tested prior to surgery. For daily volumetrics animals are under brief halothane anesthetic (rapid immobilization and quick recovery), both legs are shaved and equally marked using waterproof marker on legs. Legs are first dipped in water, then dipped into instrument to each marked level then measured by Buxco edema software(Chen/Victor). Data is recorded by one person, while the other is dipping the limb to marked area.

Blood-plasma protein measurements: Blood is drawn, spun, and serum separated prior to surgery and then at conclusion for total protein and Ca2+ comparison.

Limb Weight Comparison: After drawing blood, the animal is prepared for tissue collection. The limbs are amputated using a quillitine, then both experimental and control legs are cut at the ligature and weighed. A second weighing is done as the tibio-cacaneal joint is disarticulated and the foot is weighed.

Histological Preparations: The transverse muscle located behind the knee (popliteal) area is dissected and arranged in a metal mold, filled with freezeGel, dipped into cold methylbutane, placed into labeled sample bags at - 80EC until sectioning. Upon sectioning, the muscle is observed under fluorescent microscopy for lymphatics..

The studies described in this example tested activity of agonists or antagonists of the invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 30: Suppression of TNF alpha-induced adhesion molecule expression by a Agonist or Antagonist of the Invention

The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules (CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an inflammatory response. The local concentration of cytokines and growth factor participate in the modulation of the expression of these CAMs.

Tumor necrosis factor alpha (TNF-a), a potent proinflammatory cytokine, is a stimulator of all three CAMs on endothelial cells and may be involved in a wide variety of inflammatory responses, often resulting in a pathological outcome.

The potential of an agonist or antagonist of the invention to mediate a suppression of TNF-a induced CAM expression can be examined. A modified ELISA assay which uses ECs as a solid phase absorbent is employed to measure the amount of CAM expression on TNF-a treated ECs when co-stimulated with a member of the FGF family of proteins.

To perform the experiment, human umbilical vein endothelial cell (HUVEC) cultures are obtained from pooled cord harvests and maintained in growth medium (EGM-2; Clonetics, San Diego, CA) supplemented with 10% FCS and 1% penicillin/streptomycin in a 37 degree C humidified incubator containing 5% CO_2. HUVECs are seeded in 96-well

plates at concentrations of 1 x 10^4 cells/well in EGM medium at 37 degree C for 18-24 hrs or until confluent. The monolayers are subsequently washed 3 times with a serum-free solution of RPMI-1640 supplemented with 100 U/ml penicillin and 100 mg/ml streptomycin, and treated with a given cytokine and/or growth factor(s) for 24 h at 37 degree C. Following incubation, the cells are then evaluated for CAM expression.

Human Umbilical Vein Endothelial cells (HUVECs) are grown in a standard 96 well plate to confluence. Growth medium is removed from the cells and replaced with 90 ul of 199 Medium (10% FBS). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10 ul volumes). Plates are incubated at 37 degree C for either 5 h (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to remove medium and 100 µl of 0.1% paraformaldehyde-PBS(with Ca++ and Mg++) is added to each well. Plates are held at 4°C for 30 min.

Fixative is then removed from the wells and wells are washed 1X with PBS(+Ca,Mg)+0.5% BSA and drained. Do not allow the wells to dry. Add 10 µl of diluted primary antibody to the test and control wells. Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin and Anti-E-selectin-Biotin are used at a concentration of 10 µg/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified environment. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA.

Then add 20 µl of diluted ExtrAvidin-Alkaline Phosphotase (1:5,000 dilution) to each well and incubated at 37°C for 30 min. Wells are washed X3 with PBS(+Ca,Mg)+0.5% BSA. 1 tablet of p-Nitrophenol Phosphate pNPP is dissolved in 5 ml of glycine buffer (pH 10.4). 100 µl of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphotase in glycine buffer: 1:5,000 (10^0) > $10^{-0.5}$ > 10^{-1} > $10^{-1.5}$. 5 µl of each dilution is added to triplicate wells and the resulting AP content in each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 µl of pNNP reagent must then be added to each of the standard wells. The plate must be incubated at 37°C for 4h. A volume of 50 µl of 3M NaOH is added to all wells. The results are quantified on a plate reader at 405 nm. The background subtraction option is used on blank wells filled with glycine buffer only. The template is set up to indicate the concentration of AP-conjugate in each standard well [5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng]. Results are indicated as amount of bound AP-conjugate in each sample.

The studies described in this example tested activity of agonists or antagonists of the

invention. However, one skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides or polypeptides of the invention (e.g., gene therapy).

Example 31: Production Of Polypeptide of the Invention For High-Throughput Screening Assays

The following protocol produces a supernatant containing polypeptide of the present invention to be tested. This supernatant can then be used in the Screening Assays described in Examples 33-42.

First, dilute Poly-D-Lysine (644 587 Boehringer-Mannheim) stock solution (1mg/ml in PBS) 1:20 in PBS (w/o calcium or magnesium 17-516F Biowhittaker) for a working solution of 50ug/ml. Add 200 ul of this solution to each well (24 well plates) and incubate at RT for 20 minutes. Be sure to distribute the solution over each well (note: a 12-channel pipetter may be used with tips on every other channel). Aspirate off the Poly-D-Lysine solution and rinse with 1ml PBS (Phosphate Buffered Saline). The PBS should remain in the well until just prior to plating the cells and plates may be poly-lysine coated in advance for up to two weeks.

Plate 293T cells (do not carry cells past P+20) at 2 x 10^5 cells/well in .5ml DMEM(Dulbecco's Modified Eagle Medium)(with 4.5 G/L glucose and L-glutamine (12-604F Biowhittaker))/10% heat inactivated FBS(14-503F Biowhittaker)/1x Penstrep(17-602E Biowhittaker). Let the cells grow overnight.

The next day, mix together in a sterile solution basin: 300 ul Lipofectamine (18324-012 Gibco/BRL) and 5ml Optimem I (31985070 Gibco/BRL)/96-well plate. With a small volume multi-channel pipetter, aliquot approximately 2ug of an expression vector containing a polynucleotide insert, produced by the methods described in Examples 8-10, into an appropriately labeled 96-well round bottom plate. With a multi-channel pipetter, add 50ul of the Lipofectamine/Optimem I mixture to each well. Pipette up and down gently to mix. Incubate at RT 15-45 minutes. After about 20 minutes, use a multi-channel pipetter to add 150ul Optimem I to each well. As a control, one plate of vector DNA lacking an insert should be transfected with each set of transfections.

Preferably, the transfection should be performed by tag-teaming the following tasks. By tag-teaming, hands on time is cut in half, and the cells do not spend too much time on

PBS. First, person A aspirates off the media from four 24-well plates of cells, and then person B rinses each well with .5-1ml PBS. Person A then aspirates off PBS rinse, and person B, using a12-channel pipetter with tips on every other channel, adds the 200ul of DNA/Lipofectamine/Optimem I complex to the odd wells first, then to the even wells, to each row on the 24-well plates. Incubate at 37 degree C for 6 hours.

While cells are incubating, prepare appropriate media, either 1%BSA in DMEM with 1x penstrep, or HGS CHO-5 media (116.6 mg/L of CaCl2 (anhyd); 0.00130 mg/L $CuSO_4$-$5H_2O$; 0.050 mg/L of $Fe(NO_3)_3$-$9H_2O$; 0.417 mg/L of $FeSO_4$-$7H_2O$; 311.80 mg/L of Kcl; 28.64 mg/L of $MgCl_2$; 48.84 mg/L of $MgSO_4$; 6995.50 mg/L of NaCl; 2400.0 mg/L of $NaHCO_3$; 62.50 mg/L of NaH_2PO_4-H_20; 71.02 mg/L of Na_2HPO4; .4320 mg/L of $ZnSO_4$-$7H_2O$; .002 mg/L of Arachidonic Acid ; 1.022 mg/L of Cholesterol; .070 mg/L of DL-alpha-Tocopherol-Acetate; 0.0520 mg/L of Linoleic Acid; 0.010 mg/L of Linolenic Acid; 0.010 mg/L of Myristic Acid; 0.010 mg/L of Oleic Acid; 0.010 mg/L of Palmitric Acid; 0.010 mg/L of Palmitic Acid; 100 mg/L of Pluronic F-68; 0.010 mg/L of Stearic Acid; 2.20 mg/L of Tween 80; 4551 mg/L of D-Glucose; 130.85 mg/ml of L- Alanine; 147.50 mg/ml of L-Arginine-HCL; 7.50 mg/ml of L-Asparagine-H_20; 6.65 mg/ml of L-Aspartic Acid; 29.56 mg/ml of L-Cystine-2HCL-H_20; 31.29 mg/ml of L-Cystine-2HCL; 7.35 mg/ml of L-Glutamic Acid; 365.0 mg/ml of L-Glutamine; 18.75 mg/ml of Glycine; 52.48 mg/ml of L-Histidine-HCL-H_20; 106.97 mg/ml of L-Isoleucine; 111.45 mg/ml of L-Leucine; 163.75 mg/ml of L-Lysine HCL; 32.34 mg/ml of L-Methionine; 68.48 mg/ml of L-Phenylalainine; 40.0 mg/ml of L-Proline; 26.25 mg/ml of L-Serine; 101.05 mg/ml of L-Threonine; 19.22 mg/ml of L-Tryptophan; 91.79 mg/ml of L-Tryrosine-2Na-$2H_20$; and 99.65 mg/ml of L-Valine; 0.0035 mg/L of Biotin; 3.24 mg/L of D-Ca Pantothenate; 11.78 mg/L of Choline Chloride; 4.65 mg/L of Folic Acid; 15.60 mg/L of i-Inositol; 3.02 mg/L of Niacinamide; 3.00 mg/L of Pyridoxal HCL; 0.031 mg/L of Pyridoxine HCL; 0.319 mg/L of Riboflavin; 3.17 mg/L of Thiamine HCL; 0.365 mg/L of Thymidine; 0.680 mg/L of Vitamin B_{12}; 25 mM of HEPES Buffer; 2.39 mg/L of Na Hypoxanthine; 0.105 mg/L of Lipoic Acid; 0.081 mg/L of Sodium Putrescine-2HCL; 55.0 mg/L of Sodium Pyruvate; 0.0067 mg/L of Sodium Selenite; 20uM of Ethanolamine; 0.122 mg/L of Ferric Citrate; 41.70 mg/L of Methyl-B-Cyclodextrin complexed with Linoleic Acid; 33.33 mg/L of Methyl-B-Cyclodextrin complexed with Oleic Acid; 10 mg/L of Methyl-B-Cyclodextrin complexed with Retinal Acetate. Adjust

osmolarity to 327 mOsm) with 2mm glutamine and 1x penstrep. (BSA (81-068-3 Bayer) 100gm dissolved in 1L DMEM for a 10% BSA stock solution). Filter the media and collect 50 ul for endotoxin assay in 15ml polystyrene conical.

The transfection reaction is terminated, preferably by tag-teaming, at the end of the incubation period. Person A aspirates off the transfection media, while person B adds 1.5ml appropriate media to each well. Incubate at 37 degree C for 45 or 72 hours depending on the media used: 1%BSA for 45 hours or CHO-5 for 72 hours.

On day four, using a 300ul multichannel pipetter, aliquot 600ul in one 1ml deep well plate and the remaining supernatant into a 2ml deep well. The supernatants from each well can then be used in the assays described in Examples 33-40.

It is specifically understood that when activity is obtained in any of the assays described below using a supernatant, the activity originates from either the polypeptide of the present invention directly (e.g., as a secreted protein) or by polypeptide of the present invention inducing expression of other proteins, which are then secreted into the supernatant. Thus, the invention further provides a method of identifying the protein in the supernatant characterized by an activity in a particular assay.

Example 32: Construction of GAS Reporter Construct

One signal transduction pathway involved in the differentiation and proliferation of cells is called the Jaks-STATs pathway. Activated proteins in the Jaks-STATs pathway bind to gamma activation site "GAS" elements or interferon-sensitive responsive element ("ISRE"), located in the promoter of many genes. The binding of a protein to these elements alter the expression of the associated gene.

GAS and ISRE elements are recognized by a class of transcription factors called Signal Transducers and Activators of Transcription, or "STATs." There are six members of the STATs family. Stat1 and Stat3 are present in many cell types, as is Stat2 (as response to IFN-alpha is widespread). Stat4 is more restricted and is not in many cell types though it has been found in T helper class I, cells after treatment with IL-12. Stat5 was originally called mammary growth factor, but has been found at higher concentrations in other cells including myeloid cells. It can be activated in tissue culture cells by many cytokines.

The STATs are activated to translocate from the cytoplasm to the nucleus upon

tyrosine phosphorylation by a set of kinases known as the Janus Kinase ("Jaks") family. Jaks represent a distinct family of soluble tyrosine kinases and include Tyk2, Jak1, Jak2, and Jak3. These kinases display significant sequence similarity and are generally catalytically inactive in resting cells.

The Jaks are activated by a wide range of receptors summarized in the Table below. (Adapted from review by Schidler and Darnell, Ann. Rev. Biochem. 64:621-51 (1995).) A cytokine receptor family, capable of activating Jaks, is divided into two groups: (a) Class 1 includes receptors for IL-2, IL-3, IL-4, IL-6, IL-7, IL-9, IL-11, IL-12, IL-15, Epo, PRL, GH, G-CSF, GM-CSF, LIF, CNTF, and thrombopoietin; and (b) Class 2 includes IFN-a, IFN-g, and IL-10. The Class 1 receptors share a conserved cysteine motif (a set of four conserved cysteines and one tryptophan) and a WSXWS motif (a membrane proximal region encoding Trp-Ser-Xxx-Trp-Ser (SEQ ID NO:1686)).

Thus, on binding of a ligand to a receptor, Jaks are activated, which in turn activate STATs, which then translocate and bind to GAS elements. This entire process is encompassed in the Jaks-STATs signal transduction pathway.

Therefore, activation of the Jaks-STATs pathway, reflected by the binding of the GAS or the ISRE element, can be used to indicate proteins involved in the proliferation and differentiation of cells. For example, growth factors and cytokines are known to activate the Jaks-STATs pathway. (See Table below.) Thus, by using GAS elements linked to reporter molecules, activators of the Jaks-STATs pathway can be identified.

Ligand	tyk2	Jak1	Jak2	Jak3	STATS	GAS(elements) or ISRE
		JAKs				
IFN family						
IFN-a/B	+	+	-	-	1,2,3	ISRE
IFN-g		+	+	-	1	GAS
(IRF1>Lys6>IFP)						
Il-10	+	?	?	-	1,3	
gp130 family						
IL-6 (Pleiotrohic)	+	+	+	?	1,3	GAS
(IRF1>Lys6>IFP)						
Il-11(Pleiotrohic)	?	+	?	?	1,3	
OnM(Pleiotrohic)	?	+	+	?	1,3	
LIF(Pleiotrohic)	?	+	+	?	1,3	
CNTF(Pleiotrohic)	-/+	+	+	?	1,3	
G-CSF(Pleiotrohic)	?	+	?	?	1,3	
IL-12(Pleiotrohic)	+	-	+	+	1,3	
g-C family						
IL-2 (lymphocytes)	-	+	-	+	1,3,5	GAS
IL-4 (lymph/myeloid)	-	+	-	+	6	GAS (IRF1 = IFP
>>Ly6)(IgH)						
IL-7 (lymphocytes)	-	+	-	+	5	GAS
IL-9 (lymphocytes)	-	+	-	+	5	GAS
IL-13 (lymphocyte)	-	+	?	?	6	GAS
IL-15	?	+	?	+	5	GAS
gp140 family						
IL-3 (myeloid)	-	-	+	-	5	GAS
(IRF1>IFP>>Ly6)						
IL-5 (myeloid)	-	-	+	-	5	GAS
GM-CSF (myeloid)	-	-	+	-	5	GAS

<u>Growth hormone family</u>						
GH	?	-	+	-	5	
PRL	?	+/-	+	-	1,3,5	
EPO	?	-	+	-	5	GAS(B-CAS>IRF1=IFP>>Ly6)
<u>Receptor Tyrosine Kinases</u>						
EGF	?	+	+	-	1,3	GAS (IRF1)
PDGF	?	+	+	-	1,3	
CSF-1	?	+	+	-	1,3	GAS (not IRF1)

To construct a synthetic GAS containing promoter element, which is used in the Biological Assays described in Examples 33-34, a PCR based strategy is employed to generate a GAS-SV40 promoter sequence. The 5' primer contains four tandem copies of the GAS binding site found in the IRF1 promoter and previously demonstrated to bind STATs upon induction with a range of cytokines (Rothman et al., Immunity 1:457-468 (1994).), although other GAS or ISRE elements can be used instead. The 5' primer also contains 18bp of sequence complementary to the SV40 early promoter sequence and is flanked with an XhoI site. The sequence of the 5' primer is:

5':GCGCCTCGAGATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCC GAAATGATTTCCCCGAAATATCTGCCATCTCAATTAG:3' (SEQ ID NO:1687)

The downstream primer is complementary to the SV40 promoter and is flanked with a Hind III site: 5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:1688)

PCR amplification is performed using the SV40 promoter template present in the B-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is digested with XhoI/Hind III and subcloned into BLSK2-. (Stratagene.) Sequencing with forward and reverse primers confirms that the insert contains the following sequence:

5':<u>CTCGAG</u>ATTTCCCCGAAATCTAGATTTCCCCGAAATGATTTCCCCGAAA TGATTTCCCCGAAATATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCG CCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCT CCGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCC TCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTA GGCTTTTGCAAA<u>AAGCTT</u>:3' (SEQ ID NO:1689)

With this GAS promoter element linked to the SV40 promoter, a GAS:SEAP2 reporter construct is next engineered. Here, the reporter molecule is a secreted alkaline phosphatase, or "SEAP." Clearly, however, any reporter molecule can be instead of SEAP, in this or in any of the other Examples. Well known reporter molecules that can be used instead of SEAP include chloramphenicol

acetyltransferase (CAT), luciferase, alkaline phosphatase, B-galactosidase, green fluorescent protein (GFP), or any protein detectable by an antibody.

The above sequence confirmed synthetic GAS-SV40 promoter element is subcloned into the pSEAP-Promoter vector obtained from Clontech using HindIII and XhoI, effectively replacing the SV40 promoter with the amplified GAS:SV40 promoter element, to create the GAS-SEAP vector. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

Thus, in order to generate mammalian stable cell lines expressing the GAS-SEAP reporter, the GAS-SEAP cassette is removed from the GAS-SEAP vector using SalI and NotI, and inserted into a backbone vector containing the neomycin resistance gene, such as pGFP-1 (Clontech), using these restriction sites in the multiple cloning site, to create the GAS-SEAP/Neo vector. Once this vector is transfected into mammalian cells, this vector can then be used as a reporter molecule for GAS binding as described in Examples 33-34.

Other constructs can be made using the above description and replacing GAS with a different promoter sequence. For example, construction of reporter molecules containing NFK-B and EGR promoter sequences are described in Examples 35 and 36. However, many other promoters can be substituted using the protocols described in these Examples. For instance, SRE, IL-2, NFAT, or Osteocalcin promoters can be substituted, alone or in combination (e.g., GAS/NF-KB/EGR, GAS/NF-KB, Il-2/NFAT, or NF-KB/GAS). Similarly, other cell lines can be used to test reporter construct activity, such as HELA (epithelial), HUVEC (endothelial), Reh (B-cell), Saos-2 (osteoblast), HUVAC (aortic), or Cardiomyocyte.

Example 33: High-Throughput Screening Assay for T-cell Activity.

The following protocol is used to assess T-cell activity by identifying factors, and determining whether supernate containing a polypeptide of the invention proliferates and/or differentiates T-cells. T-cell activity is assessed using the

GAS/SEAP/Neo construct produced in Example 32. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The T-cell used in this assay is Jurkat T-cells (ATCC Accession No. TIB-152), although Molt-3 cells (ATCC Accession No. CRL-1552) and Molt-4 cells (ATCC Accession No. CRL-1582) cells can also be used.

Jurkat T-cells are lymphoblastic CD4+ Th1 helper cells. In order to generate stable cell lines, approximately 2 million Jurkat cells are transfected with the GAS-SEAP/neo vector using DMRIE-C (Life Technologies)(transfection procedure described below). The transfected cells are seeded to a density of approximately 20,000 cells per well and transfectants resistant to 1 mg/ml genticin selected. Resistant colonies are expanded and then tested for their response to increasing concentrations of interferon gamma. The dose response of a selected clone is demonstrated.

Specifically, the following protocol will yield sufficient cells for 75 wells containing 200 ul of cells. Thus, it is either scaled up, or performed in multiple to generate sufficient cells for multiple 96 well plates. Jurkat cells are maintained in RPMI + 10% serum with 1%Pen-Strep. Combine 2.5 mls of OPTI-MEM (Life Technologies) with 10 ug of plasmid DNA in a T25 flask. Add 2.5 ml OPTI-MEM containing 50 ul of DMRIE-C and incubate at room temperature for 15-45 mins.

During the incubation period, count cell concentration, spin down the required number of cells (10^7 per transfection), and resuspend in OPTI-MEM to a final concentration of 10^7 cells/ml. Then add 1ml of 1 x 10^7 cells in OPTI-MEM to T25 flask and incubate at 37 degree C for 6 hrs. After the incubation, add 10 ml of RPMI + 15% serum.

The Jurkat:GAS-SEAP stable reporter lines are maintained in RPMI + 10% serum, 1 mg/ml Genticin, and 1% Pen-Strep. These cells are treated with supernatants containing polypeptide of the present invention or polypeptide of the present invention induced polypeptides as produced by the protocol described in Example 31.

On the day of treatment with the supernatant, the cells should be washed and

resuspended in fresh RPMI + 10% serum to a density of 500,000 cells per ml. The exact number of cells required will depend on the number of supernatants being screened. For one 96 well plate, approximately 10 million cells (for 10 plates, 100 million cells) are required.

Transfer the cells to a triangular reservoir boat, in order to dispense the cells into a 96 well dish, using a 12 channel pipette. Using a 12 channel pipette, transfer 200 ul of cells into each well (therefore adding 100, 000 cells per well).

After all the plates have been seeded, 50 ul of the supernatants are transferred directly from the 96 well plate containing the supernatants into each well using a 12 channel pipette. In addition, a dose of exogenous interferon gamma (0.1, 1.0, 10 ng) is added to wells H9, H10, and H11 to serve as additional positive controls for the assay.

The 96 well dishes containing Jurkat cells treated with supernatants are placed in an incubator for 48 hrs (note: this time is variable between 48-72 hrs). 35 ul samples from each well are then transferred to an opaque 96 well plate using a 12 channel pipette. The opaque plates should be covered (using sellophene covers) and stored at -20 degree C until SEAP assays are performed according to Example 37. The plates containing the remaining treated cells are placed at 4 degree C and serve as a source of material for repeating the assay on a specific well if desired.

As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate Jurkat T cells. Over 30 fold induction is typically observed in the positive control wells.

The above protocol may be used in the generation of both transient, as well as, stable transfected cells, which would be apparent to those of skill in the art.

Example 34: High-Throughput Screening Assay Identifying Myeloid Activity

The following protocol is used to assess myeloid activity of polypeptide of the present invention by determining whether polypeptide of the present invention proliferates and/or differentiates myeloid cells. Myeloid cell activity is assessed using

the GAS/SEAP/Neo construct produced in Example 32. Thus, factors that increase SEAP activity indicate the ability to activate the Jaks-STATS signal transduction pathway. The myeloid cell used in this assay is U937, a pre-monocyte cell line, although TF-1, HL60, or KG1 can be used.

To transiently transfect U937 cells with the GAS/SEAP/Neo construct produced in Example 32, a DEAE-Dextran method (Kharbanda et. al., 1994, Cell Growth & Differentiation, 5:259-265) is used. First, harvest 2x10e^7 U937 cells and wash with PBS. The U937 cells are usually grown in RPMI 1640 medium containing 10% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 mg/ml streptomycin.

Next, suspend the cells in 1 ml of 20 mM Tris-HCl (pH 7.4) buffer containing 0.5 mg/ml DEAE-Dextran, 8 ug GAS-SEAP2 plasmid DNA, 140 mM NaCl, 5 mM KCl, 375 uM $Na_2HPO_4.7H_2O$, 1 mM $MgCl_2$, and 675 uM $CaCl_2$. Incubate at 37 degrees C for 45 min.

Wash the cells with RPMI 1640 medium containing 10% FBS and then resuspend in 10 ml complete medium and incubate at 37 degree C for 36 hr.

The GAS-SEAP/U937 stable cells are obtained by growing the cells in 400 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 400 ug/ml G418 for couple of passages.

These cells are tested by harvesting $1x10^8$ cells (this is enough for ten 96-well plates assay) and wash with PBS. Suspend the cells in 200 ml above described growth medium, with a final density of $5x10^5$ cells/ml. Plate 200 ul cells per well in the 96-well plate (or $1x10^5$ cells/well).

Add 50 ul of the supernatant prepared by the protocol described in Example 31. Incubate at 37 degee C for 48 to 72 hr. As a positive control, 100 Unit/ml interferon gamma can be used which is known to activate U937 cells. Over 30 fold induction is typically observed in the positive control wells. SEAP assay the supernatant according to the protocol described in Example 37.

Example 35: High-Throughput Screening Assay Identifying Neuronal Activity.

When cells undergo differentiation and proliferation, a group of genes are activated through many different signal transduction pathways. One of these genes, EGR1 (early growth response gene 1), is induced in various tissues and cell types upon activation. The promoter of EGR1 is responsible for such induction. Using the EGR1 promoter linked to reporter molecules, activation of cells can be assessed by polypeptide of the present invention.

Particularly, the following protocol is used to assess neuronal activity in PC12 cell lines. PC12 cells (rat phenochromocytoma cells) are known to proliferate and/or differentiate by activation with a number of mitogens, such as TPA (tetradecanoyl phorbol acetate), NGF (nerve growth factor), and EGF (epidermal growth factor). The EGR1 gene expression is activated during this treatment. Thus, by stably transfecting PC12 cells with a construct containing an EGR promoter linked to SEAP reporter, activation of PC12 cells by polypeptide of the present invention can be assessed.

The EGR/SEAP reporter construct can be assembled by the following protocol. The EGR-1 promoter sequence (-633 to +1)(Sakamoto K et al., Oncogene 6:867-871 (1991)) can be PCR amplified from human genomic DNA using the following primers:

5' GCGCTCGAGGGATGACAGCGATAGAACCCCGG -3' (SEQ ID NO: 1690)

5' GCGAAGCTTCGCGACTCCCCGGATCCGCCTC-3' (SEQ ID NO: 1691)

Using the GAS:SEAP/Neo vector produced in Example 32, EGR1 amplified product can then be inserted into this vector. Linearize the GAS:SEAP/Neo vector using restriction enzymes XhoI/HindIII, removing the GAS/SV40 stuffer. Restrict the EGR1 amplified product with these same enzymes. Ligate the vector and the EGR1 promoter.

To prepare 96 well-plates for cell culture, two mls of a coating solution (1:30 dilution of collagen type I (Upstate Biotech Inc. Cat#08-115) in 30% ethanol (filter

sterilized)) is added per one 10 cm plate or 50 ml per well of the 96-well plate, and allowed to air dry for 2 hr.

PC12 cells are routinely grown in RPMI-1640 medium (Bio Whittaker) containing 10% horse serum (JRH BIOSCIENCES, Cat. # 12449-78P), 5% heat-inactivated fetal bovine serum (FBS) supplemented with 100 units/ml penicillin and 100 ug/ml streptomycin on a precoated 10 cm tissue culture dish. One to four split is done every three to four days. Cells are removed from the plates by scraping and resuspended with pipetting up and down for more than 15 times.

Transfect the EGR/SEAP/Neo construct into PC12 using the Lipofectamine protocol described in Example 31. EGR-SEAP/PC12 stable cells are obtained by growing the cells in 300 ug/ml G418. The G418-free medium is used for routine growth but every one to two months, the cells should be re-grown in 300 ug/ml G418 for couple of passages.

To assay for neuronal activity, a 10 cm plate with cells around 70 to 80% confluent is screened by removing the old medium. Wash the cells once with PBS (Phosphate buffered saline). Then starve the cells in low serum medium (RPMI-1640 containing 1% horse serum and 0.5% FBS with antibiotics) overnight.

The next morning, remove the medium and wash the cells with PBS. Scrape off the cells from the plate, suspend the cells well in 2 ml low serum medium. Count the cell number and add more low serum medium to reach final cell density as $5x10^5$ cells/ml.

Add 200 ul of the cell suspension to each well of 96-well plate (equivalent to $1x10^5$ cells/well). Add 50 ul supernatant produced by Example 31, 37 degree C for 48 to 72 hr. As a positive control, a growth factor known to activate PC12 cells through EGR can be used, such as 50 ng/ul of Neuronal Growth Factor (NGF). Over fifty-fold induction of SEAP is typically seen in the positive control wells. SEAP assay the supernatant according to Example 37.

Example 36: High-Throughput Screening Assay for T-cell Activity

NF-KB (Nuclear Factor KB) is a transcription factor activated by a wide variety of agents including the inflammatory cytokines IL-1 and TNF, CD30 and CD40, lymphotoxin-alpha and lymphotoxin-beta, by exposure to LPS or thrombin, and by expression of certain viral gene products. As a transcription factor, NF-KB regulates the expression of genes involved in immune cell activation, control of apoptosis (NF- KB appears to shield cells from apoptosis), B and T-cell development, anti-viral and antimicrobial responses, and multiple stress responses.

In non-stimulated conditions, NF- KB is retained in the cytoplasm with I-KB (Inhibitor KB). However, upon stimulation, I- KB is phosphorylated and degraded, causing NF- KB to shuttle to the nucleus, thereby activating transcription of target genes. Target genes activated by NF- KB include IL-2, IL-6, GM-CSF, ICAM-1 and class 1 MHC.

Due to its central role and ability to respond to a range of stimuli, reporter constructs utilizing the NF-KB promoter element are used to screen the supernatants produced in Example 31. Activators or inhibitors of NF-KB would be useful in treating, preventing, and/or diagnosing diseases. For example, inhibitors of NF-KB could be used to treat those diseases related to the acute or chronic activation of NF-KB, such as rheumatoid arthritis.

To construct a vector containing the NF-KB promoter element, a PCR based strategy is employed. The upstream primer contains four tandem copies of the NF-KB binding site (GGGGACTTTCCC) (SEQ ID NO:1692), 18 bp of sequence complementary to the 5' end of the SV40 early promoter sequence, and is flanked with an XhoI site:

5':GCGGCCTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGAC TTTCCATCCTGCCATCTCAATTAG:3' (SEQ ID NO:1693)

The downstream primer is complementary to the 3' end of the SV40 promoter and is flanked with a Hind III site:

5':GCGGCAAGCTTTTTGCAAAGCCTAGGC:3' (SEQ ID NO:1688)

PCR amplification is performed using the SV40 promoter template present in the pB-gal:promoter plasmid obtained from Clontech. The resulting PCR fragment is

digested with XhoI and Hind III and subcloned into BLSK2-. (Stratagene) Sequencing with the T7 and T3 primers confirms the insert contains the following sequence:

5':CTCGAGGGGACTTTCCCGGGGACTTTCCGGGGACTTTCCGGGACTTTCC
ATCTGCCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCC
ATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGA
CTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTA
TTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAAA
GCTT:3' (SEQ ID NO:1694)

Next, replace the SV40 minimal promoter element present in the pSEAP2-promoter plasmid (Clontech) with this NF-KB/SV40 fragment using XhoI and HindIII. However, this vector does not contain a neomycin resistance gene, and therefore, is not preferred for mammalian expression systems.

In order to generate stable mammalian cell lines, the NF-KB/SV40/SEAP cassette is removed from the above NF-KB/SEAP vector using restriction enzymes SalI and NotI, and inserted into a vector containing neomycin resistance. Particularly, the NF-KB/SV40/SEAP cassette was inserted into pGFP-1 (Clontech), replacing the GFP gene, after restricting pGFP-1 with SalI and NotI.

Once NF-KB/SV40/SEAP/Neo vector is created, stable Jurkat T-cells are created and maintained according to the protocol described in Example 33. Similarly, the method for assaying supernatants with these stable Jurkat T-cells is also described in Example 33. As a positive control, exogenous TNF alpha (0.1,1, 10 ng) is added to wells H9, H10, and H11, with a 5-10 fold activation typically observed.

Example 37: Assay for SEAP Activity

As a reporter molecule for the assays described in Examples 33-36, SEAP activity is assayed using the Tropix Phospho-light Kit (Cat. BP-400) according to the following general procedure. The Tropix Phospho-light Kit supplies the Dilution, Assay, and Reaction Buffers used below.

Prime a dispenser with the 2.5x Dilution Buffer and dispense 15 ul of 2.5x dilution buffer into Optiplates containing 35 ul of a supernatant. Seal the plates with a plastic sealer and incubate at 65 degree C for 30 min. Separate the Optiplates to avoid uneven heating.

Cool the samples to room temperature for 15 minutes. Empty the dispenser and prime with the Assay Buffer. Add 50 ml Assay Buffer and incubate at room temperature 5 min. Empty the dispenser and prime with the Reaction Buffer (see the table below).. Add 50 ul Reaction Buffer and incubate at room temperature for 20 minutes. Since the intensity of the chemiluminescent signal is time dependent, and it takes about 10 minutes to read 5 plates on luminometer, one should treat 5 plates at each time and start the second set 10 minutes later.

Read the relative light unit in the luminometer. Set H12 as blank, and print the results. An increase in chemiluminescence indicates reporter activity.

Reaction Buffer Formulation:

# of plates	Rxn buffer diluent (ml)	CSPD (ml)
10	60	3
11	65	3.25
12	70	3.5
13	75	3.75
14	80	4
15	85	4.25
16	90	4.5
17	95	4.75
18	100	5
19	105	5.25
20	110	5.5
21	115	5.75
22	120	6

23	125	6.25
24	130	6.5
25	135	6.75
26	140	7
27	145	7.25
28	150	7.5
29	155	7.75
30	160	8
31	165	8.25
32	170	8.5
33	175	8.75
34	180	9
35	185	9.25
36	190	9.5
37	195	9.75
38	200	10
39	205	10.25
40	210	10.5
41	215	10.75
42	220	11
43	225	11.25
44	230	11.5
45	235	11.75
46	240	12
47	245	12.25
48	250	12.5
49	255	12.75
50	260	13

Example 38: High-Throughput Screening Assay Identifying Changes in Small

Molecule Concentration and Membrane Permeability

Binding of a ligand to a receptor is known to alter intracellular levels of small molecules. such as calcium, potassium, sodium, and pH, as well as alter membrane potential. These alterations can be measured in an assay to identify supernatants which bind to receptors of a particular cell. Although the following protocol describes an assay for calcium, this protocol can easily be modified to detect changes in potassium, sodium, pH, membrane potential, or any other small molecule which is detectable by a fluorescent probe.

The following assay uses Fluorometric Imaging Plate Reader ("FLIPR") to measure changes in fluorescent molecules (Molecular Probes) that bind small molecules. Clearly, any fluorescent molecule detecting a small molecule can be used instead of the calcium fluorescent molecule, fluo-4 (Molecular Probes, Inc.; catalog no. F-14202), used here.

For adherent cells, seed the cells at 10,000 -20,000 cells/well in a Co-star black 96-well plate with clear bottom. The plate is incubated in a CO_2 incubator for 20 hours. The adherent cells are washed two times in Biotek washer with 200 ul of HBSS (Hank's Balanced Salt Solution) leaving 100 ul of buffer after the final wash.

A stock solution of 1 mg/ml fluo-4 is made in 10% pluronic acid DMSO. To load the cells with fluo-4 , 50 ul of 12 ug/ml fluo-4 is added to each well. The plate is incubated at 37 degrees C in a CO_2 incubator for 60 min. The plate is washed four times in the Biotek washer with HBSS leaving 100 ul of buffer.

For non-adherent cells, the cells are spun down from culture media. Cells are re-suspended to 2-5x10^6 cells/ml with HBSS in a 50-ml conical tube. 4 ul of 1 mg/ml fluo-4 solution in 10% pluronic acid DMSO is added to each ml of cell suspension. The tube is then placed in a 37 degrees C water bath for 30-60 min. The cells are washed twice with HBSS, resuspended to 1x10^6 cells/ml, and dispensed into a microplate. 100 ul/well. The plate is centrifuged at 1000 rpm for 5 min. The plate is then washed once in Denley Cell Wash with 200 ul, followed by an aspiration step to 100 ul final volume.

For a non-cell based assay, each well contains a fluorescent molecule, such as fluo-4 . The supernatant is added to the well, and a change in fluorescence is detected.

To measure the fluorescence of intracellular calcium, the FLIPR is set for the following parameters: (1) System gain is 300-800 mW; (2) Exposure time is 0.4 second; (3) Camera F/stop is F/2; (4) Excitation is 488 nm; (5) Emission is 530 nm; and (6) Sample addition is 50 ul. Increased emission at 530 nm indicates an extracellular signaling event caused by the a molecule, either polypeptide of the present invention or a molecule induced by polypeptide of the present invention, which has resulted in an increase in the intracellular Ca^{++} concentration.

Example 40: High-Throughput Screening Assay Identifying Tyrosine Kinase Activity

The Protein Tyrosine Kinases (PTK) represent a diverse group of transmembrane and cytoplasmic kinases. Within the Receptor Protein Tyrosine Kinase RPTK) group are receptors for a range of mitogenic and metabolic growth factors including the PDGF, FGF, EGF, NGF, HGF and Insulin receptor subfamilies. In addition there are a large family of RPTKs for which the corresponding ligand is unknown. Ligands for RPTKs include mainly secreted small proteins, but also membrane-bound and extracellular matrix proteins.

Activation of RPTK by ligands involves ligand-mediated receptor dimerization, resulting in transphosphorylation of the receptor subunits and activation of the cytoplasmic tyrosine kinases. The cytoplasmic tyrosine kinases include receptor associated tyrosine kinases of the src-family (e.g., src, yes, lck, lyn, fyn) and non-receptor linked and cytosolic protein tyrosine kinases, such as the Jak family, members of which mediate signal transduction triggered by the cytokine superfamily of receptors (e.g., the Interleukins, Interferons, GM-CSF, and Leptin).

Because of the wide range of known factors capable of stimulating tyrosine kinase activity, identifying whether polypeptide of the present invention or a molecule induced by polypeptide of the present invention is capable of activating tyrosine

kinase signal transduction pathways is of interest. Therefore, the following protocol is designed to identify such molecules capable of activating the tyrosine kinase signal transduction pathways.

Seed target cells (e.g., primary keratinocytes) at a density of approximately 25,000 cells per well in a 96 well Loprodyne Silent Screen Plates purchased from Nalge Nunc (Naperville, IL). The plates are sterilized with two 30 minute rinses with 100% ethanol, rinsed with water and dried overnight. Some plates are coated for 2 hr with 100 ml of cell culture grade type I collagen (50 mg/ml), gelatin (2%) or polylysine (50 mg/ml), all of which can be purchased from Sigma Chemicals (St. Louis, MO) or 10% Matrigel purchased from Becton Dickinson (Bedford,MA), or calf serum, rinsed with PBS and stored at 4 degree C. Cell growth on these plates is assayed by seeding 5,000 cells/well in growth medium and indirect quantitation of cell number through use of alamarBlue as described by the manufacturer Alamar Biosciences, Inc. (Sacramento, CA) after 48 hr. Falcon plate covers #3071 from Becton Dickinson (Bedford,MA) are used to cover the Loprodyne Silent Screen Plates. Falcon Microtest III cell culture plates can also be used in some proliferation experiments.

To prepare extracts, A431 cells are seeded onto the nylon membranes of Loprodyne plates (20,000/200ml/well) and cultured overnight in complete medium. Cells are quiesced by incubation in serum-free basal medium for 24 hr. After 5-20 minutes treatment with EGF (60ng/ml) or 50 ul of the supernatant produced in Example 31, the medium was removed and 100 ml of extraction buffer ((20 mM HEPES pH 7.5, 0.15 M NaCl, 1% Triton X-100, 0.1% SDS, 2 mM $Na3VO4$, 2 mM $Na4P2O7$ and a cocktail of protease inhibitors (# 1836170) obtained from Boeheringer Mannheim (Indianapolis, IN) is added to each well and the plate is shaken on a rotating shaker for 5 minutes at $4^{o}C$. The plate is then placed in a vacuum transfer manifold and the extract filtered through the 0.45 mm membrane bottoms of each well using house vacuum. Extracts are collected in a 96-well catch/assay plate in the bottom of the vacuum manifold and immediately placed on ice. To obtain extracts clarified by centrifugation, the content of each well, after

detergent solubilization for 5 minutes, is removed and centrifuged for 15 minutes at 4 degree C at 16,000 x g.

Test the filtered extracts for levels of tyrosine kinase activity. Although many methods of detecting tyrosine kinase activity are known, one method is described here.

Generally, the tyrosine kinase activity of a supernatant is evaluated by determining its ability to phosphorylate a tyrosine residue on a specific substrate (a biotinylated peptide). Biotinylated peptides that can be used for this purpose include PSK1 (corresponding to amino acids 6-20 of the cell division kinase cdc2-p34) and PSK2 (corresponding to amino acids 1-17 of gastrin). Both peptides are substrates for a range of tyrosine kinases and are available from Boehringer Mannheim.

The tyrosine kinase reaction is set up by adding the following components in order. First, add 10ul of 5uM Biotinylated Peptide, then 10ul ATP/Mg_{2+} (5mM ATP/50mM $MgCl_2$), then 10ul of 5x Assay Buffer (40mM imidazole hydrochloride, pH7.3, 40 mM beta-glycerophosphate, 1mM EGTA, 100mM $MgCl_2$, 5 mM $MnCl_2$, 0.5 mg/ml BSA), then 5ul of Sodium Vanadate(1mM), and then 5ul of water. Mix the components gently and preincubate the reaction mix at 30 degree C for 2 min. Initial the reaction by adding 10ul of the control enzyme or the filtered supernatant.

The tyrosine kinase assay reaction is then terminated by adding 10 ul of 120mm EDTA and place the reactions on ice.

Tyrosine kinase activity is determined by transferring 50 ul aliquot of reaction mixture to a microtiter plate (MTP) module and incubating at 37 degree C for 20 min. This allows the streptavadin coated 96 well plate to associate with the biotinylated peptide. Wash the MTP module with 300ul/well of PBS four times. Next add 75 ul of anti-phospotyrosine antibody conjugated to horse radish peroxidase(anti-P-Tyr-POD(0.5u/ml)) to each well and incubate at 37 degree C for one hour. Wash the well as above.

Next add 100ul of peroxidase substrate solution (Boehringer Mannheim) and incubate at room temperature for at least 5 mins (up to 30 min). Measure the absorbance of the sample at 405 nm by using ELISA reader. The level of bound

peroxidase activity is quantitated using an ELISA reader and reflects the level of tyrosine kinase activity.

Example 41: High-Throughput Screening Assay Identifying Phosphorylation Activity

As a potential alternative and/or compliment to the assay of protein tyrosine kinase activity described in Example 40, an assay which detects activation (phosphorylation) of major intracellular signal transduction intermediates can also be used. For example, as described below one particular assay can detect tyrosine phosphorylation of the Erk-1 and Erk-2 kinases. However, phosphorylation of other molecules, such as Raf, JNK, p38 MAP, Map kinase kinase (MEK), MEK kinase, Src, Muscle specific kinase (MuSK), IRAK, Tec, and Janus, as well as any other phosphoserine, phosphotyrosine, or phosphothreonine molecule, can be detected by substituting these molecules for Erk-1 or Erk-2 in the following assay.

Specifically, assay plates are made by coating the wells of a 96-well ELISA plate with 0.1ml of protein G (1ug/ml) for 2 hr at room temp, (RT). The plates are then rinsed with PBS and blocked with 3% BSA/PBS for 1 hr at RT. The protein G plates are then treated with 2 commercial monoclonal antibodies (100ng/well) against Erk-1 and Erk-2 (1 hr at RT) (Santa Cruz Biotechnology). (To detect other molecules, this step can easily be modified by substituting a monoclonal antibody detecting any of the above described molecules.) After 3-5 rinses with PBS, the plates are stored at 4 degree C until use.

A431 cells are seeded at 20,000/well in a 96-well Loprodyne filterplate and cultured overnight in growth medium. The cells are then starved for 48 hr in basal medium (DMEM) and then treated with EGF (6ng/well) or 50 ul of the supernatants obtained in Example 31 for 5-20 minutes. The cells are then solubilized and extracts filtered directly into the assay plate.

After incubation with the extract for 1 hr at RT, the wells are again rinsed. As a positive control, a commercial preparation of MAP kinase (10ng/well) is used in place of A431 extract. Plates are then treated with a commercial polyclonal (rabbit)

antibody (1ug/ml) which specifically recognizes the phosphorylated epitope of the Erk-1 and Erk-2 kinases (1 hr at RT). This antibody is biotinylated by standard procedures. The bound polyclonal antibody is then quantitated by successive incubations with Europium-streptavidin and Europium fluorescence enhancing reagent in the Wallac DELFIA instrument (time-resolved fluorescence). An increased fluorescent signal over background indicates a phosphorylation by polypeptide of the present invention or a molecule induced by polypeptide of the present invention.

Example 42: Assay for the Stimulation of Bone Marrow CD34+ Cell Proliferation

This assay is based on the ability of human CD34+ to proliferate in the presence of hematopoietic growth factors and evaluates the ability of isolated polypeptides expressed in mammalian cells to stimulate proliferation of CD34+ cells.

It has been previously shown that most mature precursors will respond to only a single signal. More immature precursors require at least two signals to respond. Therefore, to test the effect of polypeptides on hematopoietic activity of a wide range of progenitor cells, the assay contains a given polypeptide in the presence or absence of other hematopoietic growth factors. Isolated cells are cultured for 5 days in the presence of Stem Cell Factor (SCF) in combination with tested sample. SCF alone has a very limited effect on the proliferation of bone marrow (BM) cells, acting in such conditions only as a "survival" factor. However, combined with any factor exhibiting stimulatory effect on these cells (e.g., IL-3), SCF will cause a synergistic effect. Therefore, if the tested polypeptide has a stimulatory effect on a hematopoietic progenitors, such activity can be easily detected. Since normal BM cells have a low level of cycling cells, it is likely that any inhibitory effect of a given polypeptide, or agonists or antagonists thereof, might not be detected. Accordingly, assays for an inhibitory effect on progenitors is preferably tested in cells that are first subjected to *in vitro* stimulation with SCF+IL+3, and then contacted with the compound that is being evaluated for inhibition of such induced proliferation.

Briefly, CD34+ cells are isolated using methods known in the art. The cells

are thawed and resuspended in medium (QBSF 60 serum-free medium with 1% L-glutamine (500ml) Quality Biological, Inc., Gaithersburg, MD Cat# 160-204-101). After several gentle centrifugation steps at 200 x g, cells are allowed to rest for one hour. The cell count is adjusted to 2.5 x 10^5 cells/ml. During this time, 100 μl of sterile water is added to the peripheral wells of a 96-well plate. The cytokines that can be tested with a given polypeptide in this assay is rhSCF (R&D Systems, Minneapolis, MN, Cat# 255-SC) at 50 ng/ml alone and in combination with rhSCF and rhIL-3 (R&D Systems, Minneapolis, MN, Cat# 203-ML) at 30 ng/ml. After one hour, 10 μl of prepared cytokines, 50 μl of the supernatants prepared in Example 31 (supernatants at 1:2 dilution = 50 μl) and 20 μl of diluted cells are added to the media which is already present in the wells to allow for a final total volume of 100 μl. The plates are then placed in a 37°C/5% CO_2 incubator for five days.

Eighteen hours before the assay is harvested, 0.5 μCi/well of [3H] Thymidine is added in a 10 μl volume to each well to determine the proliferation rate. The experiment is terminated by harvesting the cells from each 96-well plate to a filtermat using the Tomtec Harvester 96. After harvesting, the filtermats are dried, trimmed and placed into OmniFilter assemblies consisting of one OmniFilter plate and one OmniFilter Tray. 60 μl Microscint is added to each well and the plate sealed with TopSeal-A press-on sealing film A bar code 15 sticker is affixed to the first plate for counting. The sealed plates is then loaded and the level of radioactivity determined via the Packard Top Count and the printed data collected for analysis. The level of radioactivity reflects the amount of cell proliferation.

The studies described in this example test the activity of a given polypeptide to stimulate bone marrow CD34+ cell proliferation. One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof. As a nonlimiting example, potential antagonists tested in this assay would be expected to inhibit cell proliferation in the presence of cytokines and/or to increase the inhibition of cell proliferation in the presence of cytokines and a given polypeptide. In contrast, potential agonists tested in this assay would be expected to enhance cell

proliferation and/or to decrease the inhibition of cell proliferation in the presence of cytokines and a given polypeptide.

The ability of a gene to stimulate the proliferation of bone marrow CD34+ cells indicates that polynucleotides and polypeptides corresponding to the gene are useful for the diagnosis and treatment of disorders affecting the immune system and hematopoiesis. Representative uses are described in the "Immune Activity" and "Infectious Disease" sections above, and elsewhere herein.

Example 43: Assay for Extracellular Matrix Enhanced Cell Response (EMECR)

The objective of the Extracellular Matrix Enhanced Cell Response (EMECR) assay is to identify gene products (e.g., isolated polypeptides) that act on the hematopoietic stem cells in the context of the extracellular matrix (ECM) induced signal.

Cells respond to the regulatory factors in the context of signal(s) received from the surrounding microenvironment. For example, fibroblasts, and endothelial and epithelial stem cells fail to replicate in the absence of signals from the ECM. Hematopoietic stem cells can undergo self-renewal in the bone marrow, but not in *in vitro* suspension culture. The ability of stem cells to undergo self-renewal *in vitro* is dependent upon their interaction with the stromal cells and the ECM protein fibronectin (fn). Adhesion of cells to fn is mediated by the $\alpha_5.\beta_1$ and $\alpha_4.\beta_1$ integrin receptors, which are expressed by human and mouse hematopoietic stem cells. The factor(s) which integrate with the ECM environment and responsible for stimulating stem cell self-renewal has not yet been identified. Discovery of such factors should be of great interest in gene therapy and bone marrow transplant applications

Briefly, polystyrene, non tissue culture treated, 96-well plates are coated with fn fragment at a coating concentration of 0.2 $\mu g/cm^2$. Mouse bone marrow cells are plated (1,000 cells/well) in 0.2 ml of serum-free medium. Cells cultured in the presence of IL-3 (5 ng/ml) + SCF (50 ng/ml) would serve as the positive control,

conditions under which little self-renewal but pronounced differentiation of the stem cells is to be expected. Gene products of the invention (e.g., including, but not limited to, polynucleotides and polypeptides of the present invention, and supernatants produced in Example 31), are tested with appropriate negative controls in the presence and absence of SCF(5.0 ng/ml), where test factor supernates represent 10% of the total assay volume. The plated cells are then allowed to grow by incubating in a low oxygen environment (5% CO_2, 7% O_2, and 88% N_2) tissue culture incubator for 7 days. The number of proliferating cells within the wells is then quantitated by measuring thymidine incorporation into cellular DNA. Verification of the positive hits in the assay will require phenotypic characterization of the cells, which can be accomplished by scaling up of the culture system and using appropriate antibody reagents against cell surface antigens and FACScan.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or antagonists and fragments and variants thereof.

If a particular polypeptide of the present invention is found to be a stimulator of hematopoietic progenitors, polynucleotides and polypeptides corresponding to the gene encoding said polypeptide may be useful for the diagnosis and treatment of disorders affecting the immune system and hematopoiesis. Representative uses are described in the "Immune Activity" and "Infectious Disease" sections above, and elsewhere herein. The gene product may also be useful in the expansion of stem cells and committed progenitors of various blood lineages, and in the differentiation and/or proliferation of various cell types.

Additionally, the polynucleotides and/or polypeptides of the gene of interest and/or agonists and/or antagonists thereof, may also be employed to inhibit the proliferation and differentiation of hematopoietic cells and therefore may be employed to protect bone marrow stem cells from chemotherapeutic agents during chemotherapy. This antiproliferative effect may allow administration of higher doses of chemotherapeutic agents and, therefore, more effective chemotherapeutic treatment.

Moreover, polynucleotides and polypeptides corresponding to the gene of interest may also be useful for the treatment and diagnosis of hematopoietic related disorders such as, for example, anemia, pancytopenia, leukopenia, thrombocytopenia or leukemia since stromal cells are important in the production of cells of hematopoietic lineages. The uses include bone marrow cell ex-vivo culture, bone marrow transplantation, bone marrow reconstitution, radiotherapy or chemotherapy of neoplasia.

Example 44: Human Dermal Fibroblast and Aortic Smooth Muscle Cell Proliferation

The polypeptide of interest is added to cultures of normal human dermal fibroblasts (NHDF) and human aortic smooth muscle cells (AoSMC) and two co-assays are performed with each sample. The first assay examines the effect of the polypeptide of interest on the proliferation of normal human dermal fibroblasts (NHDF) or aortic smooth muscle cells (AoSMC). Aberrant growth of fibroblasts or smooth muscle cells is a part of several pathological processes, including fibrosis, and restenosis. The second assay examines IL6 production by both NHDF and SMC. IL6 production is an indication of functional activation. Activated cells will have increased production of a number of cytokines and other factors, which can result in a proinflammatory or immunomodulatory outcome. Assays are run with and without co-TNFa stimulation, in order to check for costimulatory or inhibitory activity.

Briefly, on day 1, 96-well black plates are set up with 1000 cells/well (NHDF) or 2000 cells/well (AoSMC) in 100 μl culture media. NHDF culture media contains: Clonetics FB basal media, 1mg/ml hFGF, 5mg/ml insulin, 50mg/ml gentamycin, 2%FBS, while AoSMC culture media contains Clonetics SM basal media, 0.5 μg/ml hEGF, 5mg/ml insulin, 1μg/ml hFGF, 50mg/ml gentamycin, 50 μg/ml Amphotericin B, 5%FBS. After incubation at 37°C for at least 4-5 hours, culture media is aspirated and replaced with growth arrest media. Growth arrest media for NHDF contains fibroblast basal media, 50mg/ml gentamycin, 2% FBS, while growth arrest media for AoSMC contains SM basal media, 50mg/ml gentamycin, 50μg/ml Amphotericin B,

0.4% FBS. Incubate at 37°C until day 2.

On day 2, serial dilutions and templates of the polypeptide of interest are designed such that they always include media controls and known-protein controls. For both stimulation and inhibition experiments, proteins are diluted in growth arrest media. For inhibition experiments, TNFa is added to a final concentration of 2ng/ml (NHDF) or 5ng/ml (AoSMC). Add 1/3 vol media containing controls or polypeptides of the present invention and incubate at 37°C/5% CO_2 until day 5.

Transfer 60µl from each well to another labeled 96-well plate, cover with a plate-sealer, and store at 4°C until Day 6 (for IL6 ELISA). To the remaining 100 µl in the cell culture plate, aseptically add Alamar Blue in an amount equal to 10% of the culture volume (10µl). Return plates to incubator for 3 to 4 hours. Then measure fluorescence with excitation at 530nm and emission at 590nm using the CytoFluor. This yields the growth stimulation/inhibition data.

On day 5, the IL6 ELISA is performed by coating a 96 well plate with 50-100 ul/well of Anti-Human IL6 Monoclonal antibody diluted in PBS, pH 7.4, incubate ON at room temperature.

On day 6, empty the plates into the sink and blot on paper towels. Prepare Assay Buffer containing PBS with 4% BSA. Block the plates with 200 µl/well of Pierce Super Block blocking buffer in PBS for 1-2 hr and then wash plates with wash buffer (PBS, 0.05% Tween-20). Blot plates on paper towels. Then add 50 µl/well of diluted Anti-Human IL-6 Monoclonal, Biotin-labeled antibody at 0.50 mg/ml. Make dilutions of IL-6 stock in media (30, 10, 3, 1, 0.3, 0 ng/ml). Add duplicate samples to top row of plate. Cover the plates and incubate for 2 hours at RT on shaker. Plates are washed with wash buffer and blotted on paper towels. Dilute EU-labeled Streptavidin 1:1000 in Assay buffer, and add 100 µl/well. Cover the plate and incubate 1 h at RT. Plates are again washed with wash buffer and blotted on paper towels. Add 100 µl/well of Enhancement Solution and shake for 5 minutes. Read the plate on the Wallac DELFIA Fluorometer. Readings from triplicate samples in each assay are tabulated and averaged.

A positive result in this assay suggests AoSMC cell proliferation and that the

polypeptide of the present invention may be involved in dermal fibroblast proliferation and/or smooth muscle cell proliferation. A positive result also suggests many potential uses of polypeptides, polynucleotides, agonists and/or antagonists of the polynucleotide/polypeptide of the present invention which gives a positive result. For example, inflammation and immune responses, wound healing, and angiogenesis, as detailed throughout this specification. Particularly, polypeptides of the present invention and polynucleotides of the present invention may be used in wound healing and dermal regeneration, as well as the promotion of vasculargenesis, both of the blood vessels and lymphatics. The growth of vessels can be used in the treatment of, for example, cardiovascular diseases. Additionally, antagonists of polypeptides and polynucleotides of the invention may be useful in treating diseases, disorders, and/or conditions which involve angiogenesis by acting as an anti-vascular (e.g., anti-angiogenesis). These diseases, disorders, and/or conditions are known in the art and/or are described herein, such as, for example, malignancies, solid tumors, benign tumors, for example hemangiomas, acoustic neuromas, neurofibromas, trachomas, and pyogenic granulomas; artherosclerotic plaques; ocular angiogenic diseases, for example, diabetic retinopathy, retinopathy of prematurity, macular degeneration, corneal graft rejection, neovascular glaucoma, retrolental fibroplasia, rubeosis, retinoblastoma, uvietis and Pterygia (abnormal blood vessel growth) of the eye; rheumatoid arthritis; psoriasis; delayed wound healing; endometriosis; vasculogenesis; granulations; hypertrophic scars (keloids); nonunion fractures; scleroderma; trachoma; vascular adhesions; myocardial angiogenesis; coronary collaterals; cerebral collaterals; arteriovenous malformations; ischemic limb angiogenesis; Osler-Webber Syndrome; plaque neovascularization; telangiectasia; hemophiliac joints; angiofibroma; fibromuscular dysplasia; wound granulation; Crohn's disease; and atherosclerosis. Moreover, antagonists of polypeptides and polynucleotides of the invention may be useful in treating anti-hyperproliferative diseases and/or anti-inflammatory known in the art and/or described herein.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or

antagonists and fragments and variants thereof.

Example 45: Cellular Adhesion Molecule (CAM) Expression on Endothelial Cells

The recruitment of lymphocytes to areas of inflammation and angiogenesis involves specific receptor-ligand interactions between cell surface adhesion molecules (CAMs) on lymphocytes and the vascular endothelium. The adhesion process, in both normal and pathological settings, follows a multi-step cascade that involves intercellular adhesion molecule-1 (ICAM-1), vascular cell adhesion molecule-1 (VCAM-1), and endothelial leukocyte adhesion molecule-1 (E-selectin) expression on endothelial cells (EC). The expression of these molecules and others on the vascular endothelium determines the efficiency with which leukocytes may adhere to the local vasculature and extravasate into the local tissue during the development of an inflammatory response. The local concentration of cytokines and growth factor participate in the modulation of the expression of these CAMs.

Briefly, endothelial cells (e.g., Human Umbilical Vein Endothelial cells (HUVECs)) are grown in a standard 96 well plate to confluence, growth medium is removed from the cells and replaced with 100 µl of 199 Medium (10% fetal bovine serum (FBS)). Samples for testing and positive or negative controls are added to the plate in triplicate (in 10 µl volumes). Plates are then incubated at 37°C for either 5 h (selectin and integrin expression) or 24 h (integrin expression only). Plates are aspirated to remove medium and 100 µl of 0.1% paraformaldehyde-PBS(with Ca++ and Mg++) is added to each well. Plates are held at 4°C for 30 min. Fixative is removed from the wells and wells are washed 1X with PBS(+Ca,Mg) + 0.5% BSA and drained. 10 µl of diluted primary antibody is added to the test and control wells. Anti-ICAM-1-Biotin, Anti-VCAM-1-Biotin and Anti-E-selectin-Biotin are used at a concentration of 10 µg/ml (1:10 dilution of 0.1 mg/ml stock antibody). Cells are incubated at 37°C for 30 min. in a humidified environment. Wells are washed three times with PBS(+Ca,Mg) + 0.5% BSA. 20 µl of diluted ExtrAvidin-Alkaline

Phosphotase (1:5,000 dilution, refered to herein as the working dilution) are added to each well and incubated at 37°C for 30 min. Wells are washed three times with PBS(+Ca,Mg)+0.5% BSA. Dissolve 1 tablet of p-Nitrophenol Phosphate pNPP per 5 ml of glycine buffer (pH 10.4). 100 µl of pNPP substrate in glycine buffer is added to each test well. Standard wells in triplicate are prepared from the working dilution of the ExtrAvidin-Alkaline Phosphotase in glycine buffer: 1:5,000 (10^0) > $10^{-0.5}$ > 10^{-1} > $10^{-1.5}$. 5 µl of each dilution is added to triplicate wells and the resulting AP content in each well is 5.50 ng, 1.74 ng, 0.55 ng, 0.18 ng. 100 µl of pNNP reagent is then added to each of the standard wells. The plate is incubated at 37°C for 4h. A volume of 50 µl of 3M NaOH is added to all wells. The plate is read on a plate reader at 405 nm using the background subtraction option on blank wells filled with glycine buffer only. Additionally, the template is set up to indicate the concentration of AP-conjugate in each standard well [5.50 ng; 1.74 ng; 0.55 ng; 0.18 ng]. Results are indicated as amount of bound AP-conjugate in each sample.

Example 46: Alamar Blue Endothelial Cells Proliferation Assay

This assay may be used to quantitatively determine protein mediated inhibition of bFGF-induced proliferation of Bovine Lymphatic Endothelial Cells (LECs), Bovine Aortic Endothelial Cells (BAECs) or Human Microvascular Uterine Myometrial Cells (UTMECs). This assay incorporates a fluorometric growth indicator based on detection of metabolic activity. A standard Alamar Blue Proliferation Assay is prepared in EGM-2MV with 10 ng /ml of bFGF added as a source of endothelial cell stimulation. This assay may be used with a variety of endothelial cells with slight changes in growth medium and cell concentration. Dilutions of the protein batches to be tested are diluted as appropriate. Serum-free medium (GIBCO SFM) without bFGF is used as a non-stimulated control and Angiostatin or TSP-1 are included as a known inhibitory controls.

Briefly, LEC, BAECs or UTMECs are seeded in growth media at a density of 5000 to 2000 cells/well in a 96 well plate and placed at 37-C overnight. After the

overnight incubation of the cells, the growth media is removed and replaced with GIBCO EC-SFM. The cells are treated with the appropriate dilutions of the protein of interest or control protein sample(s) (prepared in SFM) in triplicate wells with additional bFGF to a concentration of 10 ng/ ml. Once the cells have been treated with the samples, the plate(s) is/are placed back in the 37° C incubator for three days. After three days 10 ml of stock alamar blue (Biosource Cat# DAL1100) is added to each well and the plate(s) is/are placed back in the 37°C incubator for four hours. The plate(s) are then read at 530nm excitation and 590nm emission using the CytoFluor fluorescence reader. Direct output is recorded in relative fluorescence units.

Alamar blue is an oxidation-reduction indicator that both fluoresces and changes color in response to chemical reduction of growth medium resulting from cell growth. As cells grow in culture, innate metabolic activity results in a chemical reduction of the immediate surrounding environment. Reduction related to growth causes the indicator to change from oxidized (non-fluorescent blue) form to reduced (fluorescent red) form. i.e. stimulated proliferation will produce a stronger signal and inhibited proliferation will produce a weaker signal and the total signal is proportional to the total number of cells as well as their metabolic activity. The background level of activity is observed with the starvation medium alone. This is compared to the output observed from the positive control samples (bFGF in growth medium) and protein dilutions.

Example 47: Detection of Inhibition of a Mixed Lymphocyte Reaction

This assay can be used to detect and evaluate inhibition of a Mixed Lymphocyte Reaction (MLR) by gene products (e.g., isolated polypeptides). Inhibition of a MLR may be due to a direct effect on cell proliferation and viability, modulation of costimulatory molecules on interacting cells, modulation of adhesiveness between lymphocytes and accessory cells, or modulation of cytokine production by accessory cells. Multiple cells may be targeted by these polypeptides

since the peripheral blood mononuclear fraction used in this assay includes T, B and natural killer lymphocytes, as well as monocytes and dendritic cells.

Polypeptides of interest found to inhibit the MLR may find application in diseases associated with lymphocyte and monocyte activation or proliferation. These include, but are not limited to, diseases such as asthma, arthritis, diabetes, inflammatory skin conditions, psoriasis, eczema, systemic lupus erythematosus, multiple sclerosis, glomerulonephritis, inflammatory bowel disease, crohn's disease, ulcerative colitis, arteriosclerosis, cirrhosis, graft vs. host disease, host vs. graft disease, hepatitis, leukemia and lymphoma.

Briefly, PBMCs from human donors are purified by density gradient centrifugation using Lymphocyte Separation Medium (LSM®, density 1.0770 g/ml, Organon Teknika Corporation, West Chester, PA). PBMCs from two donors are adjusted to 2 x 10^6 cells/ml in RPMI-1640 (Life Technologies, Grand Island, NY) supplemented with 10% FCS and 2 mM glutamine. PBMCs from a third donor is adjusted to 2 x 10^5 cells/ml. Fifty microliters of PBMCs from each donor is added to wells of a 96-well round bottom microtiter plate. Dilutions of test materials (50 μl) is added in triplicate to microtiter wells. Test samples (of the protein of interest) are added for final dilution of 1:4; rhuIL-2 (R&D Systems, Minneapolis, MN, catalog number 202-IL) is added to a final concentration of 1 μg/ml; anti-CD4 mAb (R&D Systems, clone 34930.11, catalog number MAB379) is added to a final concentration of 10 μg/ml. Cells are cultured for 7-8 days at 37°C in 5% CO_2, and 1 μC of [^{3}H] thymidine is added to wells for the last 16 hrs of culture. Cells are harvested and thymidine incorporation determined using a Packard TopCount. Data is expressed as the mean and standard deviation of triplicate determinations.

Samples of the protein of interest are screened in separate experiments and compared to the negative control treatment, anti-CD4 mAb, which inhibits proliferation of lymphocytes and the positive control treatment, IL-2 (either as recombinant material or supernatant), which enhances proliferation of lymphocytes.

One skilled in the art could easily modify the exemplified studies to test the activity of polynucleotides (e.g., gene therapy), antibodies, agonists, and/or

antagonists and fragments and variants thereof.

It will be clear that the invention may be practiced otherwise than as particularly described in the foregoing description and examples. Numerous modifications and variations of the present invention are possible in light of the above teachings and, therefore, are within the scope of the appended claims.

The entire disclosure of each document cited (including patents, patent applications, journal articles, abstracts, laboratory manuals, books, or other disclosures) in the Background of the Invention, Detailed Description, and Examples is hereby incorporated herein by reference. Further, the hard copy of the sequence listing submitted herewith and the corresponding computer readable form are both incorporated herein by reference in their entireties. Moreover, the hard copy of and the corresponding computer readable form of the Sequence Listing of Serial No. 60/124,270 are also incorporated herein by reference in their entireties.

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209059

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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ATCC Deposit No. 209059

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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Page 2
ATCC Deposit No. 209059

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application No.	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209060

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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ATCC Deposit No. 209060

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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Page 2
ATCC Deposit No. 209060

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application No.	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209061

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
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CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

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FINLAND

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UNITED KINGDOM

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Page 2
ATCC Deposit No. 209061

DENMARK

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209062

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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ATCC Deposit No. 209062

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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Page 2
ATCC Deposit No. 209062

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application No.	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209063

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
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ATCC Deposit No. 209063

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. 209063

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later that at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209064

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☑ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer [illegible] PCT/Internal [illegible] Processing Div. (703) 305-[illegible]	Authorized officer

ATCC Deposit No. 209064

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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Page 2
ATCC Deposit No. 209064

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209065

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209065

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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Page 2
ATCC Deposit No. 209065

DENMARK

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SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209066

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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ATCC Deposit No. 209066

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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Page 2
ATCC Deposit No. 209066

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application No.	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209067

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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ATCC Deposit No. 209067

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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Page 2
ATCC Deposit No. 209067

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later that at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application No.	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209068

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
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Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209068

CANADA

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FINLAND

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UNITED KINGDOM

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Page 2
ATCC Deposit No. 209068

DENMARK

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA106PCT	International application No.	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
20 May 1997	209069

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☑ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer Jeni McDaniel PCT/Internat'l Appl Processing Div. (703) 305-3639	Authorized officer

ATCC Deposit No. 209069

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. 209069

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
12 January 1998	209579

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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Authorized officer Joyd [illegible] PCT/Internat'l Appl Processing Div. (703) [illegible]	Authorized officer

Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209579

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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Page 2
ATCC Deposit No. 209579

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
12 January 1998	209578

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

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Authorized officer Jerry McDowell PCT/International Appl Processing Div. (703) 305-3300	Authorized officer

Form PCT/RO/134 (July 1992)

ATCC Deposit No. 209578

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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Page 2
ATCC Deposit No. 209578

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
16 July 1998	203067

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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Authorized officer Jeryl McDowell PCT/Internat'l Appl Processing Div. (703) 305-3339	Authorized officer

Form PCT/RO/134 (July 1992)

ATCC Deposit No. 203067

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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Page 2
ATCC Deposit No. 203067

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
16 July 1998	203068

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

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Authorized officer Jerry McDowell PCT/Internat'l Appl Processing Div. (703) 305-3339	Authorized officer

Form PCT/RO/134 (July 1992)

ATCC Deposit No. 203068

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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Page 2
ATCC Deposit No. 203068

DENMARK

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
1 February 1999	203609

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

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Authorized officer Jeryl McDowell PCT/Internat'l Appl Processing Div. (703) 305-3639	Authorized officer

ATCC Deposit No. 203609

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

The applicant hereby requests that the application has been laid open to public inspection (by the Norwegian Patent Office), or has been finally decided upon by the Norwegian Patent Office without having been laid open inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Norwegian Patent Office not later than at the time when the application is made available to the public under Sections 22 and 33(3) of the Norwegian Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on the list of recognized experts drawn up by the Norwegian Patent Office or any person approved by the applicant in the individual case.

AUSTRALIA

The applicant hereby gives notice that the furnishing of a sample of a microorganism shall only be effected prior to the grant of a patent, or prior to the lapsing, refusal or withdrawal of the application, to a person who is a skilled addressee without an interest in the invention (Regulation 3.25(3) of the Australian Patents Regulations).

FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. 203609

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later that at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
1 February 1999	203610

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

For receiving Office use only	For International Bureau use only
☑ This sheet was received with the international application	☐ This sheet was received by the International Bureau on:
Authorized officer Jerry [illegible] PCT/[illegible] Processing Div. (703) 305-3639	Authorized officer

ATCC Deposit No. 203610

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. 203610

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
17 November 1998	203485

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

The indications listed below will be submitted to the International Bureau later *(specify the general nature of the indications e.g., "Accession Number of Deposit")*

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Authorized officer: Joni McDowell, PCT/Internat'l Appl Processing Div., (703) 305-3639	Authorized officer

ATCC Deposit No. 203485

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. 203485

DENMARK

The applicant hereby requests that, until the application has been laid open to public inspection (by the Danish Patent Office), or has been finally decided upon by the Danish Patent office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the Danish Patent Office not later that at the time when the application is made available to the public under Sections 22 and 33(3) of the Danish Patents Act. If such a request has been filed by the applicant, any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Danish Patent Office or any person by the applicant in the individual case.

SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
18 June 1999	PTA-252

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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Authorized officer Jaryl McDowell PCT/Internat'l Appl Processing Div. (703) 305-3639	Authorized officer

Form PCT/RO/134 (July 1992)

ATCC Deposit No. PTA-252

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

The applicant hereby requests that the furnishing of a sample of a microorganism shall only be made available to an expert. The request to this effect must be filed by the applicant with the International Bureau before the completion of the technical preparations for the international publication of the application.

Page 2
ATCC Deposit No. PTA-252

DENMARK

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SWEDEN

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NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
18 June 1999	PTA-253

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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Authorized officer Jeryl McDowell PCT International Appl Processing Div. (703) 305-3639	Authorized officer

ATCC Deposit No. PTA-253

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

The applicant hereby requests that, until the application has been laid open to public inspection (by the National Board of Patents and Regulations), or has been finally decided upon by the National Board of Patents and Registration without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art.

UNITED KINGDOM

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Page 2
ATCC Deposit No. PTA-253

DENMARK

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SWEDEN

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NETHERLANDS

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Applicant's or agent's file reference number	PA106PCT	International application	UNASSIGNED

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM

(PCT Rule 13*bis*)

A. The indications made below relate to the microorganism referred to in the description on page 121, line N/A.

B. IDENTIFICATION OF DEPOSIT — Further deposits are identified on an additional sheet ☐

Name of depositary institution American Type Culture Collection

Address of depositary institution *(including postal code and country)*
10801 University Boulevard
Manassas, Virginia 20110-2209
United States of America

Date of deposit	Accession Number
22 December 1999	PTA-1081

C. ADDITIONAL INDICATIONS *(leave blank if not applicable)* — This information is continued on an additional sheet ☐

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE *(if the indications are not for all designated States)*

Europe
In respect to those designations in which a European Patent is sought a sample of the deposited microorganism will be made available until the publication of the mention of the grant of the European patent or until the date on which application has been refused or withdrawn or is deemed to be withdrawn, only by the issue of such a sample to an expert nominated by the person requesting the sample (Rule 28 (4) EPC).

E. SEPARATE FURNISHING OF INDICATIONS *(leave blank if not applicable)*

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Authorized officer Jeri McDowell PCT/Internat'l Appl Processing Div. (703) 305-3639	Authorized officer

ATCC Deposit No. PTA-1081

CANADA

The applicant requests that, until either a Canadian patent has been issued on the basis of an application or the application has been refused, or is abandoned and no longer subject to reinstatement, or is withdrawn, the Commissioner of Patents only authorizes the furnishing of a sample of the deposited biological material referred to in the application to an independent expert nominated by the Commissioner, the applicant must, by a written statement, inform the International Bureau accordingly before completion of technical preparations for publication of the international application.

NORWAY

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AUSTRALIA

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FINLAND

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UNITED KINGDOM

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Page 2
ATCC Deposit No. PTA-1081

DENMARK

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The applicant hereby requests that, until the application has been laid open to public inspection (by the Swedish Patent Office), or has been finally decided upon by the Swedish Patent Office without having been laid open to public inspection, the furnishing of a sample shall only be effected to an expert in the art. The request to this effect shall be filed by the applicant with the International Bureau before the expiration of 16 months from the priority date (preferably on the Form PCT/RO/134 reproduced in annex Z of Volume I of the PCT Applicant's Guide). If such a request has been filed by the applicant any request made by a third party for the furnishing of a sample shall indicate the expert to be used. That expert may be any person entered on a list of recognized experts drawn up by the Swedish Patent Office or any person approved by a applicant in the individual case.

NETHERLANDS

The applicant hereby requests that until the date of a grant of a Netherlands patent or until the date on which the application is refused or withdrawn or lapsed, the microorganism shall be made available as provided in the 31F(1) of the Patent Rules only by the issue of a sample to an expert. The request to this effect must be furnished by the applicant with the Netherlands Industrial Property Office before the date on which the application is made available to the public under Section 22C or Section 25 of the Patents Act of the Kingdom of the Netherlands, whichever of the two dates occurs earlier.

What Is Claimed Is:

1. An isolated nucleic acid molecule comprising a polynucleotide having a nucleotide sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polynucleotide fragment of SEQ ID NO:X or a polynucleotide fragment of the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;

(b) a polynucleotide encoding a polypeptide fragment of SEQ ID NO:Y or a polypeptide fragment encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;

(c) a polynucleotide encoding a polypeptide fragment of a polypeptide encoded by SEQ ID NO:X or a polypeptide fragment encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;

(d) a polynucleotide encoding a polypeptide domain of SEQ ID NO:Y or a polypeptide domain encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;

(e) a polynucleotide encoding a polypeptide epitope of SEQ ID NO:Y or a polypeptide epitope encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X;

(f) a polynucleotide encoding a polypeptide of SEQ ID NO:Y or the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X, having biological activity;

(g) a polynucleotide which is a variant of SEQ ID NO:X;

(h) a polynucleotide which is an allelic variant of SEQ ID NO:X;

(i) a polynucleotide which encodes a species homologue of the SEQ ID NO:Y;

(j) a polynucleotide capable of hybridizing under stringent conditions to any one of the polynucleotides specified in (a)-(i), wherein said polynucleotide does not hybridize under stringent conditions to a nucleic acid molecule having a nucleotide

sequence of only A residues or of only T residues.

2. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding a protein.

3. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises a nucleotide sequence encoding the sequence identified as SEQ ID NO:Y or the polypeptide encoded by the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X.

4. The isolated nucleic acid molecule of claim 1, wherein the polynucleotide fragment comprises the entire nucleotide sequence of SEQ ID NO:X or the cDNA sequence included in the related cDNA clone, which is hybridizable to SEQ ID NO:X.

5. The isolated nucleic acid molecule of claim 2, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

6. The isolated nucleic acid molecule of claim 3, wherein the nucleotide sequence comprises sequential nucleotide deletions from either the C-terminus or the N-terminus.

7. A recombinant vector comprising the isolated nucleic acid molecule of claim 1.

8. A method of making a recombinant host cell comprising the isolated nucleic acid molecule of claim 1.

9. A recombinant host cell produced by the method of claim 8.

10. The recombinant host cell of claim 9 comprising vector sequences.

11. An isolated polypeptide comprising an amino acid sequence at least 95% identical to a sequence selected from the group consisting of:

(a) a polypeptide fragment of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;

(b) a polypeptide fragment of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone, having biological activity;

(c) a polypeptide domain of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;

(d) a polypeptide epitope of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;

(e) a full length protein of SEQ ID NO:Y or of the sequence encoded by the cDNA included in the related cDNA clone;

(f) a variant of SEQ ID NO:Y;

(g) an allelic variant of SEQ ID NO:Y; or

(h) a species homologue of the SEQ ID NO:Y.

12. The isolated polypeptide of claim 11, wherein the full length protein comprises sequential amino acid deletions from either the C-terminus or the N-terminus.

13. An isolated antibody that binds specifically to the isolated polypeptide of claim 11.

14. A recombinant host cell that expresses the isolated polypeptide of claim 11.

15. A method of making an isolated polypeptide comprising:

(a) culturing the recombinant host cell of claim 14 under conditions such that said polypeptide is expressed; and

(b) recovering said polypeptide.

16. The polypeptide produced by claim 15.

17. A method for preventing, treating, or ameliorating a medical condition, comprising administering to a mammalian subject a therapeutically effective amount of the polypeptide of claim 11 or the polynucleotide of claim 1.

18. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or absence of a mutation in the polynucleotide of claim 1; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or absence of said mutation.

19. A method of diagnosing a pathological condition or a susceptibility to a pathological condition in a subject comprising:

(a) determining the presence or amount of expression of the polypeptide of claim 11 in a biological sample; and

(b) diagnosing a pathological condition or a susceptibility to a pathological condition based on the presence or amount of expression of the polypeptide.

20. A method for identifying a binding partner to the polypeptide of claim 11 comprising:

(a) contacting the polypeptide of claim 11 with a binding partner; and

(b) determining whether the binding partner effects an activity of the polypeptide.

21. The gene corresponding to the cDNA sequence of SEQ ID NO:Y.

22. A method of identifying an activity in a biological assay, wherein the method comprises:

(a) expressing SEQ ID NO:X in a cell;

(b) isolating the supernatant;

(c) detecting an activity in a biological assay; and

(d) identifying the protein in the supernatant having the activity.

23. The product produced by the method of claim 20.

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<210> 9
<211> 1101
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (730)
<223> n equals a,t,g, or c

<220>
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<222> (983)
<223> n equals a,t,g, or c

<220>
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<222> (1055)
<223> n equals a,t,g, or c

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<211> 1373
<212> DNA
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<222> (1364)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1373)
<223> n equals a,t,g, or c

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tgagcagatc atccaggaga tctacagcca gatccagagc aaaaagaaga tcctggcaac 180
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<210> 11
<211> 3804
<212> DNA
<213> Homo sapiens

<400> 11
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<210> 12
<211> 2157
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (806)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (846)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1517)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2110)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2116)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2137)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2150)
<223> n equals a,t,g, or c

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<210> 13
<211> 1117
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1102)
<223> n equals a,t,g, or c

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<210> 14

<211> 885
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (869)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (884)
<223> n equals a,t,g, or c

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<210> 15
<211> 1024
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (938)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1005)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1012)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1019)
<223> n equals a,t,g, or c

<400> 15
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gccagatgct caaggaggga gcgaaacact tttcaggatt agaagaggct gtgtatagaa 180
acatacaagc ttgcaaggag cttgcccaaa ccactcgtac agcatatgga ccaaatggaa 240
tgaacaaaat ggttatcaac cacttggaga agttgtttgt gacaaacgat gcagcaacta 300
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tggaattagc tgaagaactt ctgaggattg gcctgtcagt ttcagaggtc atagaaggtt 480
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aaaaccttcg agatattgat gaagtctcat ctctacttcg tacctccata atgagtaaac 600
aatatggtaa tgaagtattt ctggccaagc ttattgctca ggcatgcgta tctatttttc 660
ctgattccgg ccatttcaat gttgataaca tcagagtttg taaaattctg ggctctggta 720
tcagttcctc ttcagtattg catggcatgg tttttaagaa ggaaaccgaa gtgatgtaac 780
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aactaaggga acagtgttga taaagactgc tgaagrattg atgaatttta gtaagggagr 900
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aaat 1024

<210> 16
<211> 545
<212> DNA
<213> Homo sapiens

<220>
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<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (403)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (476)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (507)
<223> n equals a,t,g, or c

<400> 16
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atcaggactg aacacagagg actcaccatg gagtttgggc tgagctggat tttccttgct 180
gctattttaa aaggtgtcca gtgtgaggtg cagctggtgg agtctggggg aggcttggta 240
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ctcaagagat gattcaaaaa acacgytgta tytgcaaatg aacagcctga aaaccngagg 480
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ctttt 545

<210> 17
<211> 623
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (613)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (616)
<223> n equals a,t,g, or c

<400> 17
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tcaaggagga rgtgggcgaa gaggccatcg tggagctggt ggagaatggg aagaaggtga 420
aggtgaacaa ggatgacatc cagaagatga acccgcccaa gttctccaag gtggaggaca 480
tggcagagct cacgtgcctc aacgaagcct cggtgttgca caacctcaag gagcgttact 540
actcagggct catctacgta agtggctgcc gtggcacccc gcaggctggg tctgagggct 600
ccgaggtggg ggnggnggcg ggt 623

<210> 18
<211> 559

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (371)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (531)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (544)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (547)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (556)
<223> n equals a,t,g, or c

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attagtaatt ttaaaatgag grtgggaatt aactaacaga actgatagga agtgttaaca 180
tacaacaggg gagtctaaga tggcttccaa ttttcactta gaggggtaag ggtaccatta 240
acttaagatc attaatacag raaaattaat cagatttgga gtttaccaag gtttgctttt 300
ggttgtaaca atgatatatg ataaaattaa atgrataaat aagtgratgc actggtgaat 360
taatgagctg ntctcattaa gaccagagta cttatttata acaaaagtaa cttttccctt 420
tccctgggta catcaaactg tactccacag ataacagaca ccagtgagtt tttcatggtt 480
aaaaaagccc caactttgac ctataaatgt ggaccaagaa attaaaataa nctggaacca 540
gcgngcnacg gtattngga 559

<210> 19
<211> 1355
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (1045)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1355)
<223> n equals a,t,g, or c

<400> 19
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acaacggcac ctctgccagg gctaccacaa ccccagccag caagagcact ccattctcaa 180
ttcccagcca ccactctgat actcctacca cccttgccag ccatagcacc aagactgatg 240
ccagtagcac tcaccatagc acggtacctc ctctcacctc ctccaatcac agcacttctc 300
cccagttgtc tactggggtc tctttctttt tcctgtcttt tcacatttca aacctccagt 360
ttaattcctc tctggaagat cccagcaccg actactacca agagctgcag agagacattt 420
ctgaaatgtt tttgcagatt tataaacaag gggttttct gggcctctcc aatattaagt 480
tcaggccagg atctgtggtg gtacaattga ctctggcctt ccgagaaggt accatcaatg 540
tccacgacgt ggagacacag ttcaatcagt ataaaacgga agcagcctct cgatataacc 600
tgacgatctc agacgtcagc gtgagtgatg tgccatttcc tttctctgcc cagtctgggg 660
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ccattgtcta tctcattgcc ttggctgtct gtcagtgccg ccgaaagaac tacgggcagc 780
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaan 1355

<210> 20
<211> 1280
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1043)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1162)
<223> n equals a,t,g, or c

<400> 20
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tggagagcat cctctcttac cccaaggact tcacctgtgt ccaccaggcc ctgaagggct 120
tcacgaccaa aggtgtcacc tcagtctctc agatcttcca cagcccagac ctggccataa 180
gggacacctt tgtgaatgcc tctcggaccc tgtacagcag cagccccaga gtcctaagca 240
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<210> 21
<211> 1191
<212> DNA
<213> Homo sapiens

<400> 21
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tggagagcca gtttcttccc aaattactga cctaacccat ccttaacccc cagttcaagg 300
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gaactatgta ttaattagct tgattgtggt aaccatttca caatgtatac atttgccaaa 960
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catcaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaactcgtag g 1191

<210> 22
<211> 853

<212> DNA
<213> Homo sapiens

<400> 22
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accattaacc taaaacttac tatttaacct agtgtttttg ttgatgaggt ttacattatg 720
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<210> 23
<211> 474
<212> DNA
<213> Homo sapiens

<400> 23
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gccargaara agcgtcccag gaagccggcc tgccggcaag agcgggcccc agcc 474

<210> 24
<211> 2280
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (13)
<223> n equals a,t,g, or c

<400> 24
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<210> 25
<211> 1061
<212> DNA
<213> Homo sapiens

<400> 25
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<210> 26
<211> 1572
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (19)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (28)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1491)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1527)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1555)
<223> n equals a,t,g, or c

<400> 26

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gggcagctgc ggacatgtcg accccggccc ggaggaggct catgcgggat ttcaagcggt 180
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aatatgagaa aagagtttcg gccattgttg aacaaagctg gaatgattca taatagacaa 600
ctggtctgtt aatcttttttc atcattgttg tgtataattt acctctcatt agaaaggcta 660
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caaatattga atgccttatt tttgaattct ttagattttt aaattggaga aaagcactta 960
aagtttttta tatatgaata ttacatgtaa agctgttaaa atacataact tcagtgcaag 1020
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<210> 27
<211> 2005
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1976)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1977)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1978)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1979)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1986)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1988)
<223> n equals a,t,g, or c

<400> 27
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cgcctccgcc gcctagcgct gttcccgggt gtggcgctgc ttcttgccgc ggcccgcctc 180
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gttgggggaa atgttgtggg ggtggggttg agttgggggt attttctaat ttttttgta 1920
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gggggncncc cagtcccatt cgccc 2005

<210> 28
<211> 1408
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (11)
<223> n equals a,t,g, or c

<400> 28
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acacgtacga cgagtacaaa aagggcttcc tggaccaggc atctgggagt gcagtgctgc 180
tgctcaggcc cggagaccgg tgttcctcca gatgccctca gaacaggctg caggactgta 240

tgccgggcag tatgtccact cctccttttc aggatattta ttgtatccca tgtaaaaaca 300
aaaaaacaaa aaacaaagaa aagaaagaga ttttatagaa gaaaatgaca caccaaaaaa 360
tccaaatgaa aaacataatt gcttcaaaac acttacacag ttggaaagtt atatgtaagt 420
gaaaatttgg accattgtgt acaaataaaa actaagatgc atgtttaata ctccacacag 480
cagcctgtaa ttgcgaatga tgggatagag ttatgtatca agtactgaca cttggttgta 540
cccactggaa tcatattagc tgttttatgt tatatgcttc cacagtaacc tgcttattca 600
gatcagtcaa aatatatcag tatgaaagat catagctaat gaaaggcact cactcatatt 660
gtttacttta aaatatttat aaatatgcct taaagaaata caaatgataa caattacata 720
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tatcagttat gcttatatag cattaaaaat tctcctcctt tgactacaca cacaaccaca 1320
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tctgtttagc atgtatgcaa actggata 1408

<210> 29
<211> 917
<212> DNA
<213> Homo sapiens

<400> 29
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ggaccatgtg cgcgtcccgg gacgactggc gctgtgcgct ccatgcacga kttttccgcc 180
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accaacgtgg cctcccagtg aggcaagacc gaagtaaact acactcagct cgtcgacctg 300
cacgcccgat acgctgagtg tggtttgcgg atcctggcct tcccgtgtaa ccagttcggg 360
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aaaaaaaaaa aaaaaaa 917

<210> 30
<211> 577
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (501)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (534)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (568)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (575)
<223> n equals a,t,g, or c

<400> 30
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gagttcaaga ccagcgtggc caacgtggtg aaccctgtct ctactaaaaa tacaaaaatt 180
gtttagctct gtttttcata atagaaatag aaaaggtaaa attgcttttc ttctgaaaag 240
aacaagtatt gttcatccaa gaagggtttt tgtgactgaa tcagcagtgc ctgccctagt 300
catagctgtg cttcagaaac ctcagcatga ttagtgttkg agcmmaacaa ggragcaaag 360
caaatwcwgt ttttgaaatt ctatctgttg cttgaactat tttgtaataa ttaaactttg 420
gatgttgaga aatcacaact ttattggtac acttcattgc aacttgaaat tccatgggtc 480
ttaaagtgag attggaattc naatgggcgg cctttaaaaa gtaattccca accnttaagg 540
ttaaaaccca ggaaattggg gccaatcnaa aaccngg 577

<210> 31
<211> 2059
<212> DNA
<213> Homo sapiens

<400> 31
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actccttttt gcagtggaca caggactata tttctctgtg aagacaaaca ttcgaagctc 180
aacaagagac tggaaggacc ataaatttaa atggagaaag gaccctcaag acaaatgacc 240
cccatcccat gggggtaata agagcagtag cagcagcatc tctgaacatt tctctggatt 300
tgcaacccca tcatcctcag gcctctctac aagcagcagg aaacatagaa ctcagagcca 360
gatcccttat ccaactctcg acttttcctt ggtctccagt ggaagggaaa agcccatgat 420
cttcaagcag ggaagcccca gtgagtagct gcattcctag aaattgaagt ttcagrgcta 480
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aaaaaaaaaa aaaaaaaaa 2059

<210> 32
<211> 549
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (337)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (378)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (497)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (537)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (546)
<223> n equals a,t,g, or c

<400> 32
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tctagaggat ccaagcttac gtacgcgtgc atgcgacgtc atagctcttc tatagtgtca 180
cctaaattca attcactggc cgtcgtttta caacgtcgtg actgggaaaa ccctggcgtt 240
acccaactta atcgccttgc agcacatccc cctttcgcca gctggcgtaa tagcgaagag 300
gcccgcaccg attcgccctt tcccaacagt tgcgcanctg gaatggcgaa tggggacgcg 360
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acttgccagc gccctagcgc ccgctccttt cgctttcttc ccttcctttc tcgccacgtt 480
cgccggcttt ccccttnaag ctctaaatcg gtgggctccc tttaggtgtc ctatttngtg 540
ctttanggt 549

<210> 33
<211> 841
<212> DNA
<213> Homo sapiens

<400> 33
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gcagccccac agaccatggt catgccaggt ggttgtacta caatcccaga gtcagaccta 180
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gcagagacac ccaggcctgt ttcacccctc caaggagtct cggaataatt ccaagtagag 300
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atagaaagag gggttgggac ttttacttc actaggagaa cttgtaacac catggggaag 480
tcagctgaaa cttgtcttgt tttgccagga aaggaagtag ttgcctttgg tcatccatct 540
gctaatagtc acagaataca gtgaaatgac atagttttgg gttagatttt ataatgcaaa 600
gattcagatc caaaataatt tcatacccca ttttttcaca gaattcttat atagtaaatg 660
tatcaagttt aataaagcat ctcattgtca aataatatct tggattttat ttataattag 720
agggatttat gagtgattgc tctacattat ttcttcaaag gaaaggaaag gaattgaaga 780
ctttgctact ctctggtaag acttgaatgt gattatttta taaataaaag aaccactatg 840
a 841

<210> 34
<211> 863
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (19)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (58)
<223> n equals a,t,g, or c

<400> 34
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tggaatcccc ccggggcttt caaggaattc ggcacgagtt tgcttaggcg cagacgggga 120
agcggagcca acatgccagt ggcccggagc tgggtttgtc gcaaaactta tgtgaccccg 180
cggagaccct tcgagaaatc tcgtctcgac caagagctga agctgatcgg cgagtatggg 240
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gcccgggaac tgctgacgct tgatgagaag gacccacggc gtctgttcga aggcaacgcc 360
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atcctgggcc tgaagataga ggatttctta gagagacgcc tgcagaccca ggtcttcaag 480
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atcgacttct ctctgcgctc tccctacggg ggtggccgcc cgggccgcgt gaagaggaag 660
aatgccaaga agggccaggg tggggctggg gctggagacg acgaggagga ggattaagtc 720
cacctgtccc tcctgggctg ctggattgtc tcgttttcct gccaaataaa caggatcagc 780
gctttacaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 840
aaaaaaaaaa aaaaaaaaaa ttt 863

<210> 35
<211> 1230
<212> DNA
<213> Homo sapiens

<400> 35
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ggtgggtgtt ccagctggaa gtaacccctt ccgggagcct agatcctgtg ctttactctg 240
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ccttcaagtc tcaagaaaac acttttccct aactttttaga gatatttcag ccctttcctg 360
tggcctggtc ctatagccaa aatcacagat attcatgagt ttctacttga gtgagaaaac 420
tgggtgaagg aatagaattt taaatagtaa taactgcttg ttttttttgt gcaagtactt 480
ttatacataa gataaacaaa aaccttacca ccaaacatac caaaatgcac ctctttcata 540
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attaatcatt tttctatgac agcaaaaaaa 1230

<210> 36
<211> 640
<212> DNA
<213> Homo sapiens

<400> 36
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ctatccgcac tagaaagttc atgaccaacc gactacttca gaggaaacaa atggtcattg 180
atgtccttca ccccgggaag gcgacagtgc ctaagacaga aattcgggaa aaactagcca 240
aaatgtacaa gaccacaccg gatgtcatct ttgtatttgg attcagaact cattttggtg 300
gtggcaagac aactggcttt ggcatgattt atgattccct ggattatgca aagaaaaatg 360
aacccaaaca tagacttgca agacatggcc tgtatgagaa gaaaaagacc tcaagaaagc 420
aacgaaagga acgcaagaac agaatgaaga aagtcagggg gactgcaaag gccaatgttg 480
gtgctggcaa aaagccgaag gagtaaaggt gctgcaatga tgttagctgt ggccactgtg 540
gatttttcgc aagaacatta ataaactaaa aacttcaaaa aaaaaaaaaa aaaaaaaaaa 600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagg 640

<210> 37
<211> 597
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (556)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (558)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (567)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (590)
<223> n equals a,t,g, or c

<400> 37
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ccgaggaagc taaggctgcg ttggggtgag gccctcactt catccggcga ctagcaccgc 120
gtccggcagc gccagcccta cactcgcccg cgccatggcc tctgtctccg agctcgcctg 180
catctactcg gccctcattc tgcacgacga tgaggtgaca gtcacggagg ataagatcaa 240
tgccctcatt aaagcagccg gtgtaaatgt tgagcctttt tggcctggct tgtttgcaaa 300
ggccctggcc aacgtcaaca ttgggagcct catctgcaat gtaggggccg gtggacctgc 360
tccagcagct ggtgctgcac cagcaggagg tcctgccccc tccactgctg ctgctccagc 420
tgaggagaag aaagtggaag caaagaaaga agaatccgag gagtctgatg atgacatggg 480
ctttggtctt tttgactaaa cctcttttat aacatgttca ataaaaagct gaactttaaa 540
aaaaaaaaaa aaaaancncg ggggggnccg ctttaaaggg tccaagttan gtacggg 597

<210> 38
<211> 624
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<400> 38
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ttcctgtgga cgccgggkaa gcacagcamc amccccgcac ctgccctcgg cctttgtgag 540
ctttgtggtc ttcccatcag gaacactgga aagtgacatt gtgtacacgc tgcagcttgg 600
gggtttttc tttgtattgc tgtt 624

<210> 39
<211> 1029
<212> DNA
<213> Homo sapiens

<400> 39
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cgcggccgcg tcgacgctca gtcttccacc aaaggccgtt cagttctcct gggctccagc 120
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atctttctg 1029

<210> 40
<211> 1107
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1098)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1106)
<223> n equals a,t,g, or c

<400> 40
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gaaaactgcg agccagcatt acccccggga ccattctgat catcctcact ggacgccaca 180
ggggcaaggt gagagtacct gtgcttgggg cgcttcactg cagctgcctg ggtgcctgg 240
tggcaatgcg tttgcacgct aggtgtactt ttcctttatt tacctatgtt tggggcaagg 300
ggaaatgatc tgcaagatac aacttagttg ttgcaaataa gaagtgtaat ccatggtgat 360
ttattagcca tttcctgctg ttgatwatgt tacacatgty catttactca aaaacgtgtt 420
tatgtctgga gtactacctt agtagcttgc tgtggttgct tccagaactg ccgagctgta 480
tacatataca tgtagaaatt tccttacccm aatttagatg cctgtgawtt tawgaatcag 540
aagycagttt taawtgcmga aaacyaatta ttytcttttt amcttacaag agggtggttt 600
tcctgaagca gctggctagt ggcttattac ttgtgactgg acctctggtc ctcaatcgag 660
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agcccagaca ccaggaaggt gagatcttcg acacagaaaa agagaaatat gagattacgg 840
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acaaattggt gttctaaatg tcttaagaac ctaattaaat agctgactac aaaaaaaaaa 1020

aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa ccccgggggg 1080
gggcccggtt cccatttngc cctttng 1107

<210> 41
<211> 1051
<212> DNA
<213> Homo sapiens

<400> 41
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agaacaaata ttcggtgctt ttacctacct acaacgagcg cgagaacctg ccgctcatcg 120
tgtggctgct ggtgaaaagc ttctccgaga gtggaatcaa ctatgaaatt ataatcatag 180
atgatggaag cccagatgga acaagggatg ttgctgaaca gttggagaag atctatgggt 240
cagacagaat tcttctaaga ccacgagaga aaaagttggg actaggaact gcatatattc 300
atggaatgaa acatgccaca ggaaactaca tcattattat ggatgctgat ctctcacacc 360
atccaaaatt tattcctgaa tttattagga agcaaaagga gggtaatttt gatattgtct 420
ctggaactcg ctacaaagga aatggaggtg tatatggctg ggatttgaaa agaaaaataa 480
tcagccgtgg ggccaatttt ttaactcaga tcttgctgag accaggagca tctgatttaa 540
caggaagttt cagattatac cgaaaagaag ttctagagaa attaatagaa aaatgtgttt 600
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tatgaagacc acctatttta tatttcaaat taaataattt taaagttgct ggcctaatga 960
gcaatgttct caattttcgt tttcattttg ctgtattgag acctataaat aaatgtatat 1020
tttttttgc ataaarwaaa aaaaaaaac c 1051

<210> 42
<211> 2192
<212> DNA
<213> Homo sapiens

<400> 42
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gctggacccc ctggccccat tggtaatgtt ggtgctcctg gagccaaagg tgctcgcggc 120
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cggttctcct ggcgccaagg gtgaccgtgg tgagaccggc cccgctggac cccctggtgc 660
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ccgaacatga ccaaaaacca aaagtgcatt caaccttacc aaaaaaaaaa aaaaaaaaaa 2160
actcgggggg ggcccggtac caattggcct aa 2192

<210> 43
<211> 353
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (37)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (348)
<223> n equals a,t,g, or c

<400> 43
tctctaatac gactcactat agggaaagct ggttacnctg caggtaccgg tccggaattc 60
ccgggtcgac ccacgcgtcc ggtggggctt caccaagttc aatgctgatg aatttgaaga 120
catggtggct gaaaagcggc tcatcccaga tggctgtggg gtcaagtaca tccccagtcg 180
tggccctctg gacaagtggc gggccctgca ctcatgaggg cttccaatgt gctgcccccc 240
tcttaatact caccaataaa ttctacttcc tgtccaaaaa aaaaaaaaaa aaaaaaaaaa 300
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaanaa aag 353

<210> 44
<211> 3490
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (782)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1311)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2298)
<223> n equals a,t,g, or c

<400> 44
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acgcgtccgg tgaaaactgt tgcattattc ctccatcctg tctggaatac accaggtcaa 120
caccagagat ctcagatcag aatcagagat ctcagagggg aataagttca tcctcatggg 180
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gtttgagacc ctgttactgt ttgaaaatgc atgcatgtta cgatgaatct ccaacctgag 3420
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aaaaaaacct 3490

<210> 45
<211> 781
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (750)
<223> n equals a,t,g, or c

<400> 45
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tccagcagcc tggagcctca tggccaaacc aggtcctcag gcatcccagg atttccaggc 120
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actgcaggac ctggcctcac targgtgtcg tgttaataaa cccagtctga tatcccagtt 720
ggamcaagac aagaagktgg tgacagaggn aagaggaatc taccaagcac ctgtccagat 780
t 781

<210> 46
<211> 1431

<212> DNA
<213> Homo sapiens

<400> 46
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ttattgaaaa tgaagagcag gaatatgttc aaactgtgaa gtcatccaaa ggtggtcccg 180
gatcagcggt gagcccctat cctaccttca atccatcctc ggatgtcgct gccttgcata 240
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agtttcttca acaggattac agtgtagcta cctacatgct gaaaaatata gcctttaaat 1260
catttttata ttataactct gtataataga gataagtcca tttttaaaa atgttttccc 1320
caaaccataa aaccctatac aagttgttct agtaacaata catgagaaag atgtctatgt 1380
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<210> 47
<211> 1913
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1878)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1896)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (1905)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1907)
<223> n equals a,t,g, or c

<400> 47
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gaagagagaa gacatattct acacttcaaa gctttggwgc aattccccatc gaccagagtt 360
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ycttattcat tttccagtgt ctgtaaagcc aggtgaggaa gtgatcccaa aagatgaaaa 480
tggaaaaata ctatttgaca cagtggatct ctgtgccacr tgggaggccg tggagaagtg 540
taaagatgca ggattggcca agtccatcgg ggtgtccaac ttcaaccrca ggcagctgga 600
gatgatcctc aacaagccag ggctcaagta caagcctgtc tgcaaccagg tggaatgtca 660
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cctggaatct ttggatgtgt gcccagttca cagattggac cctattggtt tgtggtgggg 1860
ccagggcatc caaagacntc attggactaa ttcacnttcc cccgnanagc ccc 1913

<210> 48
<211> 1761
<212> DNA
<213> Homo sapiens

<400> 48
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cagccggctt cgaagggctt caggcggagg agtgcggcat cctgaacggc tgtgagaatg 360
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aaaaaaaaaa aaaaaaaaag g 1761

<210> 49
<211> 956
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (37)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (352)
<223> n equals a,t,g, or c

<400> 49
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traagaccac ccctcctcat cgcccctcca ggcccccggc gccccacccc ctagagtgct 720
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wmcgkcccgt ggccctgcgc ggagctgtgt ccaataaagt tcttggatgt gaaaaa 956

<210> 50
<211> 563
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (510)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (519)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (530)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (558)
<223> n equals a,t,g, or c

<400> 50
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gccacaccgc cgctgcctca gtcatgccga agcacgagtt ctctgtggac atgacctgtg 120
gaggctgtgc tgaagctgtc tctcgggtcc tcaataagct tggaggagtt aagtatgaca 180
ttgacctgcc caacaagaag gtctgcattg aatctgagca cagcatggac actctgcttg 240
caaccctgaa gaaaacagga aagactgttt cctaccttgg ccttgagtag caggggcctg 300
gtccccacag cccacaggat ggaccaaagg gggcaggatg ctgatcctcc cgctggcttc 360
cagacagacc tgggacttgg cagtcatgcc gggtgatggt gttcctgcgg agaccctcag 420
ttgtcctatt ccttcctagc ttccctgcaa taaaatcaag ctgcttttgt tggaaaaaaa 480
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tcccattcat ccggcctnaa aaa 563

<210> 51
<211> 3215
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3196)
<223> n equals a,t,g, or c

<400> 51
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cgcactgcgc ctgtcagtag tggacattgt aatccagtcg gcttgttctt gcagcattcc 120
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ttgggcggaa agtgagagcc agcagcaaaa actacatttt gcaacttgtt ggtgtggatc 360
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acaattaagg tcaagcccag aaagtgataa gtgcagggag gaaaagtgca agtccattat 540
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aatcagagct ccagtttgca tttggatgtg taaattacag taatcccatt tcccaaacct 2760
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cagatgtttt gatgttatcg cttatgttaa tagtaattcc cgtacgtgtt cattttattt 3120
tcatgctttt tcagccatgt atcaatattc acttgactaa aatcactcaa ttaatcaawa 3180
aaaaaaaaaa aaaccncggg gggggcccg gaacc                            3215
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<210> 52
<211> 626
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (571)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (572)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (573)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (618)
<223> n equals a,t,g, or c

<400> 52

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accatgcctg agggtacaat cgtgtgctgc ctggaggaga agcctggaga ccgtggcaag 120
ctggcccggg catcagggaa ctatgccacc gttatctccc acaaccctga gaccaagaag 180
acccgtgtga agctgccctc cggctccaag aaggttatct cctcagccaa cagagctgtg 240
gttggtgtgg tggctggagg tggccgaatt gacaaaccca tcttgaaggc tggccgggcg 300
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cgcagagatg cccctgctgg ccgcaaagtg ggtctcattg ctgcccgccg gactggacgt 480
ctccggggaa ccaagactgt gcaggagaaa gagaactagt gctgagggcc tcaataaagt 540
ttgtgtttat gccaaaaaaa aaaaaaaaaa nnngggggc cgctttarag rwtcctccaa 600
ggggccaact taccсttnca tgcaaa                                     626
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<210> 53
<211> 920

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (617)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (621)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (725)
<223> n equals a,t,g, or c

<400> 53
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ctctgctact atgatcccaa ttcagatgct gacagtgaaa ccgtgaaggc agcaaaggtg 120
tggaaactcg cagagtcctg gtgggtgagc agcagcagtg ccasgatgcc aagagccagc 180
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agctgtgtgt cagtgtcagc cctgtattgt atttgattat ctcctgaata aagttatgat 900
attawaaaaa aaaaaaaaaa 920

<210> 54
<211> 1090
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1024)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1034)
<223> n equals a,t,g, or c

<400> 54
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tctctggagt gacttttttct cctcgaattg aaacaagtct atggcaaaag aagctgcatt 120
tttttcacaa aagggaagat ggtaacaatg gtcacttcaa acttttgggc taaattatat 180
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aaacatatac 1090

<210> 55
<211> 1464
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (766)
<223> n equals a,t,g, or c

<400> 55
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gacgctctca gctctcggcg cacggcccag cttccttcaa aatgtctact gttcacgaaa 120
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ctctcattga gatcatctgc tccagaacca accaggagct gcaggaaatt aacagagtct 540
acaaggaaat gtacaagact gatctggaga aggacattat ttcggacaca tctggtgact 600
tccgcaagct gatggttgcc ctggcaaagg gtagaagagc agaggatggc tctgtcattg 660
attatgaact gattgaccaa gatgctcggg atctctatga cgctggagtg aagaggaaag 720
gaactgatgt tcccaagtgg atcagcatca tgaccgagcg gagtgncccc acctccagaa 780
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cctgatcaga atcatggtct cccgcagtga agtggacatg ttgaaaatta ggtctgaatt 1020
caagagaaag tacggcaagt ccctgtacta ttatatccag caagacacta agggcgacta 1080
ccagaaagcg ctgctgtacc tgtgtggtgg agatgactga agcccgacac ggcctgagcg 1140

tccagaaatg gtgctcacca tgcttccagc taacaggtct agaaaaccag cttgcgaata 1200
acagtccccg tggccatccc tgtgagggtg acgttagcat tacccccaac ctcattttag 1260
ttgcctaagc attgcctggc cttcctgtct agtctctcct gtaagccaaa gaaatgaaca 1320
ttccaaggag ttggaagtga agtctatgat gtgaaacact ttgcctcctg tgtactgtgt 1380
cataaacaga tgaataaact gaatttgtac tttaraaaaa aaaaaaaaaa aactyrgggg 1440
ggggcccgka cccattggcc ttag 1464

<210> 56
<211> 985
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (647)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (875)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (962)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (973)
<223> n equals a,t,g, or c

<400> 56
agaagttgct agtgttcaat gcagctgggg tgaaacccca ggggcaaggt ggctggcttt 60
gatctggacg ggacgctcat caccacacgc tctgggaagg tctttcccac tggccccagt 120
gactggagga tcttgtaccc agagattccc cgtaagctcc gagagctgga agccgagggc 180
tacaagctgg tgatcttcac caaccagatg agcatcgggc gcgggaagct gccagccgag 240
gagttcaagg ccaaggtgga ggctgtggtg gagaagctgg gggtcccctt ccaggtgctg 300
gtggccacgc acgcaggctt gtaccggaag ccggtgacgg gcatgtggga ccatctgcag 360
gagcaggcca acgacggcac gcccatatcc atcggggaca gcatctttgt gggagacgca 420
gccggacgcc cggccaactg ggccccgggg cggaagaaga aagacttctc ctgcgccgat 480
cgcctgtttg ccctcaacct tggcctgccc ttcgccacgc ctgaggagtt ctttctcaag 540
tggccagcag ccggcttcga gctcccagcc tttgatccga ggactgtctc ccgctcaggg 600
cctctctgcc tccccgagtc cagggccctc ctgagcgcca cccggangtg gttgtcgcag 660
tgggattccc tggggccggg aagtccacct ttctcaagaa gcacctcgtg tcggccggat 720
atgtccacgt gaacagggac acgctaggct cctggcagcg ctgtgtgacc acgtgtgara 780
cagccctgaa gcaagggaaa cgggtcgcca tcgacaacac aaacccagac gccgcgagcc 840
gcgccaggta cgtccartgt gcccgagccg cgggngtacc cctgccgctg cttcctcttc 900
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cnccccgggg atngcacccc ctgga 985

<210> 57
<211> 1246
<212> DNA
<213> Homo sapiens

<400> 57
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gccattggaa ggggcatatg tgtgttgctg ggtatttccc tggaggatac gcagaaggaa 180
ctggaacaca tggtccgaaa gattctaaac ctgcgtgtat ttgaggatga gagtgggaag 240
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ctccagtgtg tcctgaaggg aaacaagcct gatttccacc tagcaatgcc cacggagcag 360
gcagagggct tctacaacag cttcctggag cagctgcgta aaacatacag gccggagctt 420
atcaaagatg gcaagtttgg ggcctacatg caggtgcaca ttcagaatga tgggcctgtg 480
accatagagc tggaatcgcc agctcccggc actgctacct ctgacccaaa gcagctgtca 540
aagctcgaaa aacagcagca gaggaaagaa aagaccagag ctaagggacc ttctgaattc 600
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tctccaayac actcacactg tccatgttct ttttattgcc agggcccgtg ttgaagtgtc 1140
aagagagcaa tcatcaatga taatgtattg tgtgagacct ttgcatcttg taaattttct 1200
ctttttctta aaaataaata ataataaaat cctaaatctc aacaaa 1246

<210> 58
<211> 1966
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1926)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1942)
<223> n equals a,t,g, or c

<400> 58
gggagaaaga tccttcactc acagaaccag ttattagggg gttaatgaaa ttttggccta 60
aaacatgtag tcaaaaagag gtcatgttcc ttggggactg gaagaaatat tggatgtgat 120
tgaaccttca caatttgtta aaatccaaga acctttgttt aaacaaatcg ccaagtgtgt 180
atctagcccc cattttcagg tggcagaaag agcactctat tattggaata atgaatacat 240
catgagtttg atagargaaa actctaacgt catccttccc atcatgtttt ccagccttta 300
taggatttca aaagaacatt ggaatccggc tattgtggcg ttggtgtaca atgtgttgaa 360
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tcgtcagcgt gagaaaaaga aagaaaagga gcgtgaagaa ttgtggaaaa aattggagga 480
tctggagtta aagagaggtc ttagacgtga tggaataatt ccaacttaac aaaaacaatg 540
acaacaacat tactaacctg tggagtcaca cgtttatgta gtagaagatg gagcaacagt 600
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tgccttactt tttaatatgt atttataaag tattccagca aaagaggatg tagcctctgg 1560
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caaaggtgca tcgtgaccaa attgtttaaa aaaaaaaaac aaaaaaaaca aaatctaggg 1860
ctgtatttta tatatatata tatatatata tatatatata tatatatata tatatatgtc 1920
cttatnggac tctctgcttt gntatttaaa taaaaaatct tacatc 1966

<210> 59
<211> 1611
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<400> 59
cgcgtcngtg cgaattcggc acgaggggac ttcccagagc tcacaatgga ggttgatggt 60
aaggtagagt caattatgaa gaggacagct ttggtagcca atacctccaa tatgcctgtt 120
gctgctagag aagccyctat ttatactgga atcacactgt cagagtactt ccgtgacatg 180
ggctatcatg tcagtatgat ggctgactct acctctagat gggctgaggc cttagagaaa 240
tctctggtcg tttagctgaa atgcctgcag atagtggata tccagcctat cttggtgccc 300
gtctggcctc gttttatgaa cgagcaggca gggtgaaatg tcttggaaat cctgaaagag 360
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ttacatctgc cactcttggt atcgttcagg tgttctgggg cttagataag aaactagctc 480
aacgtaagca tttcccctct gtcaattggc tcatcagcta cagcaagtat atgcgtgcct 540
tggatgaata ctatgacaaa cacttcacag agttcgttcc tctgaggacg aaagctaagg 600
aaattctgca ggaagaagaa gacctggcag aaattgtaca gcttgtggga aaggcttctt 660
tggcagaaac agataaaatc actctggagg tagcaaaact tatcaaagat gatttcctac 720
aacaaaatgg atatactcct tatgacaggt tctgcccatt ctacaagaca gtagggatgc 780

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gtgacaataa aatcacatgg tccattattc gtgagcacat gggagacatc ctctataaac 900
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aatatttaat tttcaaaaac ataatgatta atgttccaat tatgcatcac ttcccccagk 1560
ataaaycagg aatgkttgtg agaaaccatt gggaactata ctctttttta a 1611

<210> 60
<211> 1849
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (100)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (977)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1846)
<223> n equals a,t,g, or c

<400> 60
gattcccggg tcgacccacg cgtccgcgcg gaatctcagt tagcggtgga gaggcagtat 60
gtccggttca atggcgactg cggaagctag cggcagcgan tgggaaaggg caggaagtcg 120
agacctcagt cacctattac cggttggagg aggtggcaaa gcgcaactcc ttgaaggaac 180
tgtggcttgt gatccatggg cgagtctacg atgtcacccg cttcctcaac gagcaccctg 240
gaggagaaga ggttctgctg gaacaagctg gtgtagatgc aagtgaaagc tttgaagatg 300
taggacactc ttctgatgcc agagaaatgc taaagcagta ctacattggt gatatccatc 360
cgagtgacct taaacctgaa agtggtagca aggacccttc aaaaaatgat acatgcaaaa 420
gttgctgggc atattggatt ttacccatca taggcgctgt tctcttaggt ttcctgtacc 480
gctactacac atcggaaagc aaatcctcct gaggaggcct tgctgaagtt agaaagtgca 540
tccactttgg ggcgaaaact agagacttgc ttgggggctg cagaagtgcc ctctcctcga 600
atcctgccag ttgcattctt ccccccttgga gccaagacga ttggccagac atcacctcag 660
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ccgtgttgaa caattgccgg tgtttcctct cttcactggt ttccatgagt acccttatat 780
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aagtgagagt tcatgacaac agaccgtttt ccatttcatc tgtattttat ctccgtgact 1740
ccaacttgtg ggtttgttct gtttttccat gagaataaaa tactggcggt ttttttcaaa 1800
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagggngga 1849

<210> 61
<211> 233
<212> DNA
<213> Homo sapiens

<400> 61
aagggtcggc ctctcaaagt gctgggatta caggcattag ccactgtgcc tggccaagaa 60
taaaaatttt ttaatcttga gaaraaacat acagktcata catataaaaa gccttgaaaa 120
tattattccc tttgactcac taattacact gctggaatat aaagaaatga tcctaaatat 180
atatgtagtt ttatggtcct aaatatgtat aaagctttat gatcactcgt gcc 233

<210> 62
<211> 2333
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (14)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2327)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2331)
<223> n equals a,t,g, or c

<400> 62
cgncgnnccg cganccccacg cgtccggtgg aagatatgtg gacttagtcc cactacaacc 60
ttagccatat attttgaggt tgtcaatcag cataatgctc caattcytca aggagggcgt 120
ggtgcaatcc agtttgtgac tcagtatcag cattcaagtg ggcagagacg catccgagtg 180
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cctgatgaga gttcatatta tcgtcaccat tttatgcgtc aagatctgac ccagtctcta 540
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cttgatagca gtagcattct tgcagatcgt attcttctca tggacacatt cttccagatt 660
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tcaattagct taaataagtt gctttgttat attttatttg aattgaacta cgctaggcct 2280

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<210> 63
<211> 1470
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1410)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1414)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1419)
<223> n equals a,t,g, or c

<400> 63
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gaggacgcaa cgtcgagaac atgamgatct tgcgtctaat gctgctccac atcaaatacc 180
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gccgctgtgt gcccattgcc aagcgcgagc tactgtgggc tggctctgcc gggctggcct 360
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gaacgagaaa ccacaatggc tccatgctgc ccttcaaacg tggcgccttc catcttgcag 540
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accttcacct tccctcccag tgtagcctcc tgtcagtggg ggctggaccc ttctaattca 1380
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<210> 64
<211> 939

<212> DNA
<213> Homo sapiens

<220>
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<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (11)
<223> n equals a,t,g, or c

<400> 64
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cgtggaagcc gaagccgcac ctcccgcatg gcccctccgg ccagccgggc ccctcagatg 180
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gttggctctt ctgctgctgc gccccggcag ccaggtctga tggcccagat ggcaaccact 300
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ggcttcagtg gaggaagtaa tgctgagcct gcgaggcctg acatcactta ccaggagcct 420
cagggaaccc agccagcaca gcagcagcag ccttgcctct atgagatcaa acagtttctg 480
gagtgtgccc agaaccaggg tgacatcaag ctctgtgagg gtttcaatga ggtgctgaaa 540
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tgtaaccatc agttaaacct ctcctgtcat tcctagcttc cttgcttcag aattgaaatg 720
gaagtggggg tgtccctact ctgtagaatc tgggactggg caaatgtttg tgtggcctcc 780
ttaaactagc tgttatgtta tgattttatt ctttgtgagt taattagaat aaagtcattt 840
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<210> 65
<211> 2068
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (308)
<223> n equals a,t,g, or c

<400> 65
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cgggcagcag gctcctgact acaggtccat tctgagcatt agtgacgarg cagccagggc 120
acaagccctg aacgagcacc tcagcacgcg tagtatgtcc aggggtactc actgtcccag 180
gcagacgtgg acgcgttcag gcagctctcg gccccgcccg ctgaccccca gctcttccac 240

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tgggacccas catgcagact ccacctttac aacagcctca ccaggaacaa ggaagtgttc 420
atacctcaag atgggaaaaa ggtgacgtgg tattgctgtg ggccaaccgt ctatgacgca 480
tctcacatgg ggcacgccag gtcctacatc tcttttgata tcttgagaag agtgttgaag 540
gattacttca aatttgatgt cttttattgc atgaacatta cggatattga tgacaagatc 600
atcaagaggg cccggcagaa ccacctgttc gagcagtatc gggagaagag gcctgaagcg 660
gcacagctct tggaggatgt tcaggccgcc ctgaagccat tttcagtaaa attaaatgag 720
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<210> 66
<211> 1391
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (16)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (20)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (27)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1343)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1358)
<223> n equals a,t,g, or c

<400> 66
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gttagcctaa gtcacttcca ccctccaatg ttgtgaatgc agtctctagc attcgctatt 180
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ccccgccgtg ggaacggcct gacagtcact cgtcaaagga agtggctgcc ggcagctctt 420
gacccggaat cggatcctag tcccaccccc tccgctccag gcttccttct gcaacaggcg 480
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aggattccac ccaggcaacc acacaacaag cccagctggc ggcagcagct gaaatcgatg 720
aagaaccagt cagtaaagca aaacagagtc ggagtgaaaa gaaggcacgg aaggctatgt 780
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aaaaaaaaaa aaaaaaaagg cgnggccgca ggcttttncc ctttggtggg ggttattttt 1380
ggcttggccc t 1391

<210> 67
<211> 659
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (139)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (475)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (585)
<223> n equals a,t,g, or c

<400> 67
gcaaggctgc tgctatgggg ccgggcggcg tgtggcgcgg ctgctcgccc cactaatgtg 60
gcgcagggcg gtttcctcgg tggcggggtc cgcggttgga gccgagcccg ggcttcggct 120
gctggccgtg cagcgyttnc ccgtagagca gcgttctgcc gggcttgcca gaccccaaac 180
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gatggtttca cttctgaggc aagaaaatgc aagagacatt tgtgtgatcc argttcctcc 360
agaaatgaga tatacagatt actttgtgat tgttagtgga acttctaccc gacacttaca 420
tgccatggcy ttctacgttg tgaaaatgta caaacacctg aaatgtaaac gtganccctc 480
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tggattcatt tgaatgcttc cagaaaacca gagaaatcta tgganttaga gaaattatgg 600
accctacgtt cttatgaatg accagttagc tcagatagca cctgaggaca gtacctgta 659

<210> 68
<211> 2981
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2858)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2948)
<223> n equals a,t,g, or c

<400> 68
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ttaccaccgt gttagaaagc agcctcagga ccggccacct ccatcactgg cgtcaccatg 120
ggggctgtgc tgggtgtctt ctccctcgcc agctgggttc catgcctctg cagcggtgcc 180
tcatgtttgc tgtgtagttg ctgtcctaac agtaagaatt ccacggtgac tcgcctcatt 240
tatgctttca ttctcctcct gagcactgtc gtatcctata tcatgcagag aaaagagatg 300
gaaacttact tgaagaagat tcctggattt tgtgaagggg gatttaaaat ccatgaggct 360

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gatataaatg cagataaaga ttgtgatgtg ctggttggtt ataaagctgt gtatcggatc 420
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agtaaagatc tccgagcggc agtacacaat gggttttggt tcttcaaaat tgctgccctt 540
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gttgttggca tgataggggc cgccctcttc atcctcattc agctggtgct gctggtagat 660
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<210> 69
<211> 603
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (584)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (590)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (595)
<223> n equals a,t,g, or c

<400> 69
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gccgccattt catctgtcct cattctctgc gcctttcgca gagcttccag cagcggtatg 120
ttgggccaga gcatccggag ttcacaacct ctgtggtccg tagagccact atgaggaggg 180
ccctgggaag aatttgccat tttcagtgkg taaggggcac ggcttcgttg ggggaggggg 240
cgcttggctg tgactcgcgc acctgcaagg ccgcctccgg gctgtggcgt gggagatgat 300
agccagaaac caggctgaga cgcagactag cattccactt agcccaagga ccagtgagga 360
agctgggcat cctagcgcgt accgctaaag gaatgggcag gtagatccgg aagccctgcc 420
tccatcagcc acctgacgcc ccctccccg ccccgcagaa agccctgaga tggcyccggg 480
aggccacggc tgtaggtgtg ttggttaaat ccgagctgga ggtcatcgga cccgaaatga 540
aggtcattgg aaaatcatga ggaaatcagg gctctggtta tggnacaggn ttttnaaact 600
agc                                                               603
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<210> 70
<211> 1101
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (195)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1080)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1081)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1090)
<223> n equals a,t,g, or c

<400> 70
aattcggcac gagcacagct catgttttcc agcctgtgtg ggagcttggt ctgaagagag 60
attaagtgat agcctactta tggatcctgg agaattcttc agaaatccat gtgtaactca 120
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tggggcacat gccttggatt tgaagagctt tcactgctga ttagtggaga gtgcttatta 300
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aagaagtttt tcaatgtctt aactacaaat acagatggca agattgagtt tatttcaaca 540
atggaaggat ataagtatcc agtatatggt gtccagtggc atccagagaa agcaccttat 600
gagtggaaga atttggatgg catttcccat gcacctaatg ctgtgaaaac cgcattttat 660
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gaagaggaga aagcattgat ttatcagttc agtccaattt atactggaaa tatttcttca 780
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gattcttttc tataatgtgc ctggctctga ttcttcattc tgtatgtgac tatttatata 960
acattagata attaaatagt gagacataaa tagagtgttt ttcatggaaa agccttctta 1020
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<210> 71
<211> 714
<212> DNA
<213> Homo sapiens

<400> 71
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gaagtcagtt cgttctctcc tctcctctct tcttgtttga acatggtgcg gactaaagca 120
gacagtgttc caggcactta cagaaaagtg gtggctgctc gagcccccag aaaggtgctt 180
ggttcttcca cctctgccac taattcgaca tcagtttcat cgaggaaaga gcatgtcctt 240
tgcaacctga tcacacaaat gatgaaaaag aatagaactt tctcattcat ctttgaataa 300
cgtctccttg tttaccctgg tattctagaa tgtaaattta cataaatgtg tttgttccaa 360
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ataatgcatt gtttggtttc ttttaccaaa ttaagtgtct agttcttgct aaaatcaagt 540
cattgcattg tgttctaatt acaagtatgt tgtatttgag atttgcttag attgttgtac 600
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<210> 72
<211> 2890
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (555)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2853)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2882)
<223> n equals a,t,g, or c

<400> 72
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gtcttcatca gcatcggttc tgccctgggc ttcaaatacc cggtggggaa caaccagacg 180
gcggtccagg acaacgtgaa ggtgtcgctg gccttcgggc tgagcatcgc cacgctggcg 240
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<210> 73
<211> 2488
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (277)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (446)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2382)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2412)
<223> n equals a,t,g, or c

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<210> 74
<211> 711
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (696)
<223> n equals a,t,g, or c

<400> 74
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acactatcta tgtaaaattc aaaactggaa aagtataaag ggtacagaga gacacctgcc 120
tcccaccgat gtccctcagc ttccacttac cctccaggag aatgaagaat ccctccattg 180
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ccactgatat tcctgtggtg tgtctagaat cagataatgg gaacattatg atccagaaac 360
acgatggcat cacggtggca gtgcacaaaa tggcctcttg atgctcatat ctgttcttca 420
gcagcctgtc ataggaactg gatcctacct atgttaatta ccttatagaa ctactaaagt 480
tccagtagtt aggccattca tttaatgtgc attaggcact tttctgttta tttaagagtc 540
aattgctttc taatgctcta tggaccgact atcaagatat tagtaagaaa ggatcatgtt 600
ttgaagcagc aggtccaggt cactttgtat atagaatttt gctgtattca ataaatctgt 660
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<210> 75
<211> 906
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (362)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (889)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (894)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (897)
<223> n equals a,t,g, or c

<400> 75
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cttaca 906

<210> 76
<211> 271
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c

<400> 76
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aaaacaaaac cctctgtatc attatgtgaa caacggtgca aaaaagagga gacacagttt 180
acccatgggt agctaactat gatagtgaaa gttgccttga accttgtttt agaaaaatgg 240
caagtgtggg tctcactctt ctagttcctg a 271

<210> 77
<211> 673
<212> DNA
<213> Homo sapiens

<400> 77
ttcggcacga gggtgaccag cggcgggtca cgtgacgcgg tgcctggcgc cgagcctccc 60
aagatggcgg tgtgcatcgc ggtgattgcc aaggagaatt accccctcta cattcgcagc 120
accccctacgg agaacgagct gaagttccac tacatggtgc acacatctct ggacgtggtg 180
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gggggggcc cgg 673

<210> 78
<211> 367
<212> DNA
<213> Homo sapiens

<400> 78
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aatacgttca cttgctattt taatccatca ctgtagatat gactcagtcc ctttgttatt 300
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ttttctc 367

<210> 79
<211> 1344
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1319)
<223> n equals a,t,g, or c

<400> 79
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<210> 80
<211> 3748
<212> DNA
<213> Homo sapiens

<400> 80
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<210> 81
<211> 1891
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1869)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1879)
<223> n equals a,t,g, or c

<400> 81
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tacttcttgg aaatgaaaaa taagatgcct tccttatctc caatagacaa gaattggccc 180
tcaagacctt acttattctt ggattctact cacaaggagc taaaaaggat tttccacttg 240
tggaggtgta aaaaatacag ggaccaattc acagaccagc agaaacttat ttatgaagag 300
aaactagaag ccagtgaact cttcaaagac aagaaggctt tatacccatc tagtgttggg 360
caaccattcc aaggggctta cctggaaatc aacaagaacc ccaagtataa gaaactcaaa 420
gatgccattg aagaaaagat catcattgct gaagtcgtga acaaaattaa ccgtgctaat 480
gggaagagta catctcggat ttcctcttta acaaacaata atctccttct tgctgaccaa 540
aagtctggac aaatcaagtc agaggttcca ytggtggatg tgaccaaggt atcaatgagc 600
tcacaaaatg atggcttctt cgccgtccac ctcaaagagg gctcagaagc agctagtaaa 660
ggagactttc tcttcagcag tgatcacctg attgaaatgg ccaccaagct ctatcgcaca 720
actctcagcc aaaccaaaca gaagctcaat attgagattt ccgatgagtt cctggtacag 780
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tctggtaaat accatatatg atcctcgaaa tgataatatc tccagaatat tgttttcacc 1740
caaatttgag tagatatttt aaacacctaa caaagtaaag ggctaaaagc cattcagata 1800

gcagtaaaac attctgtatg atgtgcaata aaacatccaa gatctttttt gaaagtgwka 1860
tttccgttna agtcccccnt taggaccccc g 1891

<210> 82
<211> 1954
<212> DNA
<213> Homo sapiens

<400> 82
ttcagtgtct ggcacactga gacacctcca agaaggagat tgatgcatca ggttcagttt 60
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atttatgggt attttttttc gaagttatta agcatattcc ttttccacga acctcttctg 180
tactttgatt gtaataggtt ggctcttaca cccattccaa atgcagttta tttttagacc 240
cgattgcaaa tagtgatgta gttttaacca gtatggatta gttcagggat gaactgctcc 300
ctccagcctt actggctctg atccacaggg ttttgttttg ttttgttttg tttttgttt 360
aagtcgagat ataaaaactg aacacgataa cacttactct taaatcaagc atcaacactt 420
tttccctgtt agaattcttt gcatttttgt gtttgtaaca gaaacgcctt aagacactat 480
gtttgggaat ataggaaact atgtgtgtcc caaggaaatc cctgtaaatt taactcacct 540
acaaaaggct ttttccccgc ctttggttgt taacggcatt cctgaaagcc acatgtgttt 600
attcattggg cttgttctta tcagcaaata ggttttctgg ttttatgact ttttgtctta 660
ttttatkttt cctacatttc tttttttttt tttttccytt agaatgccck ggraatatat 720
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accagtgaag tttttagaa cctttagaag ggtggtcttt attcaggttt tactgtaatg 840
gtaaggattg actcaagaga cagtattagt aaatttattg tgtatggatc aaaagtgaat 900
aatgtatgaa tgagagctgt aagaaggatt tttattttgt tataatttag ttaccatttt 960
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gatggcttcc agatttgtaa gattktatgt tgtatatacc attctattaa gaaacatgtc 1140
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aacttatttg tgtgactaat tgcctagatt gtaagctctt tgagggcagg gcttgtctct 1860
tacacatctt tataatcccc tgcagcggct ttcagtattt tgtacttgta ggcacctaat 1920
aaatttatta tttgctatac tgaaaaaaaa aaaa 1954

<210> 83
<211> 936
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (895)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (930)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (936)
<223> n equals a,t,g, or c

<400> 83
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caagaaactg taggcaatgt tgtcctgttg gccatcgtca ccctcatcag cgtggtccag 120
aatggattct ttgcccataa agtggagcac gaaagcagga cccagaatgg gaggagcttc 180
cagaggaccg gaacacttgc ctttgagcgg gtctacactg ccaaccagaa ctgtgtagat 240
gcgtacccca ctttcctcgc tgtgctctgg tctgcggggc tactttgcag ccaagttcct 300
gctgcgtttg ctggactgat gtacttgttt gtgaggcaaa agtactttgt cggttaccta 360
ggagagagaa cgcagagcac ccctggctac atatttgggg aaacgcatca tactcttcct 420
gttcctcatg tccgttgctg gcatattcaa ctattacctc atcttctttt tcggaagtga 480
ctttgaaaac tacataaaga cgatctccac caccatctcc cctctacttc tcattcccta 540
actctctgct gaatatgggg ttggtgttct catctaatca atacctacaa gtcatcataa 600
ttcagctctt gagagcattc tgctcttctt tagatggctg taaatctatt ggccatctgg 660
gcttcacagc ttgagttaac cttgcttttc cgggaacaaa atgatgtcat gtcagctccg 720
ccccttgaac atgaccgtgg ccccaaattt gctattccca tgcattttgt ttgtttcttc 780
acttatcctg ttctctgaag atgttttgtg accaggtttg tgttttctta aaataaaatg 840
cagagacatg ttttaagctg aaaaaaaaaa aaaaaaaacc cggggggggc ccggnaccaa 900
ttcgcccaaa agggggcgat taaaatcccn ggccgn 936

<210> 84
<211> 1513
<212> DNA
<213> Homo sapiens

<400> 84
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gtggagaccg gagaagctgt gaggttcttt agcgtcacct ccctcactgg gcagcatggg 120
ggagaagtca gagaactgtg gggttccaga ggatctgtta aatggtttga aggttacaga 180
tactcaggaa gccgagtgtg ctggccctcc agttcctgat cccaaaaatc agcattccca 240
gagtaagctg ctcagggatg atgaggccca tctccaggag gaccagggag aagaggagtg 300
ttttcatgac tgcagtgcct catttgagga ggagccagga gcggacaagg ttgagaacaa 360
atctaatgaa gatgtgaatt cctctgaact agatgaagaa tacctaatag aactggaaaa 420
aaacatgtcg gatgaagaga aacagaaaag aagagaagag agcactagac taaaggagga 480
gggaaatgaa cagtttaaga aaggagatta tatagaagct gaaagttctt atagtcgagc 540
cctcgaaatg tgcccatcct gcttccaaaa ggagaggtcg attctatttt caaatagagc 600
tgcagcaagg atgaaacagg acaagaaaga aatggccatc aatgactgca gcaaagcaat 660
tcaattaaac cccagctata tcagggcaat attgaggaga gcagagttgt atgagaagac 720
ggacaagcta gatgaagccc tggaagacta taaatctata ttagaaaaag atccatcaat 780
acatcaagca agagaagctt gtatgagatt acctaagcaa attgaagaac gtaatgaaag 840
actaaaagaa gagatgttag gtaaattaaa agatcttggg aacttggttc tccgaccttt 900

tgggctctcc acggaaaatt tccagatcaa acaggattcc tctaccggct cgtactccat 960
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tcttttatga tcagggtgaa atgtacttcc tgatgtaatg aacctaattt gatttccatt 1200
ttaaggtggt gtctgtgcag ctggtgtccc cgattctggc tgtcctatgt ccaggaagaa 1260
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cctgaaccaa acaaacctgt tggttgggag actgcccaga catgattgat gacgggttcc 1380
cgcctgctgt cccctccctg atcacacagc taacgaggct gcctccagca tttcctgatt 1440
tcctctgtgg taataaaagc tttctgtgct taaaaaaaaa aaaaaaaaaa aaacttcgag 1500
gggggggccc ggt 1513

<210> 85
<211> 1298
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<400> 85
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tggcgcggtt ggcgggggca gtcccgagcg tgaggaggtc ggcgcaggct acaacagtga 120
ggacgagtat gaggcggctg cagcacgcat cgaggctatg gaccctgcca ctgtcgagca 180
gcaggagcat tggtttgaaa aggccctacg agacaagaag ggcttcatca tcaagcagat 240
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ctccaactat gtcacagagg actttaccac ctacattaac aggaagcgga aaaacaattg 420
ccatggcaac cacattgaga tgcaggccat ggcagagatg tacaaccgtc ctgtggaggt 480
gtaccagtac agcacagaac ccatcaacac attccatggg atacatcaaa acgaggacga 540
acccattcgt gttagctacc atcggaatat ccactataat tcagtggtga atcctaacaa 600
ggccaccatt ggtgtggggc tgggcctgcc atcattcaaa ccagggtttg cagagcagtc 660
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agacaagaaa cgggccacag actgggaggc cacaaatgaa gccatcgagg agcaggtggc 780
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tggcctggag gagtggacta gccggtcccc gcggcaggag tttcagcctc gtcacctgag 960
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cagagacccg cccccagaca agagttgatg gagaccca 1298

<210> 86
<211> 2009
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1955)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1959)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2008)
<223> n equals a,t,g, or c

<400> 86
gtgttcgtcc gcttgtcact gaattggacc ctgatgctcc cataagacag aaaatgcccc 60
ttgatgatct ggatagagaa gatgaagtta gattactcaa atatctcttt actctaatcc 120
gtgctggaat gacagaagag gcacaacgac tctgtaaacg ctgtggtcaa gcatggagag 180
ctgcaacact tgaaggctgg aaactgtacc atgaccctaa tgttaatgga ggaacagaat 240
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cagaagatga gctttttaat agatacgaga gagcaattta tgcagcttta agtgggaatc 360
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tagctctctc cctatagtga gtcgtacng 2009

<210> 87
<211> 534
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (466)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (477)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (526)
<223> n equals a,t,g, or c

<400> 87
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cgagcacctt cgggccctcg actgctccga ggtgacggtg cgagccctgc ccgagggctc 120
cctcgccttc cccggagtgc cgctcctgca ggtgtccggg ccgctcctgg tggtgcagct 180
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cagcagcaac gtgctagcgg gccagctgcg aggtgtgccg gtggccggga ccctggccca 420
ctccttcgtc acttcctttt caggcagcga ggtgcccctg acccgntgtt ggggcanaag 480
tttgtgaagg gccttgggtt gacctggggg caaagccaag ttttgnttga gcaa 534

<210> 88
<211> 4302
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1015)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4270)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4274)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4296)
<223> n equals a,t,g, or c

<400> 88
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ggtggcacct ctccctttct ccacggacat cggacatcct caaaatcaga ctgtcaggtg 120
ggcagaagaa atccagacta gtagaccaca aaccataact gaacaagact ctaacaagaa 180
ttcttcaaca gcagaaatta acgaaacaac aacctcatct actgattttc tggctagagc 240
ttatggtttt gaaatggcca aagaatttgt tacatcagca ccaaaaccat ctgacttgta 300
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tgcaactact caggcaacca gacaagaaag cagcaccaca tttgtttctg atgggtccct 420
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agctgtcaac ctttctttaa ctgaggaaac atttgagggc tctgctgatg ttctggctag 960
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aaattgaatt agaaggtgct acacagtggc cacactctac ttctgcttct gccacctatg 1980
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<210> 89
<211> 2782
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (82)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (743)
<223> n equals a,t,g, or c

<400> 89
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aatgtggtgc tgaaaggaga antgagtgcc cggatgaaga ttccaagcaa tatgtgggta 120
gaagcctggg aaacagctaa gccaattcct gctagaaggc aaaggagact ctttgatgat 180
acacgggaag cagaaaaggt gctgcactat ctggcaatcc agaaacctgc agaccttgct 240
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ctcgaaaaca tttcttcagt taagaagatc ataaagcaga taatatccca ttccagtaaa 360
gttttgcact tccccaatcc agaagacaag aaattggaag aaatcattca ccagattact 420

aatgtggaag ctctcattgc cagagctcgg tcactaaaag ccaagtttgg aactgagaaa 480
tgtgaacagg aggaggaaaa ggaagatctt gaaaggtttg tgagttgcct gctggagcag 540
cctgaagtgt tagtcaccgg tgcaggaaga ggacatgctg gcaggatcat tcacaagctg 600
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gctcccccaga ggaaagaagg cagaactccg tgtcagactt cccacccccct gctggccggg 720
aattcatttt gsgcamcact gtncgcgccc tgctccctac tccaaagctc tgcctcagcg 780
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acgttgccac aaaatgttga gtatagtcaa ctctgctgtg tggatcggag ggcctgcatt 2700
tatcctacaa ataattgaat gtaatcctac attcatgtat tcattggcag tacggagtaa 2760
taaatgcagc aatgccataa aa 2782

<210> 90
<211> 1037
<212> DNA
<213> Homo sapiens

<400> 90
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acactttatc tccaagttac aaaagtttga ggtgcagagg gaaggccaga tttttttttt 120
aatgaaatta tatagattag atctcagtat ttaaactgtt cctcaatttt gtgaggctgt 180
gttggaaata acccgcctct agtgctgttg gtatgcaagg cagcggtgct taatcaatat 240

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cttctggtgg ttaccctgac tcttgactct tagaagtgcc cgagatgggg ctaaccttta 360
ttaaacagat cgcatattat gatcttgctg cagccacagt gcagctccac attaactcta 420
cagaccaaac catttgtatc tggcatcact tactaacaca cgacatgcgg cttttctgca 480
tcaactgcta tgacggttaa gaatgtcagt atacaagaag gaatagaaaa ctgatactgt 540
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tttgagataa ttctagtaca aagtataata aaactagatg tataataaac cctttaaatc 660
attggtaagt gtacaagtgg tggaactgaa gcatttactg gacaaagtaa tgttactcta 720
atggttactt gctcgtgcgt tgccacactg tgttataatt tgcttcattt ccttgctatt 780
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aacggggggg ggcccgg 1037

<210> 91
<211> 1052
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (76)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (962)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (965)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1044)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1048)
<223> n equals a,t,g, or c

<400> 91
gggcacgagt gcaggtggat gctgcactgc acccagcatc tctgcttatc aggaggctct 60
ggagccacac cgcagnaagc acacgccctt ttgagccaga catgctgact ttctaataag 120
gatgttctct ctccacagct gaaagatgaa aattctaagc tgagaagaaa gctgaatgag 180
gttcaragct tctytraagc wcawacagaa atggtgagga cgcttgagcg gaagttagaa 240
gcaaaaatga atcaaggagg aaagcgacta ccacgacctg gagtcggtgg ttcagcaggt 300

ggagcagaac ctggagctga tgaccaaacg ggctgtaaag gcagaaaacc acgtcgtgaa 360
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agccctgcgg tgcggccagg gtgccagcct gaccgtggtg aagcagaacg ccgacgtggc 480
cctgcagaac ctccgggtgg tcatgaacag tgcacaggct tccatcaagc aactggtttc 540
cggagctgag acactgaatc ttgttgccga aatccttaaa tctatagaca gaatttctga 600
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tngangggc ccaagcttac gcgtgcattc gacgtcataa ctttttccc tataagggag 1020
cgattataag cttaggcact tggnccgngg tt 1052

<210> 92
<211> 1234
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1115)
<223> n equals a,t,g, or c

<400> 92
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gttctctcgc gcgggtgtcg ctgggctgtc ggcctggacc ttgcagccgc aatggattca 120
agttcgaaat atggcaactt tgaaagatat caccaggaga ctaaagtcca tcaaaaacat 180
ccagaaaatt accaagtcta tgaaaatggt agcggcagca aaatatgccc gagctgagag 240
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tatcaagggg cctgaagaca agaagaaaca cctccttatt ggtgtgtcct cagatcgagg 360
actgtgtggt gctattcatt cctccattgc taaacagatg aaaagcgagg ttgctacact 420
aacagcagct gggaaagaag ttatgcttgt tggaattggt gacaaaatca gaggcatact 480
ttataggact cattctgacc agtttctggt ggcattcaaa gaagtgggaa gaaagccccc 540
cacttttgga gatgcgtcag tcattgccct tgaattacta aattctggat atgaatttga 600
tgaaggctcc atcatcttta ataaattcag gtctgtcatc tcctataaga cagaagaaaa 660
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tccattattt gaattactga agacagcaag atatttgtaa attatcttaa aataaacaac 1080
ttaaaataaa atcattgttt ttcttatata taagnacaat agatatagtt tttgaaatga 1140
gatgatacta aaacatttaa aaatattaat atgctactat taaaattttt tagtagaaga 1200
caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1234

<210> 93
<211> 1571
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1497)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1516)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1530)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1546)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1571)
<223> n equals a,t,g, or c

<400> 93
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gctttccctg ggtccggggg ctgccasgag ggascgggar gtctgtccac ctcacaaggc 120
aggctctgtc agcttttgtc actccctgat ttcttattct ttgttacctt ttttcgcctg 180
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aaaagttact tcttttttc cccaccagtt ataatcttca accttactag tttataacag 600
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gtttgaatta ctaatagtgg ggaataataa tttcagtttt ggttttaaac atctggnatt 1500
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aaaggggggg n 1571

<210> 94
<211> 1872
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (51)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1271)
<223> n equals a,t,g, or c

<400> 94
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aatgttgtaa taaatattcc tttgatcttg gtgtttgcaa aaaaaaaaaa aaaaaaaact 1860
cgagactagc gg 1872

<210> 95
<211> 1516
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1505)
<223> n equals a,t,g, or c

<400> 95
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cttccgggag ggcactgtct agtgcacagg caacctggcc ttsgcctcct agcccgagaa 120
gccgaatctc cctaatccct gtgacctgtg tcacctctgc atcgcgagga gggggataag 180
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aaggcgcccc caccccaact ccacgggaat ataaacaatt tgtattttcc gatcaggtgg 300
cgggacaggc ttcattggga cagccctaac ccagctgctg aatgccagag gccacgaagt 360
acgttggtct cccgaaagcc cgggcccggc cggatcacgt gggatgagct cgctgcatcg 420
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<211> 1770
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (485)
<223> n equals a,t,g, or c

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<211> 938
<212> DNA
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<223> n equals a,t,g, or c

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<222> (938)
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<211> 311
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (297)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (309)
<223> n equals a,t,g, or c

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<210> 99
<211> 620
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (368)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (570)
<223> n equals a,t,g, or c

<400> 99
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<211> 2511
<212> DNA
<213> Homo sapiens

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<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (28)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (44)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2456)
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<222> (2488)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2511)
<223> n equals a,t,g, or c

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<210> 101
<211> 2981
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (293)
<223> n equals a,t,g, or c

<400> 101

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<211> 2804
<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

<400> 103
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gccttctcca aggccctgcc ccgcagctaa gccagcactg agmtgcgtgg tgcctccagg 600
accgctgcgg gtggtaacca gtggaagacc ccagccccca gggagaggaa cccgttctat 660
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aa 722

<210> 104
<211> 1636
<212> DNA
<213> Homo sapiens

<400> 104
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aaaaaggggg gggggg 1636

<210> 105
<211> 1561
<212> DNA
<213> Homo sapiens

<400> 105
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gtatgacctc agccggccta ctgcctctca gctggaggac gagctgcagg tggggaatgt 180
tccccttaaa aaagcaaagg agtctaaaaa gcatgaaaag cttgagaaac cagagaagga 240
gaagaaaaaa aagatgaaga atgagaacgc agacaagtta cttaagagtg aaaagcaaat 300
gaagaagtct gagaaaaaga gcaagcaaga gaaagagaag agcaagaaga aaaaaggagg 360
taaaacagaa caggatggct atcagaaacc caccaacaaa cacttcacgc agagtcccaa 420
gaagtcagtg gccgacctgc tggggtcctt tgaaggcaaa cgaagactcc ttctgatcac 480
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accatgaaaa tcgaccactt tcagctagat aatgagaagc ccatgcgagt ggtggatgat 660
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aacttcctat ccaggttccg gtggaggagg aggttgctgg tgatctctgc tcctaacgat 960
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gaactgttcc caattaatgg gagctctgtt gttgagcgag aagacgtacc agcccatttg 1140
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tactgagcag aaatatgtaa ccttagactc agccagtttc ctctgcagct gctaaaacta 1500
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t 1561

<210> 106
<211> 486
<212> DNA
<213> Homo sapiens

<400> 106
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catttgccaa aaatgagtct aagtgcattt actctcttcc tggcattgat tggtggtacc 120
agtggccagt actatgatta tgattttccc ctatcaattt atgggcaatc atcaccaaac 180
tgtgcaccag aatgtaactg ccctgaaagc tacccaagtg ccatgtactg tgatgagctg 240
aaattgaaaa gtgtaccaat ggtgcctcct ggaatcaagt atctttacct taggaataac 300
cagattgacc atattgatga aaaggccttt gagaatgtaa ctgatctgca gtggctcatt 360
ctagatcaca accttctaga aaactccaag ataaaaggga gagttttctc taaattgaaa 420
caactgaaga agctgcatat aaaccacaac aacctgacag agtctgtggg cccacttccc 480
aaatct 486

<210> 107
<211> 800
<212> DNA
<213> Homo sapiens

<400> 107
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ttggcttcaa ctactattac aaatattcca atgaaggtga ttcgcatcta ggtggcggca 180
gtcgagaagg ctcgtttaaa gaaacaataa cattaaagtg gtgtacacca aggacaaata 240
acattgaatt acactattgt actggagctt atcggatttc acctgtagat gtaaatagta 300
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cacgaaagtc aggttctaaa gtcattagtc atatgcttag tagccatgga ggagagattt 420
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caaaccacca tttttaacak gcaagcggta gttccattag ccagtgttat tgtggaaaga 720
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ataaggggaa ggaaaaaagg 800

<210> 108
<211> 1058
<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (895)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1019)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1054)
<223> n equals a,t,g, or c

<400> 108
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caggcgagca cccgggagcc agcgggacct gggcaggggc gcccggagca ggccgcatgg 120
cgggccccgc gcggggatcc ggctggaaga gagcgtacac ggctcgcacg agtccggggc 180
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gcgcamcccg ggcccagccc agaccytaty ccttccttcc tgggctggar gtaktaacag 300
gatccactca ccctgcggag gcagcaccag aggagggctc cctggaggag gcggcaaccc 360
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tccccacaga agctgtgaca tgccagcctc aggggaaccc ttgggctgca ccccacttct 480
gccgaatgac tctggccacc cctcagagct gggcggcacc agacgggcgg ggaatggtgc 540
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<210> 109
<211> 1076
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (780)
<223> n equals a,t,g, or c

<400> 109
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tggaagcaga tgggattaaa tgagcgacga gactgggaga gtgccagaga gagacaccaa 120
gaggatgcag gtctgtctgc tatcagctat gccgctgccc gttgcgctgc agacccgctt 180

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa waaaaaaatt ttgggggggg cccccct 1076

<210> 110
<211> 1199
<212> DNA
<213> Homo sapiens

<400> 110
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<210> 111
<211> 3630
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3606)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3608)
<223> n equals a,t,g, or c

<400> 111
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cggccgctcc tcgctgcgct tcgcctccgc ctcctcggac tcggactcgg gtttatatcg 180
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<210> 112
<211> 1526
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1496)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1511)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1512)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1515)
<223> n equals a,t,g, or c

<400> 112
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ggctccgggc agctcggcct tgggggcttc ggggccccga gacgcggggc gtatgagtgg 180
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gagaccttct accccatatc acccatcatc gatcttcatg aatgcaatat ttatgatgtg 900
aaaaatgaca caggattcca ggaaggctat ccttacccct atccccatac cctgtactta 960
ctggacaaag ccaatttacg accacaccgc cttcaaccag atcagctgcg ggccaagatg 1020
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gcctgggtgg actcagacca gctcctctat cagcattttt ggtgtctccc agtgatcaaa 1260
aagagagtgg ttgtggaacc tgttggccca gttggtttca agccagagac attcagaaag 1320
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ccctcttgcc tctcttccac ggaagaggcc tgggccccgt ggagcctcag tgcccgtttg 1440
gcctgctgct ctcgctgaca ataaagagcc cttgcgttgc aaaaaaaaaa aaaaangggg 1500
ggccgctcaa nnggncccaa gttagt 1526

<210> 113
<211> 585
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (422)
<223> n equals a,t,g, or c

<400> 113
tcgacccacg cgtccgccca cgcgtccgcc cacgcgtccg ggagcccggt gacaggatgt 60
tggtgttggt attaggagat ctgcacatcc cacaccggtg caacagtttg ccagctaaat 120
tcaaaaaact cctggtgcca ggaaaaattc agcacattct ctgcacagga aacctttgca 180
ccaaagagag ttatgactat ctcaagactc tggctggtga tgttcatatt gtgagaggag 240
acttcgatga gaatctgaat tatccagaac agaaagttgt gactgttgga cagttcaaaa 300
ttggtctgat ccatggacat caagttattc catggggaga tatggccagc ttagccctgt 360
tgcagaggca atttgatgtg gacattctta tctygggaca cacacacaaa tttgaagcat 420
tngagcatga aaataaattc tacattaatc caggttctgc cactggggca tataatgcct 480
tggaaacaaa cattattyca tcattgtgtt gatggatatc caggcttcta cagtggkcac 540
ctatgtgtaa tcagctaatt ggagatgaag tgaaagtaga acgga 585

<210> 114
<211> 501
<212> DNA
<213> Homo sapiens

<400> 114
gatgaaaaga aggtttttgc tcttcaaatg cttaagtaaa ctaaaaggca gagctggaaa 60
taaagcccgt attgtggact ccaagtaatg ctctttctgc tacaccatac tttgtggtgt 120

ctgctcccat gtgcttcttc gctaaggctg atcaaaaaag ttagtaggtt gcttcagcta 180
taagaatttg atggtcttcc ttagtcatca tagtctgcag caatcatttt tgttcatcat 240
tgggatgtct gcttactcct gttgagtaaa tgtgatctat tcacccttgg ragctccttg 300
cacaccaaca gtattcttgg atagggacaa gtgttgtcta agtcagtgac gatttcttta 360
gcataataaa aggctccatg taggatgcta atacttgagt gaaatatgct tcataagcag 420
ccttgttttg acagagttgg tgtaaagtga ggttatgtct tggcctgagc gtcttcaaag 480
catgtgccac tttgtgcatc t 501

<210> 115
<211> 1965
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (338)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (343)
<223> n equals a,t,g, or c

<400> 115
agaggcggca ctggcggcaa gagcagacgc ccgaaccgag cgagaagagc ggcagagcct 60
tatcccctga agccgggccc cgcgtcccag mcctggccca aaggcaggag cagcagacaa 120
gagtgcagtg gtggctgccg ccgcaccagc ctcagtggca gatgacacac cacccccga 180
gcgtcggaac aagagcggta tcatcagtga gcccctcaac aagagcctgc gccgctcccg 240
cccgctctcc cactactctt cttttggcag cagtggtggt agtggcggtg gcagcatgat 300
gggcggagag tctgctgaca aggccactgc ggctgcancc tgncctccct gttggccaat 360
gggcatgacc tggcggcggc catggcggtg gacaaaagca accctacctc aaagcacaaa 420
agtggtgctg tggccagcct gctgagcaag gcagagcggg ccacggagct ggcagccgag 480
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gagcatctcc cgctgatgag cgaggcgggt gctggcctgc ctgacatgga ggctgtggca 600
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ccaggcctct tcattatgac ccccggcaggt gtgttcctgg ccgagagcgc gctgcacatg 720
gcgggcctgg ctgagtaccc catgcaggga gagctggcct ctgccatcag ctccggcaag 780
aagaagcgga aacgctgcgg catgtgcgcg ccctgccggc ggcgcatcaa ctgcgagcag 840
tgcagcagtt gtaggaatcg aaagactggc catcagattt gcaaattcag aaaatgtgag 900
gaactcaaaa agaagccttc cgctgctctg gagaaggtga tgcttccgac gggagccgcc 960
ttccggtggt ttcagtgacg gcggcggaac ccaaagctgc cctctccgtg caatgtcact 1020
gctcgtgtgg tctccagcaa gggattcggg cgaagacaaa cggatgcacc cgtctttaga 1080
accaaaaata ttctctcaca gatttcattc ctgtttttat atatatattt tttgttgtcg 1140
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cggaagaaca acaacaaaaa agaggtaaag acgaatctat aaagtaccga gacttcctgg 1260
gcaaagaatg gacaatcagt ttccttcctg tgtcgatgtc gatgttgtct gtgcaggaga 1320
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agcactactg taatttagca cagtttaact ccaccctcat ttaaacttcc tttgattctt 1440
tccgaccatg aaatagtgca tagtttgcct ggagaatcca ctcacgttca taaagagaat 1500
gttgatggcg ccgtgtagaa gccgctctgt atccatccac gcgtgcagag ctgccagcag 1560
ggagctcaca gaaggggagg gagcaccagg ccagctgagc tgcacccaca gtcccgagac 1620

tgggatcccc caccccaaca gtgattttgg aaaaaaaaat gaaagttctg ttcgtttatc 1680
cattgcgatc tggggagccc catctcgata tttccaatcc tggctacttt tcttagagaa 1740
aataagtcct ttttttctgg ccttgctaat ggcaacagaa gaaagggctt ctttgcgtgg 1800
tcccctgctg gtgggggtgg tccccagggg ccccctgcgc ctgggccccc ctsccacggc 1860
cagcttcctg ctgatgaaca tgctgtttgt attgttttag gaaaccaggc tgttttgtga 1920
ataaaacgaa tgcatgtttg tgtcacgaar maaaaaaaaa aaaaa 1965

<210> 116
<211> 1060
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (299)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1060)
<223> n equals a,t,g, or c

<400> 116
gaaacacata cattggatat gggaagatgg cggctgtgtc ggtgtatgct ccaccagttg 60
gaggcttctc ttttgataac tgccgcagaa tgccgtcttg gaagccgatt ttgcaaagag 120
gggatacaag cttccaaagg yccggaaaac tggcacgacc atcgctgggg tggtctataa 180
ggatggcata gttcttggag cagatacaag agcaactgaa gggatggttg ttgctgacaa 240
gaactgttca aaaatacact tcatatctcc taatatttat tgttgtggtg ctgggacanc 300
tgcagacaca gacatgacaa cccagctcat ttcttccaac ctggagctcc actccctctc 360
cactggccgt cttcccagag ttgtgacagc caatcggatg ctgaagcaga tgcttttcag 420
gtatcaaggt tacattggtg cagccctagt tttagggggga gtagatgtta ctggacctca 480
cctctacagc atctatcctc atggatcaac tgataagttg ccttatgtca ccatgggttc 540
tggctccttg gcagcaatgg ctgtatttga agataagttt aggccagaca tggaggagga 600
ggaagccaag aatctggtga gcgaagccat cgcagctggc atcttcaacg acctgggctc 660
cggaagcaac attgacctct gcgtcatcag caagaacaag ctggattttc tccgcccata 720
cacagtgccc aacaagaagg ggaccaggct tggccggtac aggtgtgaga aagggactac 780
tgcagtcctc actgagaaaa tcactcctct ggagattgag gtgctggaag aaacagtcca 840
aacaatggac acttcctgaa tggcatcagt gggtggctgg ccgcggttct ggaaggtggt 900
gagcattgag gcccagtaag acactcatgt ggctagtgtt tgccgaatga aactcaactc 960
aataaaaaac aaaaaccaaa ttgggcagct gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1020
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaan 1060

<210> 117
<211> 709
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (174)
<223> n equals a,t,g, or c

<400> 117
aattcggcac gagaacatcc attctaaagg gctactgtcc caaatcctgt gtgtcctttt 60
gacttgtctg atcacccaat ggaagtggat acttgtaaag tctacaccac tgtacttggc 120
gttaaatctt gctgaattcg tggtaagctg ttaccatgtc tacattttgt agantgattt 180
tggtctgcag caaaattcga tttcacttct catacccctt tccttccact tgaaatgcaa 240
tttagacaga ggccctgtgg tgaaagttgc aatattaagt ttmcctttag aagatcccyt 300
cctcaaacct cagaacccct agcagtgtta ccctwaaaca aaaatgagct cgagaaaaaa 360
gtagctcagt tacagagaag caaatcgagt tatttcccca cataaaaagt ttccccagat 420
tctaagaatt gcagtatcct gtaccctaaa atttttcaag gtgactcctg ttgtcgtctg 480
ttgataactt taataaaggt catttaagga cataagtttt taaagactcc caaagtgaaa 540
cttaaacatt ttcgggatta tcgattgcat atatcagttt atgctgtgtg ctgaattact 600
atgccatgtg ctattttagt gtttggggaa aatgaaaaat aaaatttgtt ctttagctta 660
ataaatatgt cttattttaa aaaaaaaaaa aaaaaactcg agactagct 709

<210> 118
<211> 2053
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (813)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2049)
<223> n equals a,t,g, or c

<400> 118
ctccttggcg cctgtcccca cggcccccgc agcgtgacca cgatgctccc catacccac 60
ccattcccga tacaccttac ttactgtgtg ttggcccagc cagagtgagg aaggagtttg 120
gccacattgg agatggcggt actgagcaga catgcccccca cgagtagcct gactccctgg 180
tgtgctcctg gaaggaagat cttggggacc cccccaccgg agcacaccka rggatcatct 240
ttgcccgtct cctggggacc ccccaagaaa tgtggagtcc tcgggggccg tgcactgatg 300
cggggagtgt gggaagtctg gcggttggar gggtgggtgg ggggcagtgg gggctgggcg 360
gggggagttc tggggtagga agtggtcccg ggagattttg gatggaaaag tcaggaggat 420
tgacagcaga cttgcagaat tacatagaga aattaggaac ccccaaattt catgtcaatt 480
gatctattcc ccctctttgt ttcttggggc atttttcctt tttttttttt ttttgttttt 540
tttttacccc tccttagctt tatgcgctca gaaaccaaat taaacccccc ccccatgtaa 600
caggggggca gtgacaaaag caagaacgca cgaagccagc ctggagacca ccacgtcctg 660
ccccccgcca tttatcgccc tgattggatt ttgtttttca tctgtccctg ttgcttgggt 720
tgagttgagg gtggagcctc ctggggggca ctggccactg agccccccttg gagaagtcag 780
aggggagtgg agaaggccac tgtccggcct ggnttctggg gacagtggct ggtccccaga 840
agtcctgagg gcggaggggg gggttgggca gggtctcctc aggtgtcagg agggtgctcg 900
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caggaggtcc gaagctctgt gggacctctt gggggcaagg tggggtgagg ccggggagta 1140
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aggttgcttg ggccccggag cccacgggtc tggtgatgcc atagcagcca ccaccgcggc 1260
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agggtccctc ggcaagcgcc ctgtgagtgg gccattcgga acattggaca gaagcccaaa 1500
gagccaaatt gtcacaattg tggaacccac attggcctga gatccaaaac gcttcgaggc 1560
accccaaatt acctgcccat tcgtcaggac acccacccac ccagtgttat attctgcctc 1620
gccggagtgg gtgttcccgg gggcacttgc cgaccagccc cttgcgtccc caggtttgca 1680
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cttgggtccc ctcctctgcc atcacctgaa gaccccccacg ccaaacactg aatgtcacct 1860
gtgcctgccg cctcggtcca cttgcggccc gtgtttgact caactcagct cctttaacgc 1920
taatatttcc ggcaaaatcc catgcttggg ttttgtcttt aaccttgtaa cgcttgcaat 1980
cccaataaag cattaaaagt catraaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040
gggggggggnc cgg 2053

<210> 119
<211> 1824
<212> DNA
<213> Homo sapiens

<400> 119
agttcctagc aagctgttca caagattgcc tgataagaat atggaagctg tatataaagt 60
caacatcttt agaaactcag gatgacgata acataagact gaaggaaaat acttttacca 120
tagaaaatga aaagtgttaa aatagcattt gctgttactc tggagacagt gctagccggt 180
catgaaaact gggtaaatgc agttcactgg caacctgtgt tttacaaaga tggtgtccta 240
cagcagccag tgagattatt atctgcttcc atggataaaa ccatgattct ctgggctcca 300
gatgaagagt caggagtttg gctagaacag gttcgagtag gtgaagtagg tgggaatact 360
ttgggatttt atgattgcca gttcaatgaa gatggctcca tgatcattgc tcatgctttc 420
cacggagcgt tgcacctttg gaaacagaat acagttaacc caagagagtg gactccagag 480
attgtcattt caggacactt tgatggtgtc caagacctag tctgggatcc agaaggagaa 540
tttattatca ctgttggtac tgatcagaca actagacttt ttgctccatg gaagagaaaa 600
gaccaatcac aggtgacttg gcatgaaatt gcaaggcctc agatacatgg gtatgacctg 660
aaatgtttgg caatgattaa tcggtttcag tttgtatctg gagcagatga aaaagttctt 720
cgggtttttt ctgcacctcg gaattttgtg gaaaattttt gtgccattac aggacaatca 780
ctgaatcatg tgctctgtaa tcaagatagt gatcttccag aaggagccac tgtccctgca 840
ttgggattat caaataaagc tgtctttcag ggagatatag cttctcagcc ttctgatgaa 900
gaggagctgt taactagtac tggttttgag tatcagcagg tggcctttca gccctccata 960
cttactgagc ctcccactga ggatcatctt ctgcagaata ctttgtggcc tgaagttcaa 1020
aaactatatg ggcacggtta tgaaatattt tgtgttactt gtaacagttc aaagactctg 1080
cttgcctcag cttgtaaggc agctaagaaa gagcatgcag ctatcattct ttggaacact 1140
acatcttgga aacaggtgca gaatttagtt ttccacagtt tgacagtcac gcagatggcc 1200
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aagtatttct tcactgggag tcgagacaaa aaggtggttg tctggggtga gtgtgactcc 1440
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gctgtgacag ctgtcagcgt ctgcccagtg ctccacccctt ctcaacgata cgtggttgca 1560
gtaggattgg agtgtggaaa gatttgctta tatacctgga aaaagactga tcaagttcca 1620
gaaataaatg actggaccca ctgtgtagaa acaagtcaaa gccaaagtca tacactggct 1680
atcagaaaat tatgctggaa gaattgcagt ggaaaaactg aacagaagga agcagaaggt 1740

gctgagtggt tacactttgc aagctgtggt gaagatcaca ctgtgaagat acacagagtc 1800
aataaatgtg cactgtaatg gaaa 1824

<210> 120
<211> 606
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (144)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (155)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (598)
<223> n equals a,t,g, or c

<400> 120
aggaagctgg gggaccattt tgcaccatga gtttgtgaaa aatctggatt aaaaaattac 60
tcttccagtg ttttctcatg cmaaatttyc tyctarcatg tgataatgag taaactaaaa 120
ctatttycag cttttcctca attnacattt tggtngtata cttcagagtg atgttatcta 180
agtttaagta gtttaagtat gttaaatgtg gatcttttac accacatcac agtgaacaca 240
ctggggagat gtgctttttt ggaaaactca aaggtgctag ctccctgatt caaagaaata 300
tttctcatgt ttgttcattc tagtttatat tttcatttaa aatcctttag gttaagttta 360
agctttttaa aagttagtta aaagaattga gacacaatac taatactgta ggaattggtg 420
aggccttgac ttaaaacttt ctttgtactg tgatttcctt ttgggtgtat tttgctaagt 480
gaaacttgtt aaattttttg ttaactaaat ttttttctta aaataaagac tttttcacaa 540
wraaaaaaaa aaaaaaaaaa actcgagggg gggcccgtac ccaatcgcct gtgatgtntc 600
gtatac 606

<210> 121
<211> 838
<212> DNA
<213> Homo sapiens

<400> 121
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ggtcctgcgg ctgtgatgtc ggtgttgagg cccctggaca agctgcccgg cctgaacacg 120
gccaccatct tgctggtggg cacggaggat gctcttctgc agcagctggc ggactcgatg 180
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tacagyctcc agaacacaga ggagtccctg cgccatgtgg atgccagctt cttcttgggg 360
aargtgtgtt tcctcgccac aggtggtggm rggctttagg gccaccatgg cgcarcgcct 420
ggtgcgcgtg ctgcagatct gtgctggcca cgtgcccggt gtctcagctc tgaacctgct 480
gtccctgctg agaagctctg agggcccctc cctggaggac ctgtgagggt ggctkgcccc 540

tgggctgccc cttctcatgg cttcgtgctg actccataaa cattctctgt tgaggatgtc 600
cagtcagggc ttgacaggcc caggctcagc cccccgtggc tgggaaggtt ccctgcagtg 660
ccagtgctgc agcagggaga gctgggcaga agcagcgagg gggcccagct ggcgagactg 720
tagccccctc ccactcccac actcactctt gcagagcctg tgtctttaag cagctggcgt 780
gttacatctc catttaaggt ttcctttgaa caaaaggtct gtggctaaaa aaagttta 838

<210> 122
<211> 656
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (218)
<223> n equals a,t,g, or c

<400> 122
ggcacgagcg ctcttgctgc gacgcacggt cggaagcgga ncaaggtcga ggccgggttg 60
gcgccggagc cggggccgct tggagctcgt gtggggtctc cggtccaggg cgcggcatgg 120
gcgtcctggc cgcagcggcg cgctgcctgg tccggggtgc ggaccgaatg agcaagtgga 180
cgagcaagcg gggcccgcgc agcttcaggg gccgcaangg ccggggcgcc aagggcatcg 240
gcttcctcac ctcgggctgg aggttcgtgc agatcaagga gatggtcccg gagttcgtcg 300
tcccggatct gaccggcttc aagctcaagc cctacgtgag ctacctcgcc cctgagagcg 360
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aggacttcaa ggacggtacc ttcgaccctg acaacctgga aaagtacggc ttcgagccca 480
cacaggaggg aaagctcttc cagctctacc ccaggaactt cctgcgctag ctgggcgggg 540
gaggggcggc ctgccctcat ctcatttcta ttaaacgcct ttgccagcta aaaaaaaaaa 600
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaggggggg gggcggacgc gtgggc 656

<210> 123
<211> 1386
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (8)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1283)
<223> n equals a,t,g, or c

<400> 123
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cgggtgttgg cgcaaaggtt actcccagac ccttttccgg ctgacttctg agaaggttgc 120
gcacagctgt gcccggcagt ctagaggcgc agaagaggaa gccatcgcct ggccccggct 180
ctctggacct tgtctcgctc gggagcggaa acagcggcag ccagagaact gttttaatca 240
tggacaaaca aaactcacag atgaatgctt ctcacccgga aacaaacttg ccagttgggt 300
atcctcctca gtatccaccg acagcattcc aaggacctcc aggatatagt ggctaccctg 360
ggccccaggt cagctaccca cccccaccag ccggccattc aggtcctggc ccagctggct 420
ttcctgtccc aaatcagcca gtgtataatc agccagtata taatcagcca gttggagctg 480
caggggtacc atggatgcca gcgccacagc ctccattaaa ctgtccacct ggattagaat 540
atttaagtca gatagatcag atactgattc atcagcaaat tgaacttctg gaagttttaa 600
caggttttga aactaataac aaatatgaaa ttaagaacag ctttggacag agggtttact 660
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cattgg 1386

<210> 124
<211> 845
<212> DNA
<213> Homo sapiens

<220>
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<222> (823)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (825)
<223> n equals a,t,g, or c

<400> 124
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catcgtggtg gagtactgtg aaccctgcgg cttcgaggcg acctacctgg agctggccag 180
tgctgtgaag gagcagtatc cgggcatcga gatcgagtcg cgcctcgggg gcacaggtgc 240
ctttgagata gagataaatg gacagctggt gttctccaag ctggagaatg gggggctttcc 300
ctatgagaaa gatctcattg aggccatccg aagagccagt aatggagaaa ccctagaaaa 360
gatcaccaac agccgtcctc cctgcgtcat cctgtgactg cacaggactc tgggttcctg 420
ctctgttctg ggtccaaac cttggtctcc ctttggtcct gctgggagct ccccctgcct 480
ctttcccccta cttagctcct tagcaaagag accctggcct ccactttgcc ctttgggtac 540
aaagaaggaa tagaagattc cgtggccttg gggcaggag agagacactc tccatgaaca 600
cttctccagc cacctcatac ccccttccca gggtaagtgc ccacgaaagc ccagtccact 660

cttcgcctcg gtaatacctg tctgatgcca cagattttat ttattctccc ctaacccagg 720
gcaatgtcag ctattggcag taaagtggcg ctacaaacac taaaaaaaaa aaaaaaaaaa 780
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa atntnggggg ggggcccccc 840
ccccc 845

<210> 125
<211> 1656
<212> DNA
<213> Homo sapiens

<400> 125
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tgctgcagct ggaggagctc ccccgtgctg agggggctgc tgttgcagga ggccctggga 180
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tgctgcaaga rgactcgcgc tccggcacag gctccgcagc ctcgggctcc ttgggctctg 360
gcttgggctc tgggtctggt tcaggctccc atgaaggggg cagcacctca gccagcatca 420
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tggaccatgg agtccctggt gctgcccctc aggtgggacc caggcgttct cagctgtacc 1560
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aagataaaaa cgcccaaaaa aaaaaaaaaa aaaacc 1656

<210> 126
<211> 837
<212> DNA
<213> Homo sapiens

<400> 126
tggacgttgg ccctgtttgc tttttataaa ccaaactcta tctgaaatcc caacaaaaaa 60
aatttaactc catatgtgtt cctcttgttc taatcttgtc aaccagtgca agtgaccgac 120
aaaattccag ttatttattt ccaaaatgtt tggaaacagt ataatttgac aaagaaaaat 180
gatacttctc ttttttgct gttccaccaa atacaattca aatgcttttt gttttatttt 240
tttaccaatt ccaatttcaa aatgtctcaa tggtgctata ataaataaac ttcaacactc 300

tttatgataa caacactgtg ttatattctt tgaatcctag cccatctgca gagcaatgac 360
tgtgctcacc agtaaaagat aacctttctt tctgaaatag tcaaatacga aattagaaaa 420
gccctcccta ttttaactac ctcaactggt cagaaacaca gattgtattc tatgagtccc 480
agaagatgaa aaaaatttta tacgttgata aaacttataa atttcattga ttaatctcct 540
ggaagattgg tttaaaaaga aaagtgtaat gcaagaattt aaagaaatat ttttaaagcc 600
acaattattt taatattgga tatcaactgc ttgtaaaggt gctcctcttt tttcttgtca 660
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gtactttcac ttttaaactc tagatcagaa ttgttgactt gcattcagaa cataaatgca 780
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<210> 127
<211> 1217
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1168)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1169)
<223> n equals a,t,g, or c

<400> 127
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gtacgccgag gctgcgggac cggrcctggc tgacttaatc ttcgttcccc acacatttgt 120
ttccgcagtt cgaagcccag ttgggccgac caggtggagg aggaggggga ggacgacaaa 180
tgtgtcacca gcgagctcct caaggggatc cctctggcca caggtgacac cagcccagag 240
ccagagctac tgccgggagc tccactgccg cctcccaagg aggtcatcaa cggaaacata 300
aagacagtga cagagtacaa gatagatgag gatggcaaga agttcaagat tgtccgcacc 360
ttcaggattg agacccggaa ggcttcaaag gctgtcgcaa ggaggaagaa ctggaagaag 420
ttcgggaact cagagtttga cccccccgga cccaatgtgg ccaccaccac tgtcagtgac 480
gatgtctcta tgacgttcat caccagcaaa gaggacctga actgccagga ggaggaggac 540
cctatgaaca aactcaaggg ccagaagatc gtgtcctgcc gcatctgcaa gggcgaccac 600
tggaccaccc gctgccccta caaggatacg ctggggccca tgcagaagga gctggccgag 660
cagctgggcc tgtctactgg cgagaaggag aagctgccgg gagagctaga gccggtgcag 720
gccacgcaga acaagacagg gaagtatgtg ccgccgagcc tgcgcgacgg ggccagccgc 780
cgcggggagt ccatgcagcc caaccgcaga gccgacgaca acgccaccat ccgtgtcacc 840
aacttgtcag aggacacgcg tgagaccgac ctgcaggagc tcttccggcc tttcggctcc 900
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cactgtgtac tcggtccggg acccttggcg acagaagaca gcctccgaga gcgcgggctc 1140
caagggcaat aaagcagctc cactctcnna aaaaaaaaaa aaaaaaaaag ggcggccgct 1200
cgcgatctag aactagc 1217

<210> 128
<211> 1349
<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (57)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1133)
<223> n equals a,t,g, or c

<400> 128
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gccgcgaact gcatcatgga ggtgtcctgt ggccaggcgg aaagcagtga gaagcccaac 120
gctgaggaca tgacatccaa agattactac tttgactcct acgcacactt tggcatccac 180
gaggagatgc tgaaggacga ggtgcgcacc ctcacttacc gcaactccat gtttcataac 240
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atgtttgctg ccaaggccgg ggcccgcaag gtcatcggga tcgagtgttc cagtatctct 360
gattatgcgg tgaagatcgt caaagccaac aagttagacc acgtggtgac catcatcaag 420
gggaaggtgg aggaggtgga gctcccagtg gagaaggtgg acatcatcat cagcgagtgg 480
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aaaaaaaaa aaaaaaaaa aaaaaaaa 1349

<210> 129
<211> 2318
<212> DNA
<213> Homo sapiens

<400> 129
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gcacggctcc gggtagccat ggaggacccc acgctctata ttgtcgagcg gccgcttccc 180
gggtaccccg acgccgaggc cccggagcct tcctccgctg gggctcaggc agcggaggag 240
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ctgagcctcc tggacaaaat catcggggcc gtagaccaga tccagctgac tcaagcacag 360
ctggaggagc ggcaggcgga gatggagggc gcagtgcaga gcatccaggg cgagctgagc 420
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gcaaggtcag cgtcaacgtg aagaccgtgc gcggcagcct ggagcgccag gcggggcaga 540
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tctaccagga tgaagtgaag ctgccggcca aactgagcat cagcaaatcg ctgaaagagt 660
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gccgaggtgg gcggwtcacc tgaagtcagg agttcgggac cagcctggca aacaccccat 2160
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<210> 130
<211> 2149
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (787)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (819)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1518)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2116)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2147)
<223> n equals a,t,g, or c

<400> 130
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ccacgcgtcc ggagaaggca gacgcatccc gaactcgctg gaggacaagg ctcagctctt 120
gccaggccaa attgagacat gtctgacaca agcgagagtg gtgcaggtct aactcgcttc 180
caggctgaag cttcagaaaa ggacagtagc tcgatgatgc agactctgtt gacagtgacc 240
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<210> 131
<211> 1020

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (11)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1019)
<223> n equals a,t,g, or c

<400> 131
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ggtggttagt ttctgcgact tgtgttggga ctgctgatag gaagatgtct tcaggaaatg 120
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ttaagaaact caactgccaa gtgattggtg cttctgtgga ttctcacttc tgtcatctag 360
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<210> 132
<211> 2319
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2246)
<223> n equals a,t,g, or c

<400> 132
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<210> 133
<211> 1373
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (403)
<223> n equals a,t,g, or c

<400> 133
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ggtcgttgga gtcacttccg cgtcaccagc tcctgtgcct gccagtcggt gcccctcccg 120
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gcacctcggc ccagaacaat gctaaagtag ctgtgctagg ggcctctgga ggcatcgggc 240
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ttttattttt caaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1373

<210> 134
<211> 1657
<212> DNA
<213> Homo sapiens

<400> 134
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gtaaaacaga ccatcagtaa catttcagga tttaatgaaa cctgcttgag atggagaagc 180
atcaagacag ctgatatgga ggagatgtat ttattccaca tttggggcca gagatggtat 240
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gaatttttta cggtgcacag aggacctcta ccacgcctca gactgaggaa agccaaggag 480
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tgctgtgtct gttaggcagc attgctttga tgcaatttct attgtcctat atattcaaaa 1560
gtaatgtcta cattccagta aaaatatccc gtaattaaaa aaaaaaaaaa aaaaaaaaaa 1620
aaaaaaaaaa aaaaaaaaaa aaaaaaaaag ggcggcc 1657

<210> 135
<211> 2360
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (1517)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2330)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2353)
<223> n equals a,t,g, or c

<400> 135
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gagacagtat tacacactgc tgaaccaggc cccagacatg ctgcatagat tttatggaaa 240
gaactcttct tatgtccatg gggggattgga ttcaaatgga aagccagcag atgcagtcta 300
cggacagaaa gaaatccaca ggaaagtgat gtcacaaaac ttcaccaact gccacaccaa 360
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accccagtct gttataaact gcttaagttt gtataatttt acttttttg tgtgttaatg 1680
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aactgttagt ttttttgaag tagtttttc cakgtttaat ttgtatttgg ttaaaaaaac 2280
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tcccaattaa ccntgggatt 2360

<210> 136
<211> 1042
<212> DNA
<213> Homo sapiens

<400> 136
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cccgccggcg ctgctgagtt tcttcatcta caacccgcgc ttcgggccgc gcgaaggaca 180
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aaatgtcgga ttgtgtgaag ctattgtaca gtttacaagg acatttagcc catcaaaacc 300
tgcaaaatct ttacatacac agaagaacag acagttcttc aatgaaccag aagaaaattt 360
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aatttttgta aatacagwtg acacttatga agagctccat ttaatcgktt ataaggyctg 1020
agaaagaacc ccagtttaag tt 1042

<210> 137
<211> 1037
<212> DNA
<213> Homo sapiens

<400> 137
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gcggagcggg gccgccgggg cctctccagg gccgcagcgg cagcagttgg gccccccgcc 120
ccggccggcg gaccgaagaa cgcaggaagg gggccggggg gacccgcccc cggccggccg 180
cagccatgaa ctccaacgtg gagaacctac ccccgcacat catccgcctg gtgtacaagg 240

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tcctgaccaa gatcttccac ccgaacgtgg gcgccaatgg cgagatctgc gtcaacgtgc 480
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<210> 138
<211> 1490
<212> DNA
<213> Homo sapiens

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<222> (1225)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1239)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1348)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1452)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1487)
<223> n equals a,t,g, or c

<400> 138
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caagacagta aggattcaaa ccatttgcca aaaatgagtc taagtgcatt tactctcttc 120
ctggcattga ttggtggtac cagtggccag tactatgatt atgattttcc cctatcaatt 180
tatgggcaat catcaccaaa ctgtgcacca gaatgtaact gccctgaaag ctacccaagt 240
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tatctttacc ttaggaataa ccagattgac catattgatg aaaaggcctt tgagaatgta 360
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<210> 139
<211> 1684
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (93)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (201)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1657)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1659)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1682)
<223> n equals a,t,g, or c

<400> 139
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taaaagacat tggattacct ttggatccat ttgtcaactg gaagtgctgc ttcattccac 1500
ttacaattcc taatcttgag caaattgaaa agcctatatc aataatgatt tgktaatatt 1560
attaattaaa agttacagct gtcataagat cataatttta tgaacagaaa gaactcagga 1620
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cnac 1684

<210> 140
<211> 427
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (395)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (417)
<223> n equals a,t,g, or c

<400> 140
ggacttcctc ccagcacatt cctgcactct gccgtgtcca cactgcccca cagacccagt 60
cctccaagcc tgctgccagc tccctgcaag cccctcaggt tgggccttgc cacggtgcca 120
gcaggcagcc ctgggctggg ggtaggggac tccctacagg cacgcagccc tgagacctca 180
gagggccacc ccttgagggt ggccaggccc ccagtggcca acctgagtgc tgcctctgcc 240

accagccctg ctggcccctg gttccgctgg ccccccagat gcctggctga gacacgccat 300
ggcccttcag ctggcccaca cytyttcccg gsccctggaa kttggcaytg cagcagacag 360
ytccytgggc accagrcagy taacaggaca cagcngccag cccaaacagc agcgggnatg 420
ggggcag 427

<210> 141
<211> 889
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (60)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (698)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (889)
<223> n equals a,t,g, or c

<400> 141
ggcacgaggt tgacgtcctg tagcatttgc tgttctagaa agtacagaga cacgtagaan 60
agatgggagg atctagaagg aggctgtctc ctgtgtagtg tatatttatc tgtaagtgag 120
ccgttgggga aggattgaat acagagacgc tgtctgcttg ctgccttaag acagctagct 180
gaattgctga ttaactttta aaatacccag cttggtttat ttttcttaga atctgttgct 240
aagactgggg acgctgtttt cttttacaaa gggaaatcta agttaatttc aaggcattcg 300
aaatggggaa agactattat tgcattttgg gaattgagaa aggagcttca gatgaagata 360
ttaaaaaggc ttaccgaaaa caagccctca aatttcatcc ggacaagaac aaatctcctc 420
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agagagaaat atatgrtcag tttggggagg aagggttgaa aggaggagca ggaggtactg 540
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catttttcgg agggtccaac cccttttgaaa ttttctttgg aagacgaatg ggtggtggta 660
gagattctga agaaatggaa atagrtggtg atcctttnag tgcctttggt ttcagcatga 720
atggatatcc aagagacagg aattctgtgg ggccatcccg cctcaaacaa gatcctccag 780
ttattcatga acttagagta tcacttgaag agatatatag tggttgtacc aaacgggatg 840
aaagatttct cgaaaaaggt taaaacgctg atggtaggag ttacagttn 889

<210> 142
<211> 1505
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1493)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1499)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1500)
<223> n equals a,t,g, or c

<400> 142
agtgagggaa gcgatgggcg cgggaatggc cggcccacgg gtcgcaggag acgggacgcc 60
agcttttggc tccgttccgc tggctccttc gtcagtactg acacctcggg cttgtagagc 120
acttcacgca gcaaaagcgc cccccgtcta tatcatatcg cctctcggtc ctcctaaaag 180
tcgtatgaga tggagctgga ggaggggaag gcaggcagcg gactccgcca atattatctg 240
tccaagattg aagaactcca gctgattgtg aatgataaga gccaaaacct ccggaggctg 300
caggcacaga ggaacgaact aaatgctaaa gttcgcctat tgcgggagga gctacagctg 360
ctgcaggagc agggctccta tgtgggggaa gtagtccggg ccatggataa gaagaaagtg 420
ttggtcaagg tacatcctga aggtaaattt gttgtagacg tggacaaaaa cattgacatc 480
aatgatgtga cacccaattg ccgggtggct ctaaggaatg acagctacac tctgcacaag 540
atcctgccca acaaggtaga cccattagtg tcactgatga tggtggagaa agtaccagat 600
tcaacttatg agatgattgg tggactggac aaacagatca aggagatcaa agaagtgatc 660
gagctgcctg ttaagcatcc tgagctcttc gaagcactgg gcattgctca gcccaaggga 720
gtgctgctgt atggacctcc aggcactggg aagacactgt tggcccgggc tgtggctcat 780
catacggact gtacctttat tcgtgtctct ggctctgaat tggtacagaa attcataggg 840
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gcagtagcca aggtcatgca gaaggacagt gagaaaaaca tgtccatcaa gaaattatgg 1380
aagtgagtgg acagcctttg tgtgtatctc tccaataaag ctctgtgggc caagtcaaaa 1440
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aangggggnn 1500
ccccc 1505

<210> 143
<211> 1235
<212> DNA
<213> Homo sapiens

<400> 143
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cgggcaaagg tcccaggaag gtggcgtcag catctgcagc cgcgtcgacg ttgtcggagc 120
ctccgcggag gacccaggag agccggacta ggaccagggc cctgggcctc cccacactcc 180
ccatggagaa gctggcggcc tctacagagc cccaagggcc tcggccggtc ctgggccgtg 240
agagtgtcca ggtgcccgat gaccaagact ttcgcagctt ccggtcagag tgtgaggctg 300
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agatggatcg gacgctgcac aagatcaagt gccggatgga gtgctgtgat gtgccagccg 420
agacactcta cgacgtccta cacgacattg agtaccgcaa gaaatgggac agcaacgtca 480
ttgagacttt tgacatcgcc cgcttgacag tcaacgctga cgtgggctat tactcctgga 540
ggtgtcccaa gcccctgaag aaccgtgatg tcatcaccct ccgctcctgg ctccccatgg 600
gcgctgatta catcattatg aactactcag tcaaacatcc caaataccca cctcggaaag 660
acttggtccg agctgtgtcc atccagacgg gctacctcat ccagagcaca gggcccaaga 720
gctgcgtcat cacctacctg gcccaggtgg accccaaagg ctccttaccc aagtgggtgg 780
tgaataaatc ttctcagttc ctggctccca aggccatgaa gaagatgtac aaggcgtgcc 840
tcaagtaccc cgagtggaaa cagaagcacc tgcctcactt caagccgtgg ctgcacccgg 900
agcagagccc gttgccgagc ctggcgctgt cggagctgtc ggtgcagcat gcggactcac 960
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gcggcgaggg cagcgacgac gacacctcgc tcacctgagc gycgcaccgc ttcagggacg 1080
gagacaggac cgggcgagcc ctggggcggc ggccgctcct gcactttctc cctcccccca 1140
cccggcacct ggtggcaccg ggccaggccc aggcgggtgc tgcagcctgg ctggacagag 1200
ccccaataaa cgatcccaca gcctcaaaaa aaaaa 1235

<210> 144
<211> 1420
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1385)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1396)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1400)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1410)
<223> n equals a,t,g, or c

<400> 144
gcaagaacgg agctgactga ggaaccaact ggagggtctt cactctctcc ttccccagtg 60
tacaaaacca gttttctgca acattcagga gccaaatgag gaaaaagaat caagaatctg 120
actcacagcc catctgatct gttcaaagct gtcttttcca cctgctgaaa ttcattaaat 180
cactggaggc atgcataatg aatggagaat gagtgaactt ccaatgcaac ttggattcac 240
aaacccatta tcatagccaa tatgcagatt ttaaacagca tttcacattt catttgacca 300
tgtcttcttt ttcgcatcgc ctgctgcaga attccctact agaatgtgaa acaacgaaca 360
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aggcacaaag gtgtctttgc taatgttctc ttgctacctg ccctgcttca aacgctaaat 480
ggtatgggtc tttctttgtt gccagccata ttctacaaat aagacttttc aatatagtta 540

tgagtaatat aattttatgt acatataatg ttagaatatt gtacagaatc ttggtttcta 600
cgatgcgctt ttcttgtttc aaaaagagga aaatgcttga tttttgttga tgatactttt 660
gttactgtcc ttaattttcc atagtttggt ttcttaattg tgctcactaa gcatcgatct 720
gtgctgatgc caagctatgg actatgtacg caagaccgag caatagacag aggtgcctag 780
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gctatctccc tgtgtactgt ttctcttaaa tggagcagat agaaatctgc agtgttggca 1260
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cagtttgtcc agagtccttt aaatggaaac ccccaaatcc atcccttcct ttccctaacc 1380
cccangggga tattcntagn attaagggcn cgggataagt 1420

<210> 145
<211> 1919
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1882)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1898)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1919)
<223> n equals a,t,g, or c

<400> 145
gcccacgcgt ccggccgctc gtccgcccgg cttgaggccc gcggggagcg cggcgcaatt 60
cgtcggcccg cggggggcg gcctcccggc atcttcgcgg cgaccaagga ctaccaggaa 120
ggggagcggc tggatggcg cgtccgggcc ccgskagtac aaagcgggcg acctggtctt 180
cgccaagatg aagggctacc cgcactggcc ggcccggatt gatgaactcc cagaggcgct 240
gtgaagcctt cagcaaacaa gtatcctatc ttcttttttg gcacccatga aactgcattt 300
ctaggtccca aagacctttt tccatataag gagtacaaag acaagtttgg aaagtcaaac 360
aaacggaaag gatttaacga aggattgtgg gaaatagaaa ataacccagg agtaaagttt 420
actggctacc aggcaattca gcaacagagc tcttcagaaa ctgagggaga aggtggaaat 480
actgcagatg caagcagtga ggaagaaggt gatagagtag aagaagatgg aaaaggcaaa 540
agaaagaatg aaaaagcagg ctcaaaacgg aaaaagtcat atacttcaaa gaaatcctct 600
aaacagtccc ggaaatctcc aggagatgaa gatgacaaag actgcaaaga agaggaaaac 660
aaaagcagct ctgagggtgg agatgcgggc aacgacacaa gaaacacaac ttcagacttg 720
cagaaaacca gtgaagggac ctaactacca taatgaatgc tgcatattaa gagaaaccac 780
aagaaggtta tatgtttggt tgtctaatat tcttggattt gatatgaacc aacacatagt 840

ccttgttgtc attgacagaa ccccagtttg tatgtacatt attcatattc ctctctgttg 900
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gaacacattt agtcagtttg ggttttatca atcctgttaa tgcttgtcct tggaacatct 1740
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tgtattgttt ttacagaata aatttattgg aatgtgwact ggggagtaag atttgaggtt 1860
gtaagcaaac taagttagtg tnaattggcc tccaatangt aacgtggagg cattaatgn 1919

<210> 146
<211> 1379
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (925)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1371)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1377)
<223> n equals a,t,g, or c

<400> 146
gcccacgcgt ccgcccacgc gtccgcccac gcgtccgccc acgcgtccgg taagtttaga 60
tgactggtca atatcttaaa aatgtatatt agtaagaagt tcttcctgga atttttcttt 120
cgattctggc agaataaaca ggtgttttta gttttcccac tgtctgagcc aagcaggacc 180
ctgtcccaga gcaagagatg tccccttcca tctctgaccc ttgcctggga caagctttga 240
tgggggggccc cagcttcaag gctgtggtgg gaacagcacc cccaaatgcc agcctctcct 300
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atttctggtg ggatatgcct tccagtgcca cagggccact caccccatgc atctctgtcc 420
tgcccgtcag tgctgggacg gacagcaagg gcaagcccag tgtctggcrg ataggtgggt 480
gggaacagag aggggagaat gccgtcctaa gcttctgctt ggggatcccc cacacgacct 540
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<210> 147
<211> 514
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (406)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (412)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (418)
<223> n equals a,t,g, or c

<400> 147
ttnggaaact gatcacttat caaggcttta tatattcttt acggatttag acatcaccat 60
accaagaagc ttactccatc tattccggtc tttgtaggac aggcttcatt tttcagccca 120
tgttctgtaa gccacacagt atgcctgcag aagctgctta tcggagccaa atataattgt 180
cagtacaatt taaagaccac tatgtgtccc cggagaccaa cctgtttatt tccctgaaag 240
accgcaacac cccacacaac atgtttcaga catttggacc ttgttagata agacacttgt 300
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ctgcggacgc gtgggcggac gcgtgggggg accgtgggtc gaacgnaccc ancgtccncg 420
gacgcgtggg cggacgcgtg ggcggacgcg tgggcggacg cgtgggcgga cgcgtgggcg 480
gacgcgtggg cggacgcgtg ggcggacgcg tggg 514

<210> 148
<211> 2058

<212> DNA
<213> Homo sapiens

<400> 148
gtgcgcccgc gcgccccggg agcctaccca gcacgcgctc cgccccactg gttccctcca 60
gccgccgccg tccagccgag tccccactcc ggagtcgccg ctgccgcggg gacatggtcc 120
tctgcgttca gggacctcgt cctttgctgg ctgtggagcg gactgggcag cggcccctgt 180
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tggacaacta caataggtaa gaaaatgcag ccggagcctc agtccccagc agagcctgtg 1680
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cagttctgct aggtctgctt cctgcccagg aaggtgcctg cacatgagag gagagaaata 1860
cacgtctgat aagacttcat gaaataataa ttatagcaaa gaacagtttg gtggtctttt 1920
ctcttccact gatttttctg taatgacatt atacctttat tacctcttta ttttattacc 1980
tctataataa aatgatacct ttcatgtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2040
aaaaaaaaaa aaaaaaag 2058

<210> 149
<211> 1781
<212> DNA
<213> Homo sapiens

<400> 149
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taactcccag ggggttgact ggtggggtaa ctgagcctgc tttgcagtag gtcaccctgc 180
caaacaagct aatatggaaa ccacatgtaa cttagccaga ctataccttg tgtagcttca 240
agaactcgca gtacattacc agctgtgatt ctccactgaa attttttttt taagggagct 300

caaggtcaca agaagaaatg aaaggaacaa tcagcagccc tgttcagaag gtggtttgaa 360
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<210> 150
<211> 1709
<212> DNA
<213> Homo sapiens

<220>
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<222> (1612)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1660)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1678)
<223> n equals a,t,g, or c

<400> 150
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<210> 151
<211> 922
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (906)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (915)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (922)
<223> n equals a,t,g, or c

<400> 151
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cacctcgggg acattattgc gcgtggaacg gctgcttttg gaagactatt gcccagaaga 180
aaagatgttt ggttttcaca agccaaagat gtaccgaagt atagagggct gctgtatttg 240

cagagctaag tcctccagtt ctcgattcac tgacagtaaa cgctatgaaa aggacttcca 300
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tgcaagggct ggacccagtc taaagactac attgaaacca aagaaagtga aaactctatc 480
tgggaacagg ataaaaagca accagatcag taaactgcag aaggaattta aacgtcataa 540
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<210> 152
<211> 635
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (13)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (594)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (614)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (616)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (628)
<223> n equals a,t,g, or c

<400> 152
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tttgtccgcg cccaggagct acacaccttc gaggtgaccg gccaggaaac ggtcgcccag 180
atcaaggctc atgtagcctc actggagggc attgccccgg aagatcaagt cgtgctcctg 240
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ggaaaagtga gaggtcagac tcctaaggtg gccaaacagg agaagaagaa gaagaagaca 420

ggtcgggcta agcggcggat gcagtacaac cggcgctttg tcaacgttgt gcccaccttt 480
ggcaagaaga agggccccaa tgccaactct taagtctttt gtaattctgg ctttctctaa 540
taaaaaagcc acttagttca aaaaaaaaaa aaaaaamtcg ggggggcccc gkancccaat 600
ttsccctata gggngncgtt taaattcntt ggcgg 635

<210> 153
<211> 2328
<212> DNA
<213> Homo sapiens

<400> 153
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gagaaccgcg ccgccgcctc ggccccgcgg aagccccgcc gcgccatgtc ttcgcctccc 180
gaaggaaact agagactaaa gctggacacc cgcccgccgt gaaagctggt ggaatgcgaa 240
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aatgggaaag ccccagtcca cctaaaccca ctgtgttcat ctctggggtc atcgcccggg 360
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<210> 154
<211> 1268
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (80)
<223> n equals a,t,g, or c

<400> 154
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aaaaaaaa 1268

<210> 155
<211> 4299
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2813)
<223> n equals a,t,g, or c

<400> 155
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tgatgcttta gtgagggtgt tggctatcct attgtcaat 4299

<210> 156
<211> 1006
<212> DNA
<213> Homo sapiens

<400> 156
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tgtccacagc cacaaaaaga agaagatccg cacgtcaccc accttccggc ggccgaagac 180
actgcgactc cggagacagc ccaaatatcc tcggaagagc gctcccagga gaaacaagct 240
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aaggacttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1006

<210> 157
<211> 1686
<212> DNA
<213> Homo sapiens

<400> 157
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cctagggtcg ccgagagcgc ccggagggaa ccgcctggcc ttcggggacc accaattttg 180
tctggaacca ccctcccggc gtatcctact ccctgtgccg cgaggccatc gcttcactgg 240
aggggtcgat ttgtgtgtag tttggtgaca agatttgcat tcacctggcc caaacccttt 300

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<210> 158
<211> 4147
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (13)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (292)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4145)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4146)
<223> n equals a,t,g, or c

<400> 158

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ccgacctatt cgaggtcgtg gtggtcttgg aagaggtcga gggggccgtg gacgtggaat 660
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cgtanna 4147

<210> 159
<211> 1242
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1235)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1236)
<223> n equals a,t,g, or c

<400> 159
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tcaggctgga cgccatgttc cgtgccttca aatctcttga caaagatggc actggacaaa 600
tccaggtgaa catccaggag tggctgcagc tgactatgta ttcctgaact ggagccccag 660
acccgccccc tcaccgcctt gctataggag tcacctggag cctcggtctc tcccagggcc 720
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gccccagtgc ctttgtctat attctgctcc cagcctgcca ggcccaggag gaaataaaca 1140
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaanngggg gg 1242

<210> 160
<211> 2229
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (59)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (128)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (301)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2226)
<223> n equals a,t,g, or c

<400> 160
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gttgcctnag gctggtttcg gattcctggg ctcaagtgat cttcccacct aggtttccca 180

gagtgttgga attacaggcg tgagccatca catctggctt gtttatggtt agttaattca 240
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ncaatattat taaaatactc atttggaata gaattccata tgggttaacc agagtactgt 360
tgggatggtt gtggctattt gcacgtagca gatttcctgc ttttattcaa agmcaatatt 420
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gatttatacc attataccag caaagagaat gtatttcctt ttctaaatcc ttgttaagca 660
acgttagtag aacttactgc tgaccttttt atcttgagtg ttatgtgaat ttgagtttgc 720
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ccaaantgg 2229

<210> 161
<211> 1920
<212> DNA
<213> Homo sapiens

<220>
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<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (119)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1755)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1766)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1832)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1841)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1915)
<223> n equals a,t,g, or c

<400> 161
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<210> 162
<211> 2619
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2546)
<223> n equals a,t,g, or c

<400> 162
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<211> 1419
<212> DNA
<213> Homo sapiens

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<222> (230)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (624)
<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

<220>
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<222> (1187)
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<210> 164
<211> 3810
<212> DNA
<213> Homo sapiens

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<222> (189)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2523)
<223> n equals a,t,g, or c

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<211> 817
<212> DNA
<213> Homo sapiens

<400> 165
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<210> 166
<211> 1578
<212> DNA
<213> Homo sapiens

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<222> (16)
<223> n equals a,t,g,.or c

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

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<210> 167
<211> 1694
<212> DNA
<213> Homo sapiens

<400> 167
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<210> 168
<211> 1636
<212> DNA
<213> Homo sapiens

<400> 168
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<211> 667
<212> DNA
<213> Homo sapiens

<400> 169
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tacccaa 667

<210> 170
<211> 3598
<212> DNA
<213> Homo sapiens

<220>

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<223> n equals a,t,g, or c

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<222> (16)
<223> n equals a,t,g, or c

<220>
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<222> (22)
<223> n equals a,t,g, or c

<220>
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<222> (964)
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<210> 171
<211> 940
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

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<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (919)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (935)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (938)
<223> n equals a,t,g, or c

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ccaatggaga aggttgggag tggagtagca gtgatgtgat gaattacttt gcatgggaga 480
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<210> 172
<211> 1458
<212> DNA
<213> Homo sapiens

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gcagctttgc agcagcaatt agagaacatt catcttagac aagacaaagc tgaagcattt 360
gtcaatackt ggtcttctat gggtcaagaa acagttgaaa agttccggca gagaattctg 420
gctccctgta agctagagac ygttggatgg cagcttaacc ttcagatggc tcactctgct 480
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aaaaaaaaaa aaagtcga 1458

<210> 173
<211> 2709
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2622)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2659)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2670)
<223> n equals a,t,g, or c

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<211> 1013
<212> DNA
<213> Homo sapiens

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<211> 1697
<212> DNA
<213> Homo sapiens

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aaaaaaaaaa aaaaaaa 1697

<210> 176
<211> 1409
<212> DNA
<213> Homo sapiens

<400> 176
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taaagggaac aaaagctgga gctccaccgc ggtggcggcc gctctagaac tagtggatcc 120
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<210> 177
<211> 1503
<212> DNA
<213> Homo sapiens

<400> 177
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gacacgtgag cttctctctc attttaatgt gaggaaaatc atctttcaga gacaaggcac 240
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ctcacagctt ttgtagactt atttgatttt gaaacaagca gttagctaaa tctattttcc 480
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aaa 1503

<210> 178
<211> 1378
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (82)
<223> n equals a,t,g, or c

<400> 178
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cgcgtccggg gaatgccata gntaattcac cagcagtaat cctttaataa ctggcagagc 120
actttattct tctggtgagc tccctgaata tttatttttc tgattataaa ttttctatat 180
tagtagcatt ttttaattat tacttcttca ctatagagca tttactttta gtctctagat 240
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aactccttgg atttatttcc cattttaaaa tttttagcgg taagttcaga tttataatct 360
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acaaactttt ttttgtcatt aaacaatata gtataacaac tatttacaaa gcatttacat 600
tgtattagct attataggta atctagagat gatttaaagt gtatggtagg atgtgcacag 660
gttatatgca aatactacac cattttctat aagggacttg aacatcatgg actttagtat 720
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gcacatactc aataaataaa tgactgcatt gttgtaaaaa aaaaaaaaaa aaaaaaa 1378

<210> 179
<211> 2251
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2020)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2050)
<223> n equals a,t,g, or c

<400> 179
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ggcgctgccg tggctgccgt ggctgctgtg gctgctgtgc cggggcggcg gcgatgcgga 120
ctcccgcgcc cccttcaccc cgacctggcc gcggagccgc gagcgtgaag ccgccgcctt 180
ccgggaaagt cttaatagac atcgatactt gaattcttta tttcccagtg aaaactccac 240
cgccttctat ggaataaatc agttttccta tttgtttcct gaagagttta aagccattta 300
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caatgtgtct ttgccgttaa gatttgactg gagggacaag caggttgtga cacaagtgag 420
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gtataataat tatggctgca atggaggctc tactctcaat gctttgaact ggttaaacaa 600
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ccattacttt tctggttcac attctggatt ttcaatcaaa ggttattctg catatgactt 720
cagtgaccaa gaagatgaaa tggcaaaagc acttcttacc tttggccctt tggtagtcat 780
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tcctggtggc ttggcttccc tgactaaaga attaagtctc atttttactt tccatktcta 1920
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tagtcgcttt cggtgacctg tccgtacgtt t 2251

<210> 180
<211> 1000
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (20)
<223> n equals a,t,g, or c

<400> 180
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gtccggggaa ggcgggagac agcgcagttt gaatcgcggt gcgacgaagg agtaggtggt 120
gggatctcac cgtgggtccg attagccttt tctctgcctt gcttgcttga gcttcagcgg 180
aattcgaaat ggctggcggt aaggctggaa aggactccgg aaaggccaag acaaaggcgg 240
tttcccgctc gcagagagcc ggcttgcagt tcccagtggg ccgtattcat cgacacctaa 300
aatctaggac gaccagtcat ggacgtgtgg gcgcgactgc cgctgtgtac agcgcagcca 360
tcctggagta cctcaccgca gaggtacttg aactggcagg aaatgcatca aaagacttaa 420
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tgattgggaa gaaaggacaa cagaagactg tctaaaggat gcctggattc cttgttatct 600
caggactcta aatactctaa cagctgtcca gtgttggtga ttccagtgga ctgtatctct 660
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aaaaaaaaaa aaaaaaaaam maaaaaaggg gggggccccc 1000

<210> 181
<211> 1429
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (761)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1407)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1420)
<223> n equals a,t,g, or c

<400> 181
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gcccccgcacg ggctgtctgg gtgtccgcca tccagggtct ggcagagcct ctgagatgat 120
gcatgatgcc ctcccctcag cgcaggctgc agagcccggc cccacctccc tgcgcccttg 180
aggggcccca gcgtctgcag ggtgacgcct garacagcac cactgctgag gagtgaggac 240
tgtcctccca cagacctgca gtgaggggcc ctccatgcgc agatgagggg ccactgaccc 300
acctgcgctt ctgctggagg aggggaagct gggcccaaag gccmgsgrag gcagcgtggg 360
ctctgccaat gtgggctgcc cctcgcacac agggctcaca gggcaggcct tgctggggtc 420

cagggctgtt ggaggacccc gagggctgag gagcagcagg acccgcctgc tcccatcctc 480
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<210> 182
<211> 2725
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2713)
<223> n equals a,t,g, or c

<400> 182
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aggaagacac tcccaattct gtttgggagc ctgcgaaggt gcttgtgttt gtcagacaaa 120
tacagccagg cctgccaccc cttaggctcc aaagtccgga ggtgcagaaa gccaggacca 180
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gactcagtgc agataatctc aggagacact gaagaaggga ggctctgtgg acagaggagc 480
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<210> 183
<211> 1751
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (344)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (416)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1617)
<223> n equals a,t,g, or c

<400> 183
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gtggtctgtg gggtctcaga gcagaccacc tgccaggaag tggtcatcgc actagcccaa 180
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ccaacccaca gggccctctg cctcagccag agaggagtcc ctcctgggcg ctccctctga 1140
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ggcaccgggc cctcctgtgg ctgcagccac tgcagcctgt gtcctcccgc agtggccccc 1260
atgacgcaga actcctggag gtagcagcag ctcctgcccc agagtggtgt cctctggcag 1320
cccagcccca ggctctgtga cagcctagtg agggctgcaa gaccatcctg cccggaccac 1380
agaaggagag ttggcggtca cagagggctc ctctgccagg cagtgggaag ccctgggttt 1440
ggcctcagga gctgggggtg cagtggggga ctgccctagt ccttgccagg tcgccagcac 1500
cctggagaag catggggcgt agccagctcg gaacttgcca ggccccaaag gccacgactg 1560
cctgttgggg acaggagatg catggacagt gtgctcaagc tgtgggcatg tgcttgnctg 1620
cgggagaggt ccttcactgt gtgtacacag caagagcatg tgtgtgccac ttccctacc 1680
ccaacgtgaa aacctcaata aactgcccga akyakaaaaa aaaaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa a 1751

<210> 184
<211> 2200
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2096)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2140)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2157)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2181)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2184)
<223> n equals a,t,g, or c

<400> 184
ggcacgagca gcgacatact gaagggcaac ttctcaatcc gtacagccaa gatgcagcag 60
catgtgtgtg aaaccatcat ccgcatcttt aaaagacatg gagctgttca gttgtgtact 120
ccactactgc ttccccgaaa cagacaaata tatgagcaca acgaagctgc cctattcatg 180
gaccacagcg ggatgctggt gatgcttcct tttgacctgc ggatcccttt tgcaagatat 240
gtggcaagaa ataatatatt gaatttaaaa cgatactgca tagaacgtgt gttcaggccg 300
cgcaagttag atcgatttca tcccaaagaa cttctggagt gtgcatttga tattgtcact 360
tctaccacca acagctttct gcccactgct gaaattatct acactatcta tgaaatcatc 420
caagagtttc cagcacttca ggaaagaaat tacagtattt atttgaacca taccatgtta 480
ttgaaagcaa tactcttaca ctgtgggatc ccagaagata aactcagtca agtctacatt 540
attctgtatg atgctgtgac agagaagctg acgaggagag aagtggaagc taaattttgt 600
aatctgtctt tgtcttctaa tagtctgtgt cgactctaca agtttattga acagaaggga 660
gatttgcaag atcttatgcc aacaataaat tcattaataa aacagaaaac aggtattgca 720
cagttggtga agtatggctt aaaagaccta gaggaggttg ttggactgtt gaagaaactc 780
ggcatcaagt tacaggtctt gatcaatttg ggcttggttt acaaggtgca gcagcacaat 840
ggaatcatct tccagtttgt ggctttcatc aaacgaaggc aaagggctgt acctgaaatc 900
ctcgcagytg gaggcagata tgacctgctg attccccagt ttagagggcc acaagctctg 960
gggccagttc ccactgccat tggggtcagc atagctatag acaagatatc tgctgctgtc 1020
ctcaacatgg aggaatctgt tacaataagc tcttgtgacc tcctggttgt aagtkttggt 1080
cagatgtcta tgtccagggc catcaaccta acccagaaac tctggacagc aggcatcaca 1140
gcagaaatca tgtacgactg gtcacagtcc caagaggaat tacaagagta ctgcagacat 1200
catgaaatca cctatgtggc ccttgtctcg gataaagaag gaagccatgt caaggttaag 1260
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gtactgcaga aactgaggac taaagtcact gatgaaagga atggcagaga agcttccgat 1380
aatcttgcag tgcaaaatct gaaggggtca ttttctaatg cttcaggttt gtttgaaatc 1440
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cagtttttat cattagagtg ggatgctgat gaacaggcat ttaacacaac tgtgaagcag 1680
ctgctgtcac gcctgccaaa gcaaagatac ctcaaattag tctgtgatga aatttataac 1740
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agaatcttat tttaacccta aagaactgtc gttaacctca ttcaaacaga cagaggctta 1860
tactggaata atggaatgtt gtacattcat cataatttaa aattaaattc taagaagagg 1920
ctgggtgcag tggctcacac ctttaatccc agcactttgg gaagccaagg caggaagact 1980
gcttgaaacc aggagtttga gaccagcctg agcaacaaag caagacccca tctctataaa 2040
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tgagatggat catctgagcc tcaggaggtt gacgctgcan tgactgtgac tgcgccnctg 2160
actccatctg ggcaacaga ncangaccct gcttaaatac 2200

<210> 185
<211> 1987
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (523)
<223> n equals a,t,g, or c

<400> 185
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gggccaaatt cgacacgaga cgcttctcgg cagacgcagc tcgattccag ataggaaaaa 120
ggaaatatga ctttgattct tcggaggtgc ttcagggact ggactttttt ggaaacaaga 180
agtctgtccc aggtgtgtgt ggagcatcac aaacacatca gaagccccaa aatggagaga 240
aaaaagaaga gagcctaact gaaaggaaga gggagcagag caagaaaaaa aggaagacga 300
tgacttcaga aattgcttcc caagaagaag gtgctactat acagtggatg tcatctgtag 360
aagcaaagat tgaagacaaa aaagttcaga gagaaagtaa actaacttcc ggaaagttgg 420
agaatctcag aaaagaaaag ataaacttct tgcggaataa acacaaaatt cacgtccaag 480
gaaccgatct tcctgaccca attgctacat ttcagcaact tgnaccagga atataaaatc 540
aattctcgac tacttcagaa cattctagat gcaggtttcc aaatgcctac gccaatccaa 600
atgcaagcca tcccagttat gctgcatggt cgggaacttc tggcttctgc tccaactgga 660
tctggaaaaa cattagcttt tagcattcct attttaatgc agctgaaaca acccgcaaat 720
aaaggcttca gagccctgat tatatcacca acacgagaac ttgccagcca gattcacaga 780
gagttaataa aaatttctga gggaacagga ttcagaatac acatgatcca caaagcagca 840
gtggcagcca agaaatttgg acctaaatca tctaaaaagt ttgatattct tgtgactact 900
ccaaatcgac taatctattt attaaagcaa gatcccccg gaatcgacct agcaagtgtt 960
gagtggcttg tagtagacga atcagataaa ctgtttgaag atggcaaaac tgggttcaga 1020
gaccagctgg cttccatttt cctggcctgc acatcccaca aggtccgaag agctatgttc 1080
agtgcaactt ttgcatatga tgttgaacag tggtgcaaac tcaacctgga caatgtcatc 1140
agtgtgtcca ttggagcaag gaattctgca gtagaaactg tagaacaaga gcttctcttt 1200
gttggatctg agaccggaaa acttctggcc gtgagagaac ttgttaaaaa gggtttcaat 1260
ccacctgttc ttgtttttgt tcagtccatt gaaagggcta aagaactttt tcatgagctc 1320
atatatgaag gtattaatgt ggatgttatt catgcagaga gaacacaaca acagagagat 1380
aacacagtcc acagtttcag agcaggaaaa atctgggttc tgatttgtac agccttgcta 1440
gcaagaggga ttgattttaa aggtgtgaac ttggtgatca actatgactt tccaactagc 1500
tcagtggaat atatccacag gataggtcga actggaagag cagggaataa gggaaaagca 1560
attacatttt tcactgagga tgataagcca ttattaagaa gcgttgctaa tgttatacag 1620
caggctgggt gtcctgtacc agaatacata aaaggtttc agaaactact aagcaaacaa 1680
aagaaaaaga tgattaagaa accattggaa agggagagca ttagtacaac tccaaaatgt 1740
ttcttagaaa aagctaagga taaacagaaa aaggtcactg gtcagaacag caagaagaaa 1800
gtagctcttg aagacaaaag ttaaaaacag actttaaaaa tactgtccca gaaatgtaat 1860
tttatgatcc cagcatgaat gttattttca tggaatactt gaagtcttac agtcacctgt 1920
accaaacatt tgaaatcaac tacaagtaca tgggactggt gataaatgat cctaaactat 1980
caagtca 1987

<210> 186
<211> 1737
<212> DNA
<213> Homo sapiens

<400> 186
tcgagttttt tttttttttt ttttaaggta aaaaaaaaat acaccttcag tttcctggtg 60
tgatcctggt taaaatggat gatttttcat tgaaagtttt gctgattaac aattaaagtg 120
ggatgatatg tgggcaaaat cacttatgaa agtagaagca agaatcagtt ggtttgctac 180
cacataaagc catgctgttt ttggtcaaac tgtgtaaact ggaaaaattc acatcatttc 240
tgagtttaat cactttagga tatattcaca ttgttttggt gaatttgctg aattgaattg 300
tttttctttc tcaaatctgt gatctctttt ctttatcctg tttctttgtt cctttcgttt 360

gctttcttat ttttcttttg ttccattctt ttcttacttt tttccctttt cctttttttgg 420
ggaggctggc tagtagtgtg tgagaaaaga atagaagtga aatttgcata atgaatgtaa 480
aagggaaata aaagtctttt gaaggtagct atactagcac ttttgatcat cttcagggcc 540
cacaaaaatg ttgtcaagat tttaaaggtt tataattctg cttaagctct agtttggact 600
taggtatcct aactatgttg gaggtatttg cattgtttaa agttaggata aaagcaagtt 660
cctcctgtga ctgcaacgtc ttactgattg ggacagttgc caggaggata ccaacttgat 720
agcagagggg gttttatgca aacgcactca cctccgcctt ggggaatgaa agggtcactt 780
ctgcatcatc actagctagt tttctagtgt tagagaggct tacaaatgtt tgccattctc 840
ataagtgttt tgaacttgat ctttgtgact tgtgcttttt tagcttctct cttgaatcag 900
agtatcattg tcttcctcca aggagttaga atttcccagt ttaaaacaaa aagggaaatg 960
tcctaggttt tctttgtgct tctcattttt cctttgttga ttcaattcct gtgatttttg 1020
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gtaattcaca gtcctcagaa gcctattttt aaagcagaag caaaaaagaa aaacaaaata 1140
acaaaaacaa cccttcctct tttctctcat ctcacctctc tgtgttgatt actaatcatc 1200
ttagatatta ttgctagtgg atgtatggta gatgggttga agcttttctg ataattatta 1260
cacaatttaa aacaacatat atatttaaaa taaatatata cagtaaatat attgagccat 1320
gttaacctgc caatgagatc tgtgaaaaaa taatggcctc atttttctct ttttaatttc 1380
ttttaccctt ttgtgaagca gctatacgtg gcatacatgt atttaaagaa aaaaaaatag 1440
atgtagagtg tttttttttac acttttaact tagcatgtgg tgttgaagta ttactgtaga 1500
tcaagtttgt cttccgcact aagatgtgag gaaattgtga tttgttctct ccaccacaaa 1560
tgaattacac atttattatc ttctatcatt ttgaaacact gcagtttacc atgggacact 1620
gtatatattt cttgccataa tggtaaagga ctgattgata tatttaagag ttaataaatt 1680
tgtgatttct gctgaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1737

<210> 187
<211> 1132
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1131)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1132)
<223> n equals a,t,g, or c

<400> 187
ggcagagtgg acacctgcat caagaccaag tcgcagctga tgatgccagt ttcaaggccc 60
atgggcctgt ccccaacccc cagcccatcg acccagctag cctggaggag ttcaagagga 120
agatcctgga gtcccagagg cccccctgcag gcatccctgt agccccatcc agtggctgag 180
gaggctccag gcctgaggac caagggatgg cccgactcgg cggtttgcgg aggatgcagg 240
gatatgctca cagcgcccga cacaaccccc tcccgccgcc cccaaccacc cagggccacc 300
atcagacaac tccctgcatg caaacccccta gtaccctctc acacccgcac ccgcgcctca 360
cgatccctca cccagagcac acggccgcgg agatgacgtc acgcaagcaa cggcgctgac 420
gtcacatatc accgtggtga tggcgtcacg tggccatgta gacgtcacga agagatatag 480
cgatggcgtc gtgcagatgc agcacgtcgc acacagacat ggggaacttg gcatgacgtc 540
acaccgagat gcagcaacga cgtcacgggc catgtcgacg tcacacatat taatgtcaca 600
cagacgcggc gatggcatca cacagacggt gatgatgtca cacacagaca cagtgacaac 660

acacaccatg acaacgacac ctatagatat ggcaccaaca tcacatgcac gcatgccctt 720
tcacacacac tttctaccca attctcacct agtgtcacgt tcccccgacc ctggcacacg 780
ggccaaggta cccacaggat cccatcccct cccgcacagc cctgggcccc agcacctccc 840
ctcctccagc ttcctggcct cccagccact tcctcacccc cagtgcctgg acccggaggt 900
gagaacagga agccattcac ctccgctcct tgagcgtgag tgtttccagg acccccctcgg 960
ggccctgagc cgggggtgag ggtcacctgt tgtcgggagg ggagccactc cttctccccc 1020
aactcccagc cctgcctgtg gcccgttgaa atgttggtgg cacttaataa atattagtaa 1080
atccttaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa nn 1132

<210> 188
<211> 1267
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

<400> 188
ggggatggat gntctccttc agctnttttg gagacactat agaaggtacg cctgcaggta 60
ccggtccgga attcccgggt tgatccacgc gtccgcccac gcgtccgccc acgcgtccgc 120
tggacggcag ctatgcgact caccgtgctg tgtgctgtgt gcctgctgcc tggcagcctg 180
gccctgccgc tgcctcagga ggcgggaggc atgagtgagc tacagtggga acaggctcag 240
gactatctca agagatttta tctctatgac tcagaaacaa aaaatgccaa cagtttagaa 300
gccaaactca aggagatgca aaaattcttt ggcctaccta taactggaat gttaaactcc 360
cgcgtcatag aaataatgca gaagcccaga tgtggagtgc cagatgttgc agaatactca 420
ctatttccaa atagcccaaa atggacttcc aaagtggtca cctacaggat cgtatcatat 480
actcgagact taccgcatat tacagtggat cgattagtgt caaaggcttt aaacatgtgg 540
ggcaaagaga tcccccctgca tttcaggaaa gttgtatggg gaactgctga catcatgatt 600
ggctttgcgc gaggagctca tggggactcc tacccatttg atgggccagg aaacacgctg 660
gctcatgcct ttgcgcctgg gacaggtctc ggaggagatg ctcacttcga tgaggatgaa 720
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ggccattctt tgggtatggg acattcctct gatcctaatg cagtgatgta tccaacctat 840
ggaaatggag atccccaaaa ttttaaactt tcccaggatg atattaaagg cattcagaaa 900
ctatatggaa agagaagtaa ttcaagaaag aaatagaaac ttcaggcaga acatccattc 960
attcattcat tggattgtat atcattgttg cacaatcaga attgataagc actgttcctc 1020
cactccattt agcaattatg tcaccctttt ttattgcagt tggtttttga atgtctttca 1080
ctccttttaa ggataaactc ctttatggtg tgactgtgtc ttattcatct atacttgcag 1140
tgggtagatg tcaataaatg ttacatacac aaataaataa aatgtttatt ccatggtaaa 1200
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1260
aaaaata 1267

<210> 189
<211> 3787
<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (155)
<223> n equals a,t,g, or c

<400> 189
agtccggaat tcccgggttt gntgacgcgt ccgcagcaag gtgcctcgct gtgtcaacac 60
tcagcctggc ttccactgcc tgccctgccc gccccgatac agagggaacc agcccgtcgg 120
ggtcggcctg gaagcagcca agacggaaaa gcaantgtgt gagcccgaaa acccatgcaa 180
ggacaagaca cacaactgcc acaagcacgc ggagtgcatc tacctgggtc acttcagcga 240
ccccatgtac aagtgcgagt gccagasagg ctacgcgggc gacgggctca tctgcgggga 300
ggactcggac ctggacggct ggcccaacct caatctggtc tgcgccacca acgccaccta 360
ccactgcatc aaggataact gcccccatct gccaaattct gggcaggaag actttgacaa 420
ggacgggatt ggcgatgcct gtgatgatga cgatgacaat gacggtgtga ccgatgagaa 480
ggacaactgc cagctcctct tcaatccccg ccaggctgac tatgacaagg atgaggttgg 540
ggaccgctgt gacaactgcc cttacgtgca caaccctgcc cagatcgaca cagacaacaa 600
tggagagggt gacgcctgct ccgtggacat tgatggggac gatgtcttca atgaacgaga 660
caattgtccc tacgtctaca acactgacca gagggacacg gatggtgacg gtgtggggga 720
tcactgtgac aactgccccc tggtgcacaa ccctgaccag accgacgtgg acaatgacct 780
tgttggggac cagtgtgaca acaacgagga catagatgac gacggccacc agaacaacca 840
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gcttgtgttc aacccagacc aggaggactt ggacggtgat ggacggggtg atatttgtaa 1020
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aaatcccrtt aaataaatta taaacaaggg tcaattcaaa tttgaagtaa tgttttagta 2280

aggagagatt agaagacaac aggcatagca aatgacataa gctaccgatt aactaatcgg 2340
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cggttccaga tgtggatttg gcaaaacctc atttaagtaa aaggttagca gagcaaagtg 2520
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aaatatttat ttatgtgttc acatggtcaa aatttcacca ctgaaaccct gcacttagct 3720
agaacctcat ttttaaagat taacaacagg aaataaattg taaaaaaggt tttctataaa 3780
aaaaaaa 3787

<210> 190
<211> 554
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (520)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (542)
<223> n equals a,t,g, or c

<400> 190
ggcagaggga cagcaacatt tcccacagga cacgartttg tcggcccttg ccttggcaga 60
gctgaggcat tttggagatc aaagatgggt agaaaagatg ctgctactat aaaacttcct 120
gttgatcagt acagaaaaca aattggtaaa caggattata aaaaaactaa acctatttta 180
cgagcaacca aattaaaagc agaagcaaag aaaacagcaa taggcataaa ggaagttggc 240
cttgtacttg cagctatatt ggcactacta ctggctttct atgctttctt ttatctcaga 300
ctcaccacgg atgttgaccc tgatctggac caagatgaag attagctaag caacaatcaa 360
tgcatgaaag agaaataact ttacgaaagc accttttggg accaaaactt tcaatactga 420
aactgtaaca tctttaattm tttctgctaa tattttcagt ttgcagacat atgatttttg 480

atagttgcat aggatgtcag gaaaagaacc ttacctagcn atgcagtata gtatgtgcta 540
cngggatact tgta 554

<210> 191
<211> 874
<212> DNA
<213> Homo sapiens

<400> 191
ggcacagacg ggatgaggcg ctgcagtctc tgcgctttcg acgccgcccg ggggcccagg 60
cggctgatgc gtgtgggcct cgcgctgatc ttggtgggcc acgtgaacct gctgctgggg 120
gccgtgctgc atggcaccgt cctgcggcac gtggccaatc cccgcggcgc tgtcacgccg 180
gagtacaccg tagccaatgt catctctgtc ggctcggggc tgctgagcgt ttccgtggga 240
ttgtggccct cctggcgtcc aggaamcttc ttcgccctcc actgcactgg gtcctgctgg 300
camtagctct ggtgaacctg ctcttgtccg ttgcctgctc cctgggcctc cttcttgctg 360
tgtcactcac tgtggccaac ggtggccgcc gccttattgc tgactgccac ccaggactgc 420
tggatcctct ggtaccactg gatgaggggc cgggacatac tgactgcccc tttgacccca 480
caagaatcta tgatacagcc ttggctctct ggatcccttc tttgctcatg tctgcagggg 540
aggctgctct atctggttac tgctgtgtgg ctgcactcac tctacgtgga gttgggccct 600
gcaggaagga cggacttcag gggcagctag aggaaatgac agagcttgaa tctcctaaat 660
gtaaaaggca ggaaaatgag cagctactgg atcaaaatca agaaatccgg gcatcacaga 720
gaagttgggt ttaggacagc aggtgctgtt ccgagactca gtcctaaagg gttttttttc 780
ccactaagca aggggccctg acctcgggat gagataacaa attgtaataa agtaacttct 840
cttttcttct aaaaaaaaaa aaaaaaaact cgag 874

<210> 192
<211> 2103
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (140)
<223> n equals a,t,g, or c

<400> 192
tagtagtaaa caggtgggga ctccattgcc agcttggtgc cttatctact gggcagtcga 60
gttggtgtct tcatgggcag aaataggttg taaaggtggc caactctcca ggtgagagag 120
agttttgtag caggactttn ggttgtaaat cgactattac caacctactg gtgggtgaga 180
gttcaagaaa cccatgaaaa aggacatagt ggaagatgaa gatgatgact ttctgaaagg 240
cgaagtgccc cagaatgata ccgtgattgg gatcacacca agctcctttg acacgcattt 300
ccgaagtcct tcaagtagtg tgggctcccc acccgtgttg tacatgcaac ccagtcccct 360
ctgacggcag aaatttgtga ctgagatgtg acatttggga ttccccatca cttgtcatgc 420
cctcagcacc cagcttgtgc cattgggcat tgatggcatt gaactagagc gagtgcctgc 480
ctcggctgtg gcacttccag gttcgactga atcaagcatc tgaagactgg gtttttttgt 540
tgttgttgtt ccccttacag acaaaatgaa gactatcatg tgcaatcttt tacagtgggg 600
ttgatgatac atttggaagg atttgcttgt ttaatatgta catttttttgt gttaacagct 660
ttttgacaca attactgggt aatttctaat ataggcagca gactgtttta cgggttgctg 720
ttttaacatg ggtttttgtc agatccatgg tcttaggact tgactgatga gctttcagtg 780
aagaatcctc taagataaaa cttctattta aagactttaa ctagaaagtg tttattttgg 840
ctacattgtt caccttctgc tgtattggta tttgtctgtt gggatttcaa gggagtgtag 900

agaagacaga aggaaagctg agagctggcc cgacatggtc tgggacacag agttggagct 960
ggcactgaag atctccaggg acttcagaga ccaataaaag cccataggga agagagagag 1020
gatataggga aacagaatca gatgtgtaat atacttggca cagcgaaaaa atggatttaa 1080
aagacaaaaa tggaggtcca ggtagatgta attcacacag actgaaagtg agttcgggct 1140
tgtgtaaaac acatgagatt ggatttgacc ccttggctct caagtgtccc cttagatcta 1200
gaactgctcc ttggtggcca ttagatcgag tcagttttga tctgcatcac ttagttattg 1260
ggaatttctt tgttggaaac aggaaaattt ttttagatta tttggtgtac ggttttgctc 1320
acaacaatag gtggaagttg ctagtgcagt cttggtctga tggctgtgtg catcgcacat 1380
tcggcttggt gaaatccttc tctaaagcct ctttttgtat ttttataact aaacagagga 1440
agtcttcaga agacctcgct ttaaaacaaa tttgtgcaaa cactgctaga gtcattttga 1500
agctcaagca ttttcacttt gtttcttaca tgtgtacttt tttgtttact tgtgaaaatg 1560
gccatcttta agcatattta ttttctgcca ctttatttaa aggcaagcaa tattttcttg 1620
atcataaata ttttgtaatg aaatacttcc tcttttccag ggctttgtat gcacttgtat 1680
aattacattg atggcaatgt agagtttgaa tttcagtctg taaatacttt tttggaaaat 1740
agaaattttt attgctttaa agttttggat atgggtggtt ttcttttccg ggtttggtgg 1800
aaagtaattt gagaacttta aggttgtctt tttaactgct ggcaaaatgt tgattttta 1860
atattagata aaacgagtaa acgaaattcc ccagaaatta gtagtaagtg gggtctttgt 1920
gggttgggaa gtagttttaa tgtagaaaga catttacata taagtctgtt taatttcaaa 1980
ggagtttgtg aaaaaaaatc catggtgaaa atgaaacaat gacatggtta atctggaact 2040
tacgttctta taccaataaa aggtacctca atamaaaaaa aaaaaaaaaa accccggggg 2100
ggg 2103

<210> 193
<211> 1317
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1314)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1315)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1316)
<223> n equals a,t,g, or c

<400> 193
agcatagcct tcgtgtgaag gccagtgaac agcagctgag ctaattcatg aggtatttgc 60
ccttctgaag ttggaatctg taatgattta aaacatgaga ctggtccagt gggcttgttg 120
ctccagacct catgccttct gggacccaga catctctgca atctcgggaa ctggaataca 180
ccacttcttg tcaaggtact agcaagttgc cgtggataca gaaatctctg caggcaagtt 240
gctccagagc atattgcagg acaagcctgt aacgaatagt taaattcacg gcatctggat 300
tcctaatcct tttccgaaat ggcaggtgtg agtgcctgta taaaatattc tatgtttacc 360
ttcaacttct tgttctggct atgtggtatc ttgatcctag cattagcaat atgggtacga 420
gtaagcaatg actctcaagc aatttttggt tctgaagatg taggctctag ctcctacgtt 480

gctgtggaca tattgattgc tgtaggtgcc atcatcatga ttctgggctt cctgggatgc 540
tgcggtgcta taaaagaaag tcgctgcatg cttctgttgt ttttcatagg cttgcttctg 600
atcctgctcc tgcaggtggc gacaggtatc ctaggagctg ttttcaaatc taagtctgat 660
cgcattgtga atgaaactct ctatgaaaac acaaagcttt tgagcgccac aggggaaagt 720
gaaaaacaat tccaggaagc cataattgtg tttcaagaag agtttaaatg ctgcggtttg 780
gtcaatggag ctgctgattg gggaaataat tttcaacact atcctgaatt atgtgcctgt 840
ctagataagc agagaccatg ccaaagctat aatggaaaac aagtttacaa agagacctgt 900
atttctttca taaaagactt cttggcaaaa aatttgatta tagttattgg aatatcattt 960
ggactggcag ttattgagat actgggtttg gtgttttcta tggtcctgta ttgccagatc 1020
gggaacaaat gaatctgtgg atgcatcaac ctatcgtcag tcaaacccct ttaaaatgtt 1080
gctttggctt tgtaaattta aatatgtaag tgctatataa gtcaggagca gctgtctttt 1140
taaaatgtct cggctagcta gaccacagat atcttctaga catattgaac acatttaaga 1200
tttgagggat ataagggaaa atgatatgaa tgtgtatttt tactcaaaat aaaagtaact 1260
gtttacgttg aaaaaaaaaa aaaargkcgg ccgytytara gayccarctt actnnnc 1317

<210> 194
<211> 1252
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1231)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1240)
<223> n equals a,t,g, or c

<400> 194
gcccacgmgc ggccgcgcgg aggaggccaa gatggcggca gctgcggctt cgcttcgcgg 60
ggtagtgttg ggcccgcggg gcgcggggct cccgggcgcg cgtgcccggg gtctgctgtg 120
cagcgcgcgg cccgggcagc tcccgctacg gacacctcag gcagtggcct tgtcgtcgaa 180
gtctggcctt tcccgaggcc ggaaagtgat gctgtcagcg ctgggcatgc tggcggcagg 240
gggtgcgggg ctggccgtgg ctctgcattc ggctgtgagt gccagtgacc tggagctgca 300
cccccccagc tatccgtggt ctcaccgtgg cctcctctct tccttggacc acaccagcat 360
ccggaggggt ttccaggtat ataagcaggt gtgcgcctcc tgccacagca tggacttcgt 420
ggcctaccgc cacctggtgg gcgtgtgcta cacggaggat gaagctaagg agctggctgc 480
ggaggtggag gttcaagacg gccccaatga agatggggag atgttcatgc ggccagggaa 540
gctgttcgac tatttcccaa aaccataccc caacagtgag gctgctcgag ctgccaacaa 600
cggagcattg cccccctgacc tcagctacat cgtgcgagct aggcatggtg gtgaggacta 660
cgtcttctcc ctgctcacgg gctactgcga gccacccacc ggggtgtcac tgcgggaagg 720
tctctacttc aacccctact ttcctggcca ggccattgcc atggcccctc ccatctacac 780
agatgtctta gagtttgacg atggcacccc agctaccatg tcccagatag ccaaggatgt 840
gtgcaccttc ctgcgctggg catctgagcc agagcacgac catcgaaaac gcatggggct 900
caagatgttg atgatgatgg ctctgctggt gcccctggtc tacaccataa agcggcacaa 960
gtggtcagtc ctgaagagtc ggaagctggc atatcggccg cccaagtgac cctgtccagt 1020
gtctgcttgc catcctgcca gaacaggccc tcaagcccaa gagccatccc agcctgttca 1080
ggcctcagct aagcctctct tcatctggaa gaagaggcaa gggggcagga gaccaggctc 1140
tagctctggg ccctccttca gcccccatca tgggaataaa ttaattttct caatgtaaaa 1200

aaaaaaaaaa aaaactcggg gggggcccgg ncccaatttn cccttttggg gg 1252

<210> 195
<211> 1688
<212> DNA
<213> Homo sapiens

<400> 195
ggcacgagcg gaactgctcc ggagggcacg ggctccgtag caccaactgc aaggacccct 60
cccccctgcgg gcgctcccat ggcacagttc gcgttcgaga gtgacctgca ctcgctgctt 120
cagctggatg cacccatccc caatgcaccc cctgcgcgct ggcagcaaaa gccaaggaag 180
ccgcagcccg gccccctcac ccatgcgggc cgccaaccga tcccacagcg ccggcaggac 240
tccgggccga actcctggca aatccagttc caaggttcag accactccta gcaaacctgg 300
cggtgaccgc tatatccccc atcgcagtgc tgcccagatg gaggtggcca gcttcctcct 360
gagcaaggag aaccagcctg aaaacagcca gacgcccacc aagaaggaac atcagaaagc 420
ctgggctttg aacctgaacg gttttgatgt agaggaagcc aagatccttc ggctcagtgg 480
aaaaccacaa aatgcgccag agggttayca gaacagactg aaagtactct acagccaaaa 540
ggccactcct ggctccagcc ggaagacctg ccgttacatt ccttccctgc cagaccgtat 600
cctggatgcg cctgaaatcc gaaatgacta ttacctgaac cttgtggatt ggagttctgg 660
gaatgtactg gccgtggcac tggacaacag tgtgtacctg tggagtgcaa gctctggtga 720
catcctgcag cttttgcaaa tggagcagcc tggggaatat atatcctctg tggcctggat 780
caaagagggc aactacttgg ctgtgggcac cagcagtgct gaggtgcagc tatgggatgt 840
gcagcagcag aaacggcttc gaaatatgac cagtcactct gcccgagtgg gctccctaag 900
ctggaacagc tatatcctgt ccagtggttc acgttctggc cacatccacc accatgatgt 960
tcgggtagca gaacaccatg tggccacact gagtggccac agccaggaag tgtgtgggct 1020
gcgctgggcc ccagatggac gacatttggc cagtggtggt aatgataact tggtcaatgt 1080
gtggcctagt gctcctggag agggtggctg ggttcctctg cagacattca cccagcatca 1140
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gggcaccagt gatcgacaca ttcgcatctg gaatgtgtgc tctggggcct gtctgagtgc 1260
cgtggatgcc cattcccagg tgtgctccat cctctggtct ccccattaca aggagctcat 1320
ctcaggccat ggctttgcac agaaccagct agttatttgg aagtacccaa ccatggccaa 1380
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ggccacagtg gcatccgcag cagcagatga gaccctgagg ctatggcgct gttttgagtt 1500
ggaccctgcg cggcggcggg agcgggagaa ggccagtgca gccaaaagca gcctcatcca 1560
ccaaggcatc cgctgaagac caacccatca cctcagttgt tttttatttt tctaataaag 1620
tcatgtctcc cttcatgttt tttttttaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1680
aaaaaaaa 1688

<210> 196
<211> 756
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (756)
<223> n equals a,t,g, or c

<400> 196
ggcacgagcc gccctcggcg tcctctgtag cgggcgacct aggccgcggg acccggacgg 60
aggtagaggc cagggcagcg cgtccgggag cggagtccgc gcccgccgcc gccatgccgg 120

acagctggga caaggatgtg taccctgagc ccccgcgccg cacgccggtg cagcccaatc 180
ccatcgtcta catgatgaaa gcgttcgacc tcatcgtgga ccgacccgtg accctcgtga 240
gagaatttat agagcggcag cacgcaaaga acaggtatta ctactaccac cggcagtacc 300
gccgcgtgcc agacatcact gagtgcaagg aggaggacat catgtgcatg tatgaagccg 360
aaatgcagtg gaagagggac tacaaagtcg accaagaaat tatcaacatt atgcaggatc 420
ggctcaaagc ctgtcagcag agggaaggac agaactacca gcagaactgt atcaaggaag 480
tggagcagtt cacccaggtg gccaaggcct accaggaccg ctatcaggac ctgggggcct 540
acagttctgc caggaagtgc ctggccaaac agaggcagag gatgctgcaa gagagaaaag 600
ctgcaaaaga ggccgccgct gccacctcct gaggcagctg tgggtgcccc tgctgtgtgg 660
ctctgtatga ctgttgctga aatataaagc cctgcaacct gaaaaaaaaa aaaaaaaaaa 720
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaattn 756

<210> 197
<211> 1471
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (458)
<223> n equals a,t,g, or c

<400> 197
ttggctgctc ctgacctcag caaaccaaga gggtatcact gggatacatc agattggatg 60
ccaagcgttc ctctgccgga catacaagag ttccccaact atgaggtgat tgatgagcag 120
acaccccctgt actcagcaga tccaaacgcc atcgatacgg actattaccc tggaggctac 180
gacatcgaaa gtgattttcc tccaccccca gaagacttcc ccgcagctga tgagctacca 240
ccgttaccgc ccgaattcag caatcagttt gaatccatcc accctcctag agacatgcct 300
gccgcgggta gcttgggttc ttcatcaaga aaccggcaga ggttcaactt gaatcagtat 360
ttgcccaatt tttatcccct cgatatgtct gaacctcaaa caaaaggcac tggtgagaat 420
agtacttgta gagaacccca tgccccttac ccgccagngt atcaaagaca cttcgaggcg 480
cccgctgtcg agagcatgcc catgtctgtg tacgcctcca ccgcctcctg ctctgacgtg 540
tcagcctgct gcgaagtgga gtccgaggtc atgatgagtg actatgagag cggggacgac 600
ggccacttcg aagaggtgac gatcccgccc ctggattccc agcagcacac ggaagtctga 660
ctctcaactc cccccaaagt gcctgacttt agtgaaccta gaggtgatgt gagtaatccg 720
cgctgttctt tgcagcagtg cttccaagct ttttttggtg agccgaatgg gcatggctgc 780
gctggatcct gcgcctctgg acgtgctagc catttccagt gtcccaacta ctgtcatcgt 840
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aaaataatca aacgaaaaat cagtcctgtg ttgtcagcat gattcatgta tttatataga 960
tttgattatt ttaattttcc tgtctctttt ttttgtaaat tttatgtaca gatttgattt 1020
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ggtggtagtg ccattatcta gcaccctgat ttttttttt tactataacc agggtttcat 1140
tctgtctttt tccactgaag tgtgacattt tgttagtaca tttcagtgta gtcattcatt 1200
tctagctgta cataggatga aggagagatc agatacatga acatgtctta catgggttgc 1260
tgtatttaga attataaaca tttttcatta ttggaaagtg taacggggac cttctgcata 1320
cctgtttaga accaaaacca ccatgacaca gtttttatag tgtctgtata tttgtgatgc 1380
aatggtcttg taaaggtttt taatgaaaac taccattagc cagtctttct tactgacaat 1440
aaattattaa taaaataaaa aaaaaaaaaa a 1471

<210> 198
<211> 692

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<400> 198
gtgaattggt aattcgacct cccctatagg gccgaatttg ggntaccggg cccccccctt 60
agtgcggctt gctcttggaa gttcaggctc ggttgtcttt tgggagccat ggagagtgac 120
ttttatctgc gttactacgt ggggcacaag ggcaagttcg gccacgagtt cctggagttt 180
gagtttcgac cggacgggaa gttaagatat gccaacaaca gcaattacaa gaatgatgtc 240
atgatcagaa aagaggctta tgtacataaa agcgtgatgg aggaactgaa gagaataatt 300
gacgacagtg aaattaccaa agaggatgat gcattgtggc ctcctcctga ccgagtgggc 360
cggcaggagc ttgaaatcgt cattggagat gaacacattt cttttacaac atcaaaaatt 420
ggttccctta ttgatgtcaa tcaatccaag gatccagaag gcttacgagt attttattat 480
cttgtccagg acctgaagtg tttggtcttc agtcttattg gattacactt caagattaaa 540
ccaatctaga ctgaatattg gtgtggacat gggggtgggg tgggagtaga aaattttgtg 600
tatatcaggg cagtattttt ttatgaacta taaatgattg tctttaataa atatgtgata 660
aaatccaatt tttattattt tataaagacc tg 692

<210> 199
<211> 1573
<212> DNA
<213> Homo sapiens

<400> 199
ctcgtgccga attcggcacg agccggcgcc agctacgccg ctgccgctgt cactatggcc 60
cattacaaag ccgccgactc gaagcgtgag cagttccgga ggtacttgga gaagtcgggg 120
gtgctggaca cgctgaccaa ggtgttggta gccttatatg aagaaccaga gaaacctaac 180
agtgctttgg attttttaaa gcatcactta ggagctgcta ctccagaaaa tccagaaata 240
gagctgcttc gcctagaact ggccgaaatg aaagagaagt atgaagctat tgtagaagaa 300
aataaaaaac tgaaagcaaa gcttgctcag tatgaaccac ctcaggagga gaagcgtgct 360
gaataggatt cttctcagtt tgaaagacaa tgaaaaatgg ttttgtatga cttgaatagt 420
ttgtatagta tataatcttt tctgaacaga tgctatagaa ctcttttaat atgtttaatt 480
cacctatcac actctgttaa aaacacatag aatcatcaat aaaaactcaa tataactttc 540
tttgggtctt aaagcaggag aatccaaagt aaatcctgaa caaaacctaa acacagccat 600
ctaactcatt accttaaaag acattctgkt tattagtctg attaggaatg atggcactgg 660
ttgtatttta gccaagacag tttagcatgg agctattcct tggtgcagtt caggatatga 720
acacaggtac agtcattctt tgaaggtgac actgttctgt atattcccta taggcagctg 780
gagagatctg tgtgacacaa gatgcttttg tacgggttcc catgaatctt ctgctcttgt 840
ttgtgtgaca tggaacaaat aacttctttg ccaccacttt gccttagata actgtgtgtg 900
tgtgtgccag tttgaactct gacaccacat tttccttcta tgcaatcatg cctgtctgat 960
aatcttgcat tgctttcctc tgagctttag tgggtcctag ttgcacactg gcctttctgt 1020
gctgtttttc aatttgccta ataatagcag ttaccctgat tgtaatttat gtaactttaa 1080
acaggatcac actgtacccc ctgcctgcct tatttgctta ctgagcacag gacagaggca 1140
atatacaact ctgggttcac acacaagctg agatgagaag aggaatgagc catatattgg 1200
ggaaaatcat agtttgtagg tataattata tagtgctttt ctccctcaaa gtatttttct 1260
agccttgaat tcattttatc ttcattatcc ctgtgaagta ggtgggacaa gtataagggg 1320
aagaggggtg ctgaattttt aggccaaaga ctgatattaa tacaaatcac tcactaactg 1380

tagagccttg ggcattatca gtgaactact ctgagattta ctgtcttcat ctgtttaatg 1440
agtagaatgt ccgtgatgcc tacctcacag ggttgttgtg agggtcaaat gagaatgtat 1500
gtgaaagatt tgtaaatggt aaagcactat attcttgtta aaaaaaaaaa aaaaaaaaaa 1560
aaaaaaaaaa aaa 1573

<210> 200
<211> 2742
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (26)
<223> n equals a,t,g, or c

<400> 200
gggtcgaccc acgcgtccgc ccacgntccg tgaatggtga actccagaaa gccattgact 60
tattcacaga tgccatcaag ctgaatcctc gcttggccat tttgtatgcc aagagggcca 120
gtgtcttcgt caaattacag aagccaaatg ctgccatccg agactgtgac agagccattg 180
aaataaatcc tgattcagct cagccttaca agtggcgggg gaaagcacac agacttctag 240
gccactggga agaagcagcc catgatcttg cccttgcctg taaattggat tatgatgaag 300
atgctagtgc aatgctgaaa gaagttcaac ctagggcaca gaaaattgca gaacatcgga 360
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aggctcgaga agagcatgag agagcccaga gggaggaaga agccagacga cagtcaggag 480
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<223> n equals a,t,g, or c

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<222> (1512)
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<211> 419
<212> DNA
<213> Homo sapiens

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<222> (384)
<223> n equals a,t,g, or c

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<212> DNA
<213> Homo sapiens

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<220>
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2831)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2832)
<223> n equals a,t,g, or c

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<210> 205
<211> 5830
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>
<221> misc feature
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (5821)
<223> n equals a,t,g, or c

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naggggggccc 5830

<210> 206
<211> 755
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (368)
<223> n equals a,t,g, or c

<400> 206
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acagccggga cctgaacatg gactgcatca ttgccgagat taaggcacag tatgacgaca 120
ttgtcacccg cagccgggcc gaggccgagt cctggtaccg cagcaagtgt gaggagatga 180
aggccacggt gatcaggcac ggggagaccc tgcgccgcac caaggaggag atcaacgagc 240
tgaaccgcat gatccagagg ctgacggccg aggtggagaa tgccaagtgc cagaactcca 300
agctggaggc cgcggtggcc cagtctgagc agcagggtga ggcggccctc agtgatgccc 360
gctgcaanct ggccgagctg gagggcgccc tgcagaaggc caagcaggac atggcctgcc 420
tgatcaggga gtaccaggag gtgatgaact ccaagctggg cctggacatc gagatcgcca 480
cctacaggcg cctgctggag ggcgaggagc agaggctatg tgaaggcatt ggggctgtga 540
atgtctgtgt cagcagctyc cggggcgggg tcgtgtgcgg ggacctctgc gtgtcaggct 600
yccggccagt gactgcagtg tctgcagcgc tycgtgcaac gggaacgtgg cggtgagcac 660
cggcctgtgt gcgccctgcg gcaattgaca ccamctgcgg aggggttct gcggcgtggg 720
ctyctgtggt atcaagyttc cccccctttt ggggg 755

<210> 207
<211> 1996
<212> DNA
<213> Homo sapiens

<400> 207
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tccgccactc cggtagcctc atggctgcaa cctgtgagat tagcaacatt tttagcaact 180
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cctttggggc cgatgacttg gtactgaccc tgagcaaccc ccagatgtca ttggagggta 300
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gatgtgacat ggatggcgcc accctctgca attgtgccct tgaggagctg cgtctggtct 480
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cctctcccac agagtgctgg actgttccag gccctccagt gggctgatgc tgggaccctt 1860
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aaaaaaaaaa ctcgag 1996

<210> 208
<211> 1668
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1505)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1565)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1598)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1620)
<223> n equals a,t,g, or c

<400> 208
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ccaacatctg ggtcctgcct tcgacaccac cccaaggctt cctaccttgc gtgcctggag 180
tctgccccag gggcccttgt cctgggccat ggccmagaag ggggtcctgg ggcctgggca 240
gctgggggct gtggccattc tgctctatct tggattactc cggtcgggga caggagcgga 300
aggggcagaa gctycctgcg gtgtggcccc ccaagcacgc atcacaggtg gcagcagtgc 360
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ccacaaggaa gcctatgagg tcaagctggg ggcccaccag ctagactcct actccgagga 540
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gcccatctgc ctccctgcag ccaacgcctc cttccccaac ggcctccact gcactgtcac 720
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tttccctgtg tttttgggtt gggcaacttt ttggaagttt gaggagaa 1668

<210> 209
<211> 2250
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (23)
<223> n equals a,t,g, or c

<400> 209
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ggaattcgcg gccgcgtcga cattcgccgc cgcagcagcc gccgcccccg ggagccgccg 120
ggaccctcgc gtcgtcgccg ccgccgccgc ccagatcccc gcaccatgcc gtcggagaag 180
accttcaagc agcgccgcac cttcgaacaa agagtagaag atgtccgact tattcgagag 240
cagcatccaa ccaaaatccc ggtgataata gaacgataca agggtgagaa gcagcttcct 300
gttctggata aaacaaagtt ccttgtacct gaccatgtca acatgagtga gctcatcaag 360
ataattagaa ggcgcttaca gctcaatgct aatcaggcct tcttcctgtt ggtgaacgga 420
cacagcatgg tcagcgtctc cacaccaatc tcagaggtgt atgagagtga gaaagatgaa 480
gatggattcc tgtacatggt ctatgcctcc caggagacgt tcgggatgaa attgtcagtg 540
taaaaccaga aaaaatgcat ctcttctaga attgtttaaa cccttaccaa ggaaaaaaaa 600
ggggtgttac caactgagat cgatcagttc atccaatcac agatcatgaa acagtagtgt 660
tcccacctag gagtgttagg aagttgtgtt tgtgtttcaa gcagaaaaac tgagctccaa 720
gtgagcacat tcagctttgg aaactatatt atttaatgta ggctagcttg ttttcaaatt 780
ttaaaagttt aaaaataaaa tactttgcat tctaagttgc caataaaata gaccttcaag 840
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atttttacat tatgtatatt cttaactgga ctgtctcgtt tagactgtat acatcatatc 2040
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gaaaaaaaat aacatgctga ggggtgacct atatcccatg tgagtggtca ctttatttat 2160
aggatcttta aaacattttt aatgaactaa gttgaataaa ggcacaatta aaaactgtca 2220
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2250

<210> 210
<211> 838
<212> DNA
<213> Homo sapiens

<400> 210
ggcgggccta cgtgctccgc ccgctgtgag cctgtccggc ccccgcccgc tccggagcaa 60
cccgcgagct tacaccggct tctctctgtc ctcagcccgc gcgccgccat cgccgtcatg 120
ctgggcgccg ctctccgccg ctgcgctgtg gccgcaacca cccgggccga ccctcgaggc 180
ctcctgcact ccgccccggac ccccggcccc gccgtggcta tccagtcagt tcgctgctat 240
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aagccagata tagatgcctg ggaattgcgt aaagggataa acacacttgt tacctatgat 360
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ccggaggaac tgggccttga caaagtgtaa accgcatgga tgggcttccc caaggattta 600
ttgacattgc tacttgagtg tgaacagtta cctggaaata ctgatgataa catattacct 660
tatttgaaca agttttcctt tattgagtac caagccatgt aatggtaact tggactttaa 720
taaaagggaa atgagtttga actgaaaaaa aaaaaaaaaa aaactcatac agactgaagc 780
gcggtgatta aataatgaaa gagttcgacg cggccgggaa tttaggaggt aaatatcc 838

<210> 211
<211> 1213
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1206)
<223> n equals a,t,g, or c

<400> 211
gcccacgcgt ccggcaggaa ccgcggctgc tggacaagag gggtgcggtg gatactgacc 60
tttgctccgg cctcgtcgtg aagacacagc gcatctcccc gctgtaggct tcctcccaca 120
gaacccgttt cgggcctcag agcgtctggt gagatgctgt tgccgctgct gctgctgcta 180
cccatgtgct gggccgtgga ggtcaagagg ccccggggcg tctccctcac caatcatcac 240
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caggtcaacg atgactattg cgactgcaaa gatggctctg acgagccagg cacggctgcc 360
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aaccgggtca acgatggtgt ttgtgactgc tgcgatggaa cagacgagta caacagcggc 480
gtcatctgtg agaacacctg caaagagaag ggccgtaagg agagagagtc cctgcagcag 540
atggccgagg tcacccgcga agggttccgt ctgaagaaga tccttattga ggactggaag 600
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aaaaanaaaa aaa 1213

<210> 212
<211> 969
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (922)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (955)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (958)
<223> n equals a,t,g, or c

<400> 212
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aaggaaccca agcagaaatc tttgtatgta tatgtatgaa gaggttgtct gtttttagga 120
gttgtatgta aaagctaagg aaacctttc ttttggaaga tcagtataaa catgctgctt 180
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aacagcgtat tcaagcagat tccacgaatc ctcggcccag gtttaaataa ggcaggaaag 600
ttcccttccc tgctcacaca caacgaaaac atggtggcca aagtggatga ggtgaagtcc 660
acaatcaagt tccaaatgaa gaaggtgtta tgtctggctg tagctgttgg tcacgtgaag 720
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ctcaagaaaa actggcagaa tgtccgggcc ttatatatca agagcaccat gggcaagccc 840
cagcgcctat attaaggcac atttgaataa attctattac cagttaaaaa aaaaaaaaaa 900

aaaaaaaaaa aaaaaaaaaa anaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaanccncg 960
gggggggg 969

<210> 213
<211> 1694
<212> DNA
<213> Homo sapiens

<400> 213
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gcgatggcca aggtgtcggt gctgaacgtg gcggtcctgg agaacccgag ccctttccac 180
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cctatcaagg gcttggggct ccctggctgc atccctggcc tcctccctga gaactccatg 720
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aaaaaaaaaa aaaa 1694

<210> 214
<211> 1210
<212> DNA
<213> Homo sapiens

<400> 214
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tggttaccat tatccccaac ttcagtctgg acaagatcta cctcatcggg ggggacctgg 180
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<210> 215
<211> 1776
<212> DNA
<213> Homo sapiens

<400> 215
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aaggccagct tagactttaa gcgttacgta accgatcgga gattggctga gaccctggcg 360
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agaaattaaa atattttaaa taagaaaaaa aaaaaa 1776

<210> 216
<211> 1418
<212> DNA
<213> Homo sapiens

<400> 216
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gccatacaga attgtgtatt caccagcatc atgaaacagt tgtggtcttt tgagttgatc 180
ttggcagagt aaagggacgt gtcctggagc cattcctgaa tctccccttc tttgtgacag 240
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acttcactta gagactggag tcctgcttat aatcatgcat ataaccttta ctttgatgga 360
tctggccaga ggggtgttgg agcccagccc acccacatac cagtcaagct cttaggggag 420
cagaagaaaa gcaggaagaa tttaaatgtt taattttttt tttaaattga cttttctagt 480
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aaagaagaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1418

<210> 217
<211> 2200
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2188)
<223> n equals a,t,g, or c

<400> 217
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tgcctgggga cgcaaggccc tggacattgc tgagaacgag atgccgggcc tgatgcgtat 180
gcgggagcgg tactcggcct ccaagccact gaagggcgcc cgcatcgctg gctgcctgca 240
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gcagaccctg tacttcaagg acgggcccct caacatgatt ctggacgacg gggcgacct 480
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ggggccagaa aaacatgaat gcaggcagat ttcgtgaaat ctgccaccac tttataacca 2040
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<210> 218
<211> 1853
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (890)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1794)
<223> n equals a,t,g, or c

<400> 218
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tggtgggcgc cgtgaagagc cttcaggcgc tgggcgaggt catcgaggct gaacttcggt 180
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aggcccgtgt gtttcgaagc attccccag agggcctggc ccagagcgag cttatgcgac 300
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tgtgagggtg ggccctgagg agacctgtgg gccacctatt gtctaataaa gtgngcagtt 1800
gcccccaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1853

<210> 219
<211> 1093
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1090)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1091)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1092)
<223> n equals a,t,g, or c

<400> 219
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ccgagctgcc cctgcagcgc tggtcatggg cgagggcact tgtgagaagc gccgggacgc 120

cgagtatggc gccagcccgg agcaggttgc agacaatggc gatgaccact cagaaggagg 180
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aaaaaaaaan nna 1093

<210> 220
<211> 2155
<212> DNA
<213> Homo sapiens

<400> 220
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gccctgagta gggtgtgacc tccgcagccg cagaggagga gcgcasccgg cctcgaagaa 180
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<210> 221
<211> 1264
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (17)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (125)
<223> n equals a,t,g, or c

<400> 221
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gtgantgtaa catctgtcaa agatgcaaaa atagcagtgt actcttgtcc ttttgatggc 180
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<222> (2921)
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<222> (4391)
<223> n equals a,t,g, or c

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<211> 1511
<212> DNA
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<400> 226

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tgccggtgtt a 1511

<210> 227
<211> 2239
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2238)
<223> n equals a,t,g, or c

<400> 227
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gctctcctgg gaccaagaga aaatcccggt ccttgaccaa gaagctgctg atgggagctc 180
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cctgcagcac gtgcccgact accgccagaw tgtctacatc ccaggcagca atgccacact 300
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agaagtcggg caagaaggag aagaagtaac atggaggcca ggccaagagc cacagggcgg 420
cctctcccca accagcccag cttctcctta cctgcaccca ggcctcagag tttcagggct 480
aacccccaga atactggtag ggccaaggc catgctcccc ttgggaaaca gaaacaagtg 540
cccagtcagc acctacccct tccccccag gggkttgaat atgcaaaagc agttccgctg 600
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agaaccattt gccacacccc gtttagttac agctgaactc ctccatcttc caaatcaatc 720
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<210> 228
<211> 2346
<212> DNA
<213> Homo sapiens

<400> 228
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tccaacacct acaacaggca gaactgggag gatgcggact tccccattct gtgccagaca 180
tgtcttggag aaaacccata tatccgaatg accaaagaaa agtatgggaa ggaatgcaaa 240
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atgccaaagt cagatgtcaa caaagagtac tatacacaga atatggagag agagatttct 480
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aaaaaa 2346

<210> 229
<211> 2246
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2235)
<223> n equals a,t,g, or c

<400> 229
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ggctgtgcct tctgaagcag tatctattca caatgaagtt gcagtctccc gaattccagt 180
cacttttcac agaaggactg aagagtctga cagaattatt tgtcaaagag aatcacgaat 240
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attttgccac cactgctacc cctactcaaa tgaaggagat gtttcagtcg gctgggattc 360
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attttgagat tactacacta cggattgatg tcaccactga tggaagacat gctgaggtag 480
aatttacaac tgactggcag aaagatgcgg aacgcagaga tctcactata aattctatgt 540
ttttaggttt tgatggcact ttatttgact actttaatgg ttatgaagat ttaaaaaata 600
agaaagttag atttgttgga catgctaaac agagaataca agaggattat cttagaattt 660
taagatactt caggttttat gggagaattg tagacaaacc tggtgaccat gatcctgaga 720
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ctaaatgctt tcatncaggt aaataa 2246

<210> 230
<211> 2002
<212> DNA
<213> Homo sapiens

<400> 230
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aaaaaaaaaa aaaaaaaaaa aa 2002

<210> 231
<211> 994
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (394)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (853)
<223> n equals a,t,g, or c

<400> 231
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cgggagggtg gtgtgtacag agctctagga ctcacgcacc aggccagtcg cgggttttgg 120
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tttgttcgta cacctgaaag tgttcacgca agtnattcat caagtgactc atcttttgaa 420
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gacagtcgta gatacaaatt tttggatgat gatggatcca tttctcctat tgaggagtca 840
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aattgcttca tattttgcct ttaatatagt tatacttaaa taatgaacaa agatacagag 960
tatgacaatt gggattatta cagttgagcc aagc 994

<210> 232
<211> 486
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (49)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (440)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (485)
<223> n equals a,t,g, or c

<400> 232
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cgacccacgc gtccgggaac agccttctcc tgcctcctct gcacctggac aactcaactc 120
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cacccaagtg tcccccaaag agcccagtac agtgtctgcc tccagcttcc tctggctgtg 240
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ggcgrgggyt ctggstgckg cayggttctg ggggctgctg ctgatccaga tcctgatgct 420
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gaagnc 486

<210> 233
<211> 2081
<212> DNA
<213> Homo sapiens

<400> 233
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<210> 234
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (490)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (498)
<223> n equals a,t,g, or c

<400> 234
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<210> 235
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<212> DNA
<213> Homo sapiens

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<222> (807)
<223> n equals a,t,g, or c

<400> 235
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<210> 236
<211> 1045
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (973)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1001)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1014)
<223> n equals a,t,g, or c

<400> 236
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ttcttttttg ggtacacacc tgctgtctgg ggcgtggtgc tcaaccaggc cttcggcggg 180
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<210> 237
<211> 690
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (666)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (678)
<223> n equals a,t,g, or c

<400> 237
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cggcactggc ctttgacctc tccaaggtac caggcccaga ggcagccccc aggctgyggg 180
cgctgacact gggcctggca aaacgcgtgt ggagcctgga gcggcgactg gcagctgcag 240
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cagacccaga tccccagaga ggtggccctg gacctggagt caggaggcgg tgtccaggag 360
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<210> 238
<211> 1873
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (568)
<223> n equals a,t,g, or c

<400> 238

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gaagcatgga aaatctgggc agatattcct gctccaaaac gaggagaaat agtaagacag 360
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<210> 239
<211> 905
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (873)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (874)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (897)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (898)
<223> n equals a,t,g, or c

<400> 239
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gacccagcag ggcgcggcgc tgcagaacta caacaacgag ctggtcaagt gcatagagga 120
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ggggg 905

<210> 240
<211> 1484
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1457)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1471)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1480)
<223> n equals a,t,g, or c

<400> 240
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atcttataaa ttcaacagac acaaaagaat ttgatctccc ataagcaact gtgaaattac 240
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aaaggtgttc agtttcatcc ttgttaccac cgctctgaya atgggcaggg aaatttcggc 360
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<210> 241
<211> 1521
<212> DNA
<213> Homo sapiens

<400> 241
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ggtttgtgtg tttctgtttt gtttctctcc ccctgcaggg ctgtttkcgg ggtggggtgg 180
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<210> 242
<211> 1144
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1093)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1105)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1106)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1139)
<223> n equals a,t,g, or c

<400> 242
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tcccagagga gcaggaatta gaagcttatg tagatgatat agatattgat agtgatttca 180
gaaaggatga tttttattac ttgtctcaag aagacaaaga gagacagaag cgtgagcatg 240
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<210> 243

<211> 934
<212> DNA
<213> Homo sapiens

<400> 243
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<211> 915
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (210)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (243)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (244)
<223> n equals a,t,g, or c

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<211> 1276
<212> DNA
<213> Homo sapiens

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<211> 3366
<212> DNA
<213> Homo sapiens

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<210> 247
<211> 2148
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1259)
<223> n equals a,t,g, or c

<400> 247
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<210> 248
<211> 2225
<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (14)
<223> n equals a,t,g, or c

<400> 248
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aaaaa 2225

<210> 249
<211> 1204
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1197)
<223> n equals a,t,g, or c

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<210> 250
<211> 1314
<212> DNA
<213> Homo sapiens

<400> 250
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<210> 251
<211> 1159
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1132)
<223> n equals a,t,g, or c

<400> 251
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ctgttcagtg tggtctgccc cacccctgct gacmaagact gactgaaatg tnaaataata 1140
cagaccatct caactcaga 1159

<210> 252
<211> 2488
<212> DNA
<213> Homo sapiens

<220>
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<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (64)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2334)
<223> n equals a,t,g, or c

<400> 252
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ccgnggacgc gtgggttgct cggcagcttg caaagcctga caacaccttg tttgtaaaca 120
gaacactttt tgatcaggtc cttgaattcc tttgtagtcc tgacgatgac tcccgacact 180
ctgaaagaca gcaggtcctt ttagaattgc tgcaggctgg aggcatagtt caatttgaag 240
agagtcgact catccggatg gcagaaaaag ctgagttcta tcaaatttgt gaatttatgt 300
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agaagcagtc tgtatggcag aaagcaatgg atcatattga ggaacycgkg kccctgaagc 480
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aaggtattca tgtaaatcaa gaattactgc aaatatctcc ttgtatcaca gagcagttca 660
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<210> 253
<211> 1554
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (81)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1496)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1523)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1535)
<223> n equals a,t,g, or c

<400> 253
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cgggtcgacc cacgcgtccg nggacgcgtg ggttctggtt ttgctctagt gtttgggttt 120
cttcgcggct gctcaagatg aaccgactct tcgggaaagc gaaacccaag gctccgccgc 180
ccagcctgac tgactgcatt ggcacggtgg acagtagagc agaatccatt gacaagaaga 240
tttctcgatt ggatgctgag ctagtgaagt ataaggatca gatcaagaag atgagagagg 300
gtcctgcaaa gaatatggtc aagcagaaag ccttgcgagt tttaaagcaa aagaggatgt 360
atgagcagca gcgggacaat cttgcccaac agtcattcaa catggaacaa gccaattata 420
ccatccagtc tttgaaggac accaagacca cggttgatgc tatgaaactg ggagtaaagg 480
aaatgaagaa ggcatacaag caagtgaaga tcgaccagat tgaggattta caagaccagc 540
tagaggatat gatggaagat gcaaatgaaa tccaagaagc actgagtcgc agttatggca 600
ccccagaact ggatgaagat gatttagaag cagagttgga tgcactaggt gatgagcttc 660
tggctgatga agacagttct tatttggatg aggcagcatc tgcacctgca attccagaag 720
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tgggactagg aaatatttat ctttccaaat ttgccataac agatttaggt ttctttcctt 900
tctttgaagg aaagtttaat tacattgctc ttttattttt tccattaaga gactcattgc 960
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cagtttaaaa gtatttttag ctcgtatgac ttgttttcat tcattaataa taatttgaaa 1080
taaaactaag gaaatggaat cttaaaagtc tatgacagtg taactctaca gtctcaaaat 1140

gacctgataa attgataaga caaagatgag attattgggg ctgttcatat tatgattcag 1200
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aattatgaat atttcttgat atttaatgta taggacattt atttatactc aataaatatt 1440
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aggatccccc gagggggcc cangcttacg cgtgncatgc gacgtccaaa gccc 1554

<210> 254
<211> 1506
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1492)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1501)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1506)
<223> n equals a,t,g, or c

<400> 254
ctggaagaat tcgcgtggca ggagaggcgg ggcaattttg ctnagctttc tcgcgggctt 60
gcagctgcgg caagtgctgg cggcggctgc tcgcgcaagt cagctggcgt gggaactacc 120
ctttgtagct gagaacggct tgtttattgc tacaaagact ctattgacat tggtagcttc 180
agcggcagca gcttcttacg gtataaagct gttgcttcct gaagaggcta caagcatcct 240
tccctaggac tgctgtaagc tttgagcctc tagcaggaga catgcctcgg ggacgaaaga 300
gtcggcgccg ccgtaatgcg agagccgcag aagagaaccg caacaatcgc aaaatccagg 360
cctcagaggc ctccgagacc cctatggccg cctctgtggt agcgagcacc cccgaagacg 420
acctgagcgg ccccgaggaa gacccgagca ctccagagga ggcctctacc acccctgaag 480
aagcctcgag cactgcccaa gcacaaaagc cttcagtgcc ccggagcaat tttcagggca 540
ccaagaaaag tctcctgatg tctatattag cgctcatctt catcatgggc aacagcgcca 600
aggaagctct ggtctggaaa gtgctgggga agttaggaat gcagcctgga cgtcagcaca 660
gcatctttgg agatccgaag aagatcgtca cagaagagtt tgtgcgcaga gggtacctga 720
tttataaacc ggtgccccgt agcagtccgg tggagtatga gttcttctgg gggccccgag 780
cacacgtgga atcgagcaaa ctgaaagtca tgcattttgt ggcaagggtt cgtaaccgat 840
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acatagagaa aaataaaagc ctaacgaata gtaaaaaaaa aaaaaaaacc tngggggggg 1500
ncccgn 1506

<210> 255
<211> 654
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (8)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (632)
<223> n equals a,t,g, or c

<400> 255
actcaccnta ttggaaaagc tggtacgcct gcaggtcccg gtccggaatt cccgggtcga 60
cccacgcgtc cgatctttcc gcgccggtga gtagcactct ctgagagctc caatttcatc 120
cgtctgccat cggcgccatc ctgcaatcta agccacaatg gtgcgcatga atgtcctggc 180
agatgctctc aagagtatca acaatgccga aaagagaggc aaacgccagg tgcttattag 240
gccgtgctcc aaagtcatcg tccggtttct cactgtgatg atgaagcatg gttacattgg 300
cgaatttgaa atcattgatg accacagagc tgggaaaatt gttgtgaacc tcacaggcag 360
gctaaacaag tgtggggtga tcagccccag atttgacgtg caactcaaag acctggaaaa 420
atggcagaat aatctgcttc catcccgcca gtttggtttc attgtactga caacctcagc 480
tggcatcatg gaccatgaag aagcaagacg aaaacacaca ggagggaaaa tcctgggatt 540
ctttttctag ggatgtaata catatattta caaataaaat gcctcatgga caaaaaaaaa 600
aaaaaaaaaa aaaaaagggs ggsggtctag anggtccaag cttacgtacg cgtg 654

<210> 256
<211> 1992
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (558)
<223> n equals a,t,g, or c

<400> 256
gctcgccata cacctgcgca acgccatgac cacccgcaag aaggaaacat accagtctgt 60
gtacaactgg cagtatgtgc actgcctctt cctgtggtgc cgggtcctga gcactgcggg 120

ccccagcgaa scctccagcc cttggtctac ccccttgccc aagtcatcat tggctgtatc 180
aagctcatcc ccactgcccg cttctacccg ctgcgaatgc actgcatccg tgccctgacg 240
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caccggggag gatattcggc agcccgggca gtcgcagatc ggaggatgca cctgcaggat 1920
ccccttggac ataagcgtct tcagactttt cccttccgag cggagggagc ggcccgcgag 1980
ccccaagcgc tg 1992

<210> 257
<211> 2273
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2271)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2273)
<223> n equals a,t,g, or c

<400> 257
ggcacgagct ggcggggaag gagaggtcag gcgctccggg ctcgcccgct aggtcggggc 60
cgcggcgtcc cccaccctaa gtcccacctc cggccgggca tgggtacccg ggcgggcctg 120

gctcggcctg ggcccactca ctggtccaga agcagctgta ggtgcccacc aagcccatga 180
cgacgctgct ggccagggtc cagccctatt caggcaggag ctgctcttct ggggtatcgc 240
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cagaactgag cccagtgaga gcgcaccctg ggcagcctg gattcctggg gtgtccccgg 360
cagccacaca cagccatgca ctacccaact gcactcctct tcctcatcct ggccaatggg 420
gcccaggcct ttcgcatctg cgccttcaat gcccagcggc tgacactggc caaggtggcc 480
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gggacgctag aagggtcatg tgttaactat aatcacattt atggtttgga accatcaccc 2160
caaggtaaaa aaaaaataaa aggtattccc aggtatgttt ggcaaaataa aataaaggta 2220
attaaaaacc taaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaattttgcg ncn 2273

<210> 258
<211> 1504
<212> DNA
<213> Homo sapiens

<400> 258
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tattcaggga ttttttttaaa aagtcaatca gaaaagggat actggagctt cttcatgtat 180
gtaacagcat attaaactgg agacagtgat gaatcagcta caaaggtaat attgtattaa 240
aatcatgttt aagatagctg cttttatgtg tattttatat tgcatgcttt tgtaaaaaca 300
tgctgggtga tgaaagatta gtttagaga gaaaatgttc atctgtgcag aggatgcatt 360
ttcttccatt aattctggaa aaaacgttca cagttatata tatggtattt tgcaaaagga 420
ctattaatag aaccttttga gatgaattaa tgtaagaata ttttttaaat aggcttactg 480

tcaaattgca actttttttt tagatacaga gtggaaaaca gtgctaagtc atttggcacc 540
tccttacaaa tatttttcat ggtcacattt attaaatgtt actacatttc tgaattttg 600
aaaaatgtat tttatcatta aatggcatta ttttaaaggg tgaaaaactg acacagtcaa 660
ttcagaaaat ggactgaagt ctgaataagg tcattgcatt taaaaagcat ataactgtac 720
ttgactgatg agggaggtgt tactttcatt gtatataggt cttatttcat aaacagatat 780
cctgtatcaa ataaaagtat ttgttatata tttgaagtta tgcatggaaa ggagtgtgtt 840
taaattgtta caaacaataa tgcgtcatta aaggccatgc tgatcttgca taactataag 900
tactatgaat gaatttggtt ggttttggtg ttgtacagct cacatgttta cacactcagt 960
gccctaattt cccctgaggg aatcgctttt taagtgatcc ttacagtggt gttttatgtt 1020
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attaaaactt gccttaagct accagattgc ttttgccacc attggccata ctgtgtgttt 1440
gtttgtttaa tttactttca caataaactt ctgtgtagta aaaaaaaaaa aaaaaaaaaa 1500
aaaa 1504

<210> 259
<211> 1792
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (107)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (487)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1306)
<223> n equals a,t,g, or c

<400> 259
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cgggaatccc aaagggcgtg gtgagcttca aaagtgggaa ctggggctgg gccacagccg 180
gcagcagcag catcttggcg gagtttggat ccctgcactt ggaattctta cacctcactg 240
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<210> 260
<211> 2048
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (66)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (67)
<223> n equals a,t,g, or c

<400> 260
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gcggganntgg ggtcgcccga gttgggctgg ggaagccagg gacggaggtg tccggccgtc 120
acccctagag gagggcgtgc gggggtctgt tttgcatgcg agccacccct ctggctgctc 180
ctgcgggttc cctgtccagg aagaagcggt tggagttgga tgacaactta gataccgagc 240
gtcccgtcca gaaacgagct cgaagtgggc cccagcccag actgcccccc tgcctgttgc 300
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tgccccgca caagcatgtg gctcggccca ctgaggtcct ggctggtacc cagctcctct 480
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aactcgac 2048

<210> 261
<211> 1282
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1244)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1261)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1265)
<223> n equals a,t,g, or c

<400> 261
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tagtgccagc tacggtccgc ggctggggtt ccctcctccg tttctgtatc cccacgagat 120
cctatagcaa tggaactcag cgatgcaaat ctgcaaacac taacagaata tttaaagaaa 180
acacttgatc ctgatcctgc catccgacgt ccagctgaga aatttcttga atctgttgaa 240
ggaaatcaga attatccact gttgcttttg acattactgg agaagtccca ggataatgtt 300
atcaaagtat gtgcttcagt aacattcaaa aactatatta aaaggaactg gagaattgtt 360
gaagatgaac caaacaaaat ttgtgaagcc gatcgagtgg ccattaaagc caacatagtg 420
cacttgatgc ttagcagccc agagcaaatt cagaagcagt taagtgatgc aattagcatt 480
attggcagag aagattttcc acagaaatgg cctgacttgc tgacagaaat ggtgaatcgc 540

tttcagagtg gagatttcca tgttattaat ggagtcctcc gtacagcaca ttcattattt 600
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gatgcctttg ctttgccttt gactaatctt tttaaggcca ctattgaact ctgcagtacc 720
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aattcaattt ctggcttcag tttgtgagag acctcattat aagaatctat ttgaggacca 1140
gaacacgctg acaagtatct gtggaaaagg ttattgtgcc taacatggga tttagagctg 1200
ctgatggaag aagcattgaa gtaattctga ggggttacag aggngagatt tggaagggtc 1260
nggtnttggt actagacgca gg 1282

<210> 262
<211> 599
<212> DNA
<213> Homo sapiens

<400> 262
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gcgcctcagc ccagccgcgt gccttggccc atggccgcct actcttaccg ccccggccct 120
ggggccggcc ctgggcctgc tgcaggcgcg gcgctgccgg accagagctt cctgtggaac 180
gttttccaga gggtcgataa agacaggagt ggagtgatat cagacaccga gcttcagcaa 240
gctctctcca acggcacgtg gactcccttt aatccagtga ctgtcaggtc gatcatatcc 300
atgtttgacc gtgagaacaa ggccggcgtg aacttcagcg agttcacggg tgtgtggaag 360
tacatcacgg actggcagaa cgtcttccgc acgtacgacc gggacaactc cgggatgatc 420
gataagaacg agctgaagca ggccctctma gtttcggcta ccggctctct kaccagttcc 480
acgacatcct cattcgaaag kttgacaggc argggacggg gcaratcgsc ttcgacgast 540
taatccaagg ctggcatggc ctgcagaggt ttacggatat attcaaaggt ttcggcacg 599

<210> 263
<211> 1261
<212> DNA
<213> Homo sapiens

<400> 263
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gggcactcca gcgaccgtgg ggatcagcgt aggtgagctg tggccttttg cgaggtgctg 120
cagccatagc tacgtgcgtt cgctacgagg attgagcgtc tccacccagt aagtgggcaa 180
gaggcggcag gaagtgggta cgcaggggcg caaggcgcac agcctctaga cgactcgctt 240
tccctccggc caacctctga agccgcgtcc tactttgaca gctgcagggc cgcggcctgg 300
tcttctgtgc ttcaccatct acataatgaa tcccagtatg aagcagaaac aagaagaaat 360
caaagagaat ataaagaata gttctgtccc aagaagaact ctgaagatga ttcagccttc 420
tgcatctgga tctcttgttg gaagagaaaa tgagctgtcc gcaggcttgt ccaaaaggaa 480
acatcggaat gaccacttaa catctacaac ttccagccct ggggttattg tcccagaatc 540
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aaatccatcc tctcagtatt ggaaggaagt ggcagaaaaa cggagaaagg cgctgtatga 660
agcacttaag gaaaatgaga aacttcataa agaaattgaa caaaaggaca atgaaattgc 720
ccgcctgaaa aaggagaata aagaactggc agaagtagca gaacatgtac agtatatggc 780
agagctaata gagagactga atggtgaacc tctggataat tttgaatcac tggataatca 840

ggaatttgat tctgaagaag aaactgttga ggattctcta gtggaagact cagaaattgg 900
cacgtgtgct gaaggaactg tatcttcctc tacggatgca aagccatgta tatgaaatgc 960
attaatattt gactgttgag aattttactg ccgaagttta cctccactag ttctttgtag 1020
cagagtacat aactacataa tgccaactct ggaatcaaat ttccttgttt gaatcctggg 1080
accctattgc attaaagtac aaatactatg tatttttaat ctatgatggt ttatgtgaat 1140
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gttgaacatt gtgtataact tagaataatg aaatataagg agtatgtgta gaaaaaaaaa 1260
a 1261

<210> 264
<211> 1020
<212> DNA
<213> Homo sapiens

<400> 264
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acagaagggt cctgctcaaa taacactggg tgctatattg atgggtaaat gtgtacatcc 120
tattccttcc tctttatctc acaattttg tctccactaa gcaagaagta aactaacact 180
tcgtcactct aaagaaataa cttatgtaaa actcttagta accctgtttg tcttcaaatg 240
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acactgccaa cacgtcaatt ttttaaaaag cgtgggccac attgctaaga atttgttaaa 660
gcataactgt atttttttgtt ttagggcctt attgatgttt tgccgttcca atgtatgcat 720
tttttactc aataaacttg tcttaatttt agaactgtct gatgatttcg tactggaaag 780
aactactcaa agacggcagt gtaaaagcaa gtcttaggaa agtcccattt tatttgtgtc 840
taacaaacat acaggaactg aaatattttt gttaaatcct gggatgcacc gaagtaactt 900
aaaacaaacc gttcaacagg ttcccccaac cgcccacgcc acataaagaa cagacatatc 960
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<210> 265
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (557)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (565)
<223> n equals a,t,g, or c

<400> 265
ctttacggca sgmgtccgcg tcgctagcta gtcgttctga agcggcggcc agagaagagt 60
caagggcacg agcatcgggc catgcctttc ttggacatcc agaaaaggtt cggccttaac 120

atagatcgat ggttgacaat ccagagtggt gaacagccct acaagatggc tggtcgatgc 180
catgcttttg aaaaagaatg gatagaatgt gcacatggaa tcggttatac tcgggcagag 240
aaagagtgca agatagaata tgatgatttc gtagagtgtt tgcttcggca gaaaacgatg 300
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tctggaggct gattttcctg ttctctgttc tccactggaa aggttgttta cgacaaacct 480
ccttgtcaaa gtgtgtaaaa ataaaggatt gctccatcct aaaaaaaaaa aaaaaaaaaa 540
aaaatttggg gggggncccc cgtancccat t 571

<210> 266
<211> 1350
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (204)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1313)
<223> n equals a,t,g, or c

<400> 266
tgccgccatc gtcgtggggc ttctggggca gctagggctg cccgccgcgc tgcctgcgcc 60
ggaccggggc gggtccagtc ccgggcgggc cgtcgcggga gagaaataac atctgctttg 120
ctgccgagct cagaggagac cccagacccc tcccgcagcc agagggctgg agcctgctca 180
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cggctggaac gagttcatcc tgcagcccat ccacaacctg ctcatgggtg acaccaagga 360
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tgacttcttt actaacactg gctagctata ttatcttata tactaatatc atgttttaaa 1260
aatataaaat agaaattaag aatctaaawa aaawaaaaaa acgggggggcg ctntaaaggg 1320
tccaagctta acgtaagcgt gcatgggaag 1350

<210> 267
<211> 1319

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (61)
<223> n equals a,t,g, or c

<400> 267
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nccgctctag aactagtgga tcccccgggc tgcaggaatt cggcacgaga gactccgcga 120
cctactgacc cggcgactga caggctccaa ctacccggga ctcagtatta gccttcgcct 180
cactggctcc tctgcacaag aggmggcttc cggagtagcc ctcggtgaag ccccagacca 240
cagctatgag tcccttcgtg tgacgtctgc gcagaaacat gttctgcatg tccagctcaa 300
ccggcccaac aagaggaatg ccatgaacaa ggtcttctgg agagagatgg tagagtgctt 360
caacaagatt tcgagagacg ctgactgtcg ggcggtggtg atctctggtg caggaaaaat 420
gttcactgca ggtattgacc tgatggacat ggcttcggac atcctgcagc ccaaaggaga 480
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caacgtcatc gagaggtgcc ccaagcccgt gattgctgcc gtccatgggg gctgcattgg 600
cggaggtgtg gaccttgtca ccgcctgtga catccggtac tgtgcccagg atgctttctt 660
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaagg ggggggggc 1319

<210> 268
<211> 3694
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (746)
<223> n equals a,t,g, or c

<400> 268
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gaggtgtggc ggagcctgtg cgcccgcagc ctggcagaag aggctctgcg cacggacatc 120
ctgtgcaacc tgcccagcta caaggccaag atacgtgctt ttcaacatgc cttcagcact 180

aatgactgct ccaggaatgt ctacattaag aagaatggct ttactttaca tcgaaacccc 240
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tgggaagtgt ggtgggaggg ccctctgggc actgtggcag tgattggaat tgccacaaaa 360
cgggcccccca tgcagtgcca aggttatgtg gcattgctgg gcagtgatga ccagagctgg 420
ggctggaatc tggtggacaa taatctacta cataatggag aagtcaatgg cagttttcca 480
cagtgcaaca acgcaccaaa atatcagata ggagaaagaa ttcgagtcat cttggacatg 540
gaagataaga ctttagcttt tgaacgtgga tatgagttcc tgggggttgc ttttagagga 600
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<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

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<222> (31)
<223> n equals a,t,g, or c

<220>
<221> misc feature
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (460)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1233)
<223> n equals a,t,g, or c

<400> 269
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<210> 270
<211> 2057
<212> DNA
<213> Homo sapiens

<220>
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<222> (22)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2053)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2054)
<223> n equals a,t,g, or c

<400> 270
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aaggaacatc ataatggaaa tttcacagac ccctcttcag tgaatgaaaa gaagaggagg 180
gagcgggaag aaaggcagaa tattgtcctg tggagacagc cgctcattac cttgcagtat 240
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<210> 271
<211> 960
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (31)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (951)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (956)
<223> n equals a,t,g, or c

<400> 271
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agacaaagac ccgcaaaaga tgtatgccac catctatgag ctgaaagaag acaagagcta 420
caatgtcacc tccgtcctgt ttaggaaaaa gaagtgtgac tactggatca ggacttttgt 480

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<210> 272
<211> 1167
<212> DNA
<213> Homo sapiens

<400> 272
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gaggaatccc agctggggtt cccatgcccc aggctcctgc aggacttgct gggccagtcc 540
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<210> 273
<211> 2771
<212> DNA
<213> Homo sapiens

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<222> (16)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (27)
<223> n equals a,t,g, or c

<220>
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<222> (42)
<223> n equals a,t,g, or c

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<222> (64)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2715)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2717)
<223> n equals a,t,g, or c

<400> 273
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taggccgtcg ctttcgggtt ctctcatcgc ttcgtcgttc gccaatgttt gaggagaagg 180
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<210> 274
<211> 1889
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (57)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (87)
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1676)
<223> n equals a,t,g, or c

<400> 274
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tcactgattt gctttaaaaa aaataaaaga taatgattta ttgcagaaaa aaaaaaaaaa 1860
aaaaaaaaaa aaaaaataaa aaaaataaa 1889

<210> 275
<211> 604
<212> DNA
<213> Homo sapiens

<400> 275
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tcctgccatc ctctcaacag ctctgtgggg tgggtcctcc cccatacctg atgcaccgac 180
cacacagtgg aaagtgacaa agccagcgcc ttgccccagg ccccgcaggg tggagcccgt 240
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gctgtgctcg gacctggtca aggcatacca gcgctgcgtg agcgccsccc acaagggctg 360
aggagcagac atcattccct gccctggcag tgacttggag ccctgaagaa gggaccaatc 420
atgggaccac agccactgtg ccctgccgtt tcctgctggg cccctgcata tgcccctgag 480
cctggggctg ccacgtgttt aggaaacaaa gtatgcgcta ctgtctgaaa acaaataaag 540
cagatgcctt tgttttcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 600
aaag 604

<210> 276
<211> 1381

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1348)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1349)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1350)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1358)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1359)
<223> n equals a,t,g, or c

<400> 276
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ctgagctggc agaagacaag gagaattaca agaaattcta tgaggcattc tctaaaaatc 180
tcaagcttgg aatccacgaa gactccacta accgccgccg cctgtctgag ctgctgcgct 240
atcatacctc ccagtctgga gatgagatga catctctgtc agagtatgtt tctcgcatga 300
aggagacaca gaagtccatc tattacatca ctggtgagag caaagagcag gtggccaact 360
cagcttttgt ggagcgagtg cggaaacggg gcttcgaggt ggtatatatg accgagccca 420
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tgggctatat gatggccaaa aagcacctgg agatcaaccc tgaccacccc attgtggaga 780
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gtttatttta ttttcttcat ttgttctgaa aattaaagta tgcaaaataa agaatatgcc 1320

gtttttatac aaaaaaaaaa aaaaaaannn gggggggnng ccccggtccc matttccccc 1380
c 1381

<210> 277
<211> 1149
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (680)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1088)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1098)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1140)
<223> n equals a,t,g, or c

<400> 277
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atgtcaaaag gcactgatga agatattttc tctggagtct ccttctttct aacccggctc 180
tcccgatgtg aaccgagccg tcgtccgccc gccgccgccg ccgccgccgc cgccgcccgc 240
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gggagctcca gaaggggatc atgacctcct cacctgtggg cagtgccaga tgaacttccc 420
attgggggac attcttattt ttatcgagca caaacggaaa caatgcaatg gcagcctctg 480
cttagaaaaa gctgtggata agccaccttc cccttcacca atcgagatga aaaaagcatc 540
caatcccgtg gaggttggca tccaggtcac gccagaggat gacgattgtt tatcaacgtc 600
atctagagga atttgcccca aacaggaaca catagcagat aaacttctgc actggagggg 660
cctctcctcc cctcgttctn gcacatggag ctctaatccc cacgcctggg atgagtgcag 720
aatatgcccc gcaggtattt gtaaagatga gcccagcagc tacacatgta caacttgcaa 780
acagccattc accagtgcat ggtttctctt gcaacacgca cagaacactc atggattaag 840
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cccctttaac ctgctaagaa taccaggatc agtatcgaga gaggcttccg gcctgggcag 1020
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cccaccgnat agagcgcntg gggggcggta aggagatggg cctggggcaa acccttcaan 1140
ccgagttgc 1149

<210> 278

<211> 811
<212> DNA
<213> Homo sapiens

<400> 278
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tggtcggcgg ctgcagcggg gtgagcggcg gcagcggccg gggatcctgg agccatgggg 120
cgcgcgcgcg acgccatcct ggatgcgctg gagaacctga ccgccgagga gctcaagaag 180
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gatgagcagt accaggcagt gcggccgagc ccaccaaccc aagcaagatg cggaagctct 600
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acgaaaagcc agcttgaaaa aaaaaaaaaa a 811

<210> 279
<211> 1260
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1249)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1252)
<223> n equals a,t,g, or c

<400> 279
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ccactttytt tgacagtcca gcccacctcc tcttctgccc ggagaagctc caggggytgc 180
ctttktgatc acagcatctt cacaaggacc aaaggaaaat aagatttcty gtaagaacac 240
cgtgaccaca tctttaaaat gacccatttc gtggctycca caagatttac acctycacac 300
tgaggccgga agtggttttg cccctataaa acatggcgaa aagctttctt gtctccaagg 360
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gatggcgccc ctactaaagc cttggggtta gtacgcgtcg cagcagtctc ttccgacagt 480
tgtgttgtgc caatggtgga gaagaaaact tcggttcgct cccaggaccc cgggcagcgg 540
cgggtgctgg accgggctgc ccggcagcgt cgcatcaacc ggcagctgga ggccctggag 600
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gagggcccta actacctgac ggcctgtgcg ggacccccat cgcggcccca gcgccccttc 840
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acaaaactgt gtcttatctg ccaggaaaga ccagcctcac tcctgggaac tgtctggcag 1140
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaant tngggggggg 1260

<210> 280
<211> 1668
<212> DNA
<213> Homo sapiens

<400> 280
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ttgattgtsa cagcaagatc aaataacaaa acgaagcata ttgaagaaga gaacttgatt 180
gacgaagact ttcaaaatct aaaactgcgg tcgacaggct tcaccaatct tggagcagaa 240
gggagcgtct ttcctaaggt caggataacg gcctccagag acagccagat gcaaaatccc 300
tattcaagcc acagcagcat gccccgccct gactattaga atcataagaa tgtggaaccc 360
gccatggccc ccaaccaatg tacaagctat tatttagagt gtttagaaag actgatggag 420
aagtgagcac cagtaaagat ctggcctccg gggtttttct tccatctgac atctgccagc 480
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cagtacaaag tactgagaca atggttaggg ttgttttctt aattcttttc ctggtagggc 660
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agtgcctttg ttagatggaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 1668

<210> 281
<211> 2328
<212> DNA
<213> Homo sapiens

<400> 281
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ccacagcagg tagcagtctg gccaaccatg gtggatatca acagccccga aagcctaacc 120
gaagcatata aactccgtgc agccagatta gtagaaattg ctgcaaaaaa ccttcaaaaa 180

gaagtgattc acagaaaaag caaggaggta gcttggaacc taacttctgt tgaccttgtt 240
cgagcaagtg aggcacattg ccactatgtg gtagttaagc tcttttcaga aaaactcctc 300
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tttgaggaga tcatcgacct gcagagcccc ctttgaccca gtacctca 2328

<210> 282
<211> 956
<212> DNA
<213> Homo sapiens

<400> 282
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tgcggggctt ccgccgccgc ttccctgagg agccgcacgt gccgctggag carcgccgcg 180
gcttcctggc ccgcgagcag taccgcgccc tgcggcccga cctggcggat aaagtggcca 240
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ataccgttaa gcgctgtgct accggcccca ggcccagcca cccggtacct cccgagaggc 840
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<210> 283
<211> 1402
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (26)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (88)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (97)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (131)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1344)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1355)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1394)
<223> n equals a,t,g, or c

<400> 283
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ggcgggggg nagaaaagat ttttttcttc tcttaatcgg aatcgtgatg gtgttggatt 180
atttcaatgg tggggttaat atagcatgtt atcctgtcta tcttttaaag atttctgtat 240
aagactgttg agcagttttt aaaatagtgt aggataatat aaaaagcaga tagatggcgc 300
tatgtttgat tcctacaacg aaattatcac cagctttttt tcattcttaa ctctttaaag 360
gattcaaacg caactcaaat ctgtgctgga ctttaaaaaa acaattcagg accaaatttt 420
ttctcagtgt gtgtgtttat tccttatagg tgtaaatgag aagacgtgtt tttttccttc 480
accgatgctc catcctcgta tttctttttc cttgtaaatg taatcagatg ccattttata 540
tgtggacgta tttatactgg ccaaacatat tttttctttt gtcccttttt ttctttcctt 600
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ataaatggtt taaggcctaa tggntgsatg atagncataw ggkgtcaggt ttataacttt 1380
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<210> 284
<211> 675
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (20)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (520)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (560)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (618)
<223> n equals a,t,g, or c

<400> 284
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attccagatg cgagcgcggc cgcggccccg gccgctctgg gcgactgtgc tggcgctggg 120
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<212> DNA
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<211> 1398
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<210> 287
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<212> DNA
<213> Homo sapiens

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<211> 3094
<212> DNA
<213> Homo sapiens

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<210> 289
<211> 1983
<212> DNA
<213> Homo sapiens

<400> 289

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<210> 290
<211> 1298
<212> DNA
<213> Homo sapiens

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<222> (1285)
<223> n equals a,t,g, or c

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<210> 291
<211> 2459
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

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<221> misc feature
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<222> (2392)
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gaccagagaa tcgagaacca tcctagccaa catngtgaaa accccatctg tnactaaaaa 2400
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<210> 292
<211> 570
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (567)
<223> n equals a,t,g, or c

<400> 292
aattcggcac gmgccggagt gtggtacttc tcctagttgc agtcaggctt catacgctat 60
tgtcctgccc gttagagcag ccagcgggta cagaatggat tttggaagag ggagtcacca 120
ctggacctcc aaggaagcca cgtgcagaca tctacaacct tcgatctcct gacgagttta 180
ttgttggcca aaaccaggct ttgattgaac caggatgaat gcgggtgttg gaagtagaat 240
atatatatac atataaaatt ggttgggagc cacgtgtacc agtgtgtgtt gatcttggct 300
tgattcagtc tgccttgtaa cagaaactgg cgatggaata tgagaggagc cctctggaaa 360
gaaaaggaca gaccctgtgc tttcatgaaa gtgaagatct ggctgaacca gttccacaag 420
gttactgtat acatagcctg agtttaaaag gctgtgccca cttcaagaat gtcattgtta 480
gactttgaaa tttctaactg cctacctgca taaagaaaat aaaatctttt aaatcaaaaa 540
aaaaaaaaaa raaggggccc gctctanagg 570

<210> 293
<211> 2468
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2076)
<223> n equals a,t,g, or c

<400> 293
gggtttgaga agattggaca gtgcttcagg caccgtgtac acagcaatgg atgtggccac 60
aggacaggag gtggccatta agcagatgaa tcttcagcag cagcccaaga aagagctgat 120
tattaatgag atcctggtca tgagggaaaa caagaaccca aacattgtga attacttgga 180
cagttacctc gtgggagatg agctgtgggt tgttatggaa tacttggctg gaggctcctt 240
gacagatgtg gtgacagaaa cttgcatgga tgaaggccaa attgcagctg tgtgccgtga 300
gtktctgcag gctctggagt tcttgcattc gaaccagata accccagagc agagcaaacg 360
gagcaccatg gtaggaaccc catactggat ggcaccagag gttgtgacac gaaaggccta 420
tgggcccaag gttgacatct ggtccctggg catcatggcc atcgaaatga ttgaagggga 480
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cccagaactt cagaacccag agaagctgtc agctatcttc cgggactttc tgaaccgctg 600
tctcgagatg gatgtggaga agagaggttc agctaaagag ctgctacagc atcaattcct 660
gaagattgcc aagcccctct ccagcctcac tccactgatt gctgcagcta aggaggcaac 720
aaagaacaat cactaaaacc acactcaccc cagcctcatt gtgccaagcc ttctgtgaga 780
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aagagaactg caactgaatg actaatcaga tgatggccat ttctaaataa ggaatttcct 960
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aattataaac acacttgtat ccaccaaatc aagaaakgga acactgacag taagaacctt 2280
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taaaaaaa 2468

<210> 294
<211> 1080
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1038)
<223> n equals a,t,g, or c

<400> 294
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atgacaacca aatcatcacc agctctgggg ataccacctg tgccctgtgg gacattgaga 120
caggccagca gacagtgggt tttgctggac acagtgggga tgtgatgtcc ctgtccctgg 180
cccccgatgg ccgcacgttt gtgtcaggcg cctgtgatgc ctctatcaag ctgtgggacg 240
tgcgggattc catgtgccga cagaccttca tcggccatga atccgacatc aatgcagtgg 300
ctttcttccc caacggctac gccttcacca ccggctctga cgacgccacg tgccgcctct 360
tcgacctgcg ggccgatcag gagctcctca tgtactccca tgacaacatc atctgtggca 420
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ccccactgtg gagataagaa ggggatggaa tgggggaaga ggaggagcag gaggccctca 840

tccttctgct gccctggggt tggggcctca cccctctgga gggccggagg caggaggtgg 900
aaaccccagg ggctggcttt tttaaaactg gttttatttt aatttttatt atattttcag 960
tttttccata aaggagccaa ttccaactct gwaaaaaaaa aaaaaaaaaa acttcgrggg 1020
ggggcccgta cccaattngc ctttaggggg gggtttaaat taatggcggg gttttaaaag 1080

<210> 295
<211> 2695
<212> DNA
<213> Homo sapiens

<400> 295
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tccatatata cagaaattag acaaataata agtctttagt tcaacttaag catatctcaa 180
atgacttctc taaatttaaa gttgatcatg ataggatcat aaaagacaga aaagacttaa 240
gtaatcttgt aatgacaatt atttccattt ttgctgaact aaaaatattt aacttcataa 300
atatgttact acagcttcca gatttaaaga aaaaaagttt cccccactct caattaaaag 360
ttagaaccct ccacttttaa aattatacaa atatttcttt tttacattac acagaagcct 420
tctgtaccat tttacgaatt tctgtcttca taatataagt gaaaatactg tcatttcaat 480
tttctgcttt aaattgtttt taataagcat yccaaagtga tacagactta agcttttaat 540
caatcagtca ttcagttgat agacaaagtt agcgatgctt tatgctagga aacttgttga 600
cagtaacctg tgcgacttta tgcagaagac aaatgctagt aattattatg cacagaggaa 660
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cttaatccca ttgttttggt taacatctta cccatttgtt gtatttcaaa tgccattaat 1440
cattttagta caacacctat gtttataaaa atttgaaaac attacatatt gtatttaaaa 1500
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gacatggcca ttattccatg tgcttaaatg ataatttcct tattcagttt cagaagaaaa 1980
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gcaacttttg atgtaggtgt tttgctatgc ctcagaaaat atctgtctga gaatttgtta 2220
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tgatgtttag gctttatttc tgttaataag gctttttacc attgattaaa tgaaggaatg 2520
tatctttttg aagagattta tattctgtaa ataaaaattc gttgtaacaa taaagttgag 2580
ttctaactac aaaaaaaaaa aagtcgacac cgccgggaat ttaggtgtag tagtcccccg 2640
ggaaattcgg accggttact gaaggcgatc cagttttccc aaagttgggc gtatt 2695

<210> 296
<211> 1394
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1238)
<223> n equals a,t,g, or c

<400> 296
gcccacgcgt ccgagctcag tcagcagaag agataaaagc aaacaggtct gggaggcagt 60
tctgttgcca ctctctctcc tgtcaatgat ggatctcaga aataccccag ccaaatctct 120
ggacaagttc attgaagact atctcttgcc agacacgtgt ttccgcatgc aaatcaacca 180
tgccattgac atcatctgtg ggttcctgaa ggaaaggtgc ttccgaggta gctcctaccc 240
tgtgtgtgtg tccaaggtgg taaagggtgg ctcctcaggc aagggcacca ccctcagagg 300
ccgatctgac gctgacctgg ttgtcttcct cagtcctctc accacttttc aggatcagtt 360
aaatcgccgg ggagagttca tccaggaaat taggagacag ctggaagcct gtcaaagaga 420
gagagcattt tccgtgaagt ttgaggtcca ggctccacgc tggggcaacc cccgtgcgct 480
cagcttcgta ctgagttcgc tccagctcgg ggagggggtk gagttcgatg tgctgcctgc 540
ctttgatgcc ctggattttg cccgwacagg tcaattgact ggcggctata aacctaaccc 600
ccaaatctat gtcaagctca tcgaggagtg caccgacctg cagaaagagg gcgagttctc 660
cacctgcttc acagaactac agagagactt cctgaagcag cgccccacca agctcaagag 720
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gagaaggcag ctcacgaaac ccaggcctgt gatcctggac ccggcggacc ctacaggaaa 1020
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gaattaccca tgctttaaga attgggatgg gtccccagtg agctcctgga ttctgctggt 1140
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tatagtgaca ggctgtgctc catattttac agtcattttg gtcacaatcg agggtttctg 1320
gaattttcac atcccttgtc cagaattcat tcccctaaga gtaataataa ataatctcta 1380
acaccaaaaa aaaa 1394

<210> 297
<211> 998
<212> DNA
<213> Homo sapiens

<400> 297
ggcacgaggt gaaataacgg gcccatataa atccctctgc cgcccgcctg caagatggat 60
tggccgcatt gaaattcctc cgcragataa ttaaactcgg ggcctcatcc gggcaaaatt 120
acattccttg tgacgactgc gcatgctcgg aaaggggacg caatcragat cccaaacgcg 180

gtacagacca aaccgcagtc cacgttacgg atcggcttac tccgcggagt tggcctcatt 240
tctgcagtcg gcgctccctg tagtttctcc tctcgaacgc caggtggagc aaccggccgg 300
ataccgccac agccctggca ggcggcgctg tgatgcctga gctgatcctc tctcctgcca 360
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tcaagagcac ctcacagctg ctgagccgtc cgctatctgc agtggtgctg aaacgaccgg 480
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cctttctcat cctctttgcc atgtgaagga gccgtctcca cctcccatag ttctcccgcg 840
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaa 998

<210> 298
<211> 1666
<212> DNA
<213> Homo sapiens

<400> 298
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ttaggtctcc aggaaagcta acagccaggg agaggatcag tctcttgctg gaccctggca 120
gctttkttga gagcgacatg tttgtggaac acagatgtgc agattttgga atggctgctg 180
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tggtttatgt cttcagtcag gattttacag tttttggagg cagtctgtca ggagcacatg 300
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acagagcttt tgaaaatgat gttgatgcct tgtgtaatct ccgggatttc ttcaactacc 720
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ataactaagt ttattaaatt ctagaaagat aaaaaaaaaa aaaaaa 1666

<210> 299

<211> 2444
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (402)
<223> n equals a,t,g, or c

<400> 299
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gagaaagttg atgtgattgc cggctcctcc aagatgaagg gcttctcgtc ctcagagtcg 120
gagagctcca gtgagtccag ctcctctgac agcgaagmcw ccgaaacagg tcctgcctaa 180
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<222> (454)
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<220>
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<222> (470)
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<211> 2902
<212> DNA
<213> Homo sapiens

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<220>
<221> misc feature
<222> (2891)
<223> n equals a,t,g, or c

<400> 304
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<211> 1553
<212> DNA
<213> Homo sapiens

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<210> 306
<211> 1987
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (731)
<223> n equals a,t,g, or c

<400> 306
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catttcc 1987

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<211> 785
<212> DNA
<213> Homo sapiens

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cctgcgcccc tcactcctcc cgctccatct gctgctgctg ctgctgctca gtgcggcggt 180
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aaaaa 785

<210> 308
<211> 2178
<212> DNA
<213> Homo sapiens

<400> 308
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gatgcccacc cagcagcagg tcccctttct gtctgtgggt ggggacattg ggtccggac 240
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<211> 875
<212> DNA
<213> Homo sapiens

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<210> 310
<211> 756
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (613)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (638)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (684)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (756)
<223> n equals a,t,g, or c

<400> 310
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<210> 311
<211> 851
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (834)
<223> n equals a,t,g, or c

<400> 311
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tccagaagac ttgcatagcc atgtggtaaa tgagcatgca tgtaaattaa tagagttaag 180
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ttataaaatt ttattggcat tgctccattt tctgtatata aatatatctt taatgtggta 780
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ctcactaatc c 851

<210> 312
<211> 1335
<212> DNA
<213> Homo sapiens

<400> 312
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<210> 313
<211> 516
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (505)
<223> n equals a,t,g, or c

<400> 313
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ctgagggagg cgcgagggcg cggagttcca ggtcgagcag ttaggccgcg agcgactgcg 120
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ggcccccaag accatcgtgc ggggcagcaa argtgccaaa gatggggccc tcacgctgct 480
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<210> 314
<211> 1833
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (625)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1761)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1766)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1792)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1806)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1827)
<223> n equals a,t,g, or c

<400> 314
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<210> 315
<211> 1354
<212> DNA
<213> Homo sapiens

<400> 315
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aaaaaaaaa aaaaaaaaa aaaaaaaaa aaaa 1354

<210> 316
<211> 2421
<212> DNA
<213> Homo sapiens

<400> 316
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<210> 317
<211> 1092
<212> DNA
<213> Homo sapiens

<400> 317
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aaaaaaaaaa ac 1092

<210> 318
<211> 1380
<212> DNA
<213> Homo sapiens

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<210> 319
<211> 2612
<212> DNA
<213> Homo sapiens

<400> 319
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ccaaagacct acatccggca ggacaatgag agggtactgt ttgcccccat gcgcatggtg 240
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<210> 320
<211> 943
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (54)
<223> n equals a,t,g, or c

<400> 320
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tggtggagtt cagtccaatt caggtcagcc atatccaaaa gaccacaagt cattactaag 180
ttgagcaaaa gagtttttat ctattagcag aaagggcctc tctggcagca gagattaaaa 240
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gacttgaatt ccttctttgg gaccaagtta ataaaagacc aagaaactcc tgattaaact 360
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<210> 321
<211> 2959
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2948)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (2956)
<223> n equals a,t,g, or c

<400> 321
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tgctggtgtt ttccacagat gccgggtttc actttgctgg agatgggaaa cttggtggca 180
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aaagtcccaa gtgtcatgaa ggaaatggga catttgagtg tggcgcgtgc aggtgcaatg 780
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<210> 322
<211> 802
<212> DNA
<213> Homo sapiens

<400> 322
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<210> 323
<211> 1724
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1590)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1650)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1701)
<223> n equals a,t,g, or c

<400> 323
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<210> 324
<211> 2261
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1098)
<223> n equals a,t,g, or c

<400> 324
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gaatgcgttg aggaagcata aagacttgtt gggtaaaaga tacattgaac tcttcaggag 120
cacagcagct gaagttcagc aggtgctgaa tcgattctcc tcggcccctc tcattccact 180
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<210> 325
<211> 1213
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1213)
<223> n equals a,t,g, or c

<400> 325
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actccttggc gcctgcctga tcctccaaat caccacagga ctattcctag ccatgcacta 180
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cggcattatc ctcctgcttg caactatagc aacagccttc ataggctatg tcctcccgtg 420
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cattgggaca gacctagttc aatgaatctg aggaggctac tcagtagaca gtcccaccct 540
cacacgattc tttacctttc acttcatctt gcccttcatt attgcagccc tagcagcact 600
ccacctccta ttcttgcacg aaacgggatc aaacaacccc ctaggaatca cctcccattc 660
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ccttctctcc ttaatgacat taacactatt ctcaccagac ctcctaggcg acccagacaa 780
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<210> 326
<211> 2764
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (372)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2128)
<223> n equals a,t,g, or c

<400> 326
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gggacaagaa tgcctcctta cagctgctgc aaaaggagaa ggagaagctg actgtgctgg 180
aaaggagata ccactcactc acagggggca ggcctttccc gaagaccaca tcgaccctca 240
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tcctcgcaac ctggcagcca cactgcagga catcgagacc aagcgccaac tagctctgca 480
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gggc 2764

<210> 327
<211> 1764
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1398)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1758)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1759)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1762)
<223> n equals a,t,g, or c

<400> 327
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gctgtgaccg ctgtgaagaa tggtttcatg gcgattgtgt gggcatttct gaggctcgag 180
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atgctgatgg caccgattgt acaagtatag gaacaataga gcagaagtct agcgaagacc 360
aagggataaa gggtagaatt gagaaagctg caaatccaag tggcaagaag aaactcaaga 420
tcttccagcc tgtgatagag gcgcctggtg cctcaaaatg tattggcccc gggtgctgtc 480
acgtggcgca cccgactcgg tgtactgcag taatgactgt atcctcaaac acgccgcagc 540
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ctttaaaaaa aaaaaaannt cnaa 1764

<210> 328
<211> 571
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (535)
<223> n equals a,t,g, or c

<400> 328
gcccaantac tttccagccc agtaaggggt atttcaggag agcagtccac tkaaggttct 60
ttccctttaa gatatgtgca ggatcaagtt gcggcacctt ttcagctgag taaccacact 120
ggccgcatca aggtggtctt tactccgagc atctgtaaag tgacctgcac caagggcagc 180
tgtcagaaca gctgtgagaa ggggaacacc accactctca ttagtgagaa tggtcatgct 240
gccgacaccc tgacggccac gaacttccga gtggtaattt gccatcttcc atgtatgaat 300
ggtggccagt gcagttcaag ggacaaatgt cagtgccctc caaatttcac aggaaaactt 360
tgtcagatcc cagtccatgg tgccagcgtg cstaaacttt atcagcattc ccagcagcca 420
ggcaaggcat tggggacgca tgtcatccat tcaacacata ccttgcctct gaccgtgact 480
agccagcagg agtcaaagtg aaatttcctc cttaacatag tcaatatcca tgtgnaacat 540

cctcctgaag cttccgtcca gatacatcag g 571

<210> 329
<211> 473
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (37)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (449)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (467)
<223> n equals a,t,g, or c

<400> 329
cacgtagtaa tctttaaata taaatagcca cgtgtgnact actatcatat gggacagaac 60
agttccagac cacattattg ataagatgtg ttaaaataaa taagatcttt ctgtgaactt 120
ttgggaacca aatggttttg ggcatgattt cccagctcat tatatattga cacagaattt 180
tttcagaatg gcatttacta gtaccccaga aatttagcaa agtatagtta ggtacttatt 240
gtaaaatata ttgcatattt gatttaaggt ttgttatgaa cacactaatc tgatatttta 300
tatttaaacc attttcaatk ctgtaagact cagtaagagc tatttaatta tactgwaaca 360
aagaaaatct ataaataaat agcacaaata ggcacatgcg ggtgtataat actgaagtgg 420
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<210> 330
<211> 1335
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (865)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1004)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1156)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1301)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1328)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1333)
<223> n equals a,t,g, or c

<400> 330
ggcgctactg aggccgcgga ccggactgcg gttggggcgg gaagagccgg ggccgtggct 60
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aggatgagca agctgcccag ggagctgacc cgagacttgg agcgcagctg cctgccgtgg 180
cctccctggg ctcctcactg tcccacagcc agagcctctc ctcgcacctc cttccgccgc 240
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acctgctctt catctccctg ctctggatca tcgaactgaa taccaacaca ggcatccgta 360
agaacttgga gcaggagatc atccagtaca actttaaaac ttccttcttc gacatctttg 420
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<210> 331
<211> 1046
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (982)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (997)
<223> n equals a,t,g, or c

<400> 331
ggtaaaacag agagcaacat gccccagtcc ctctctctgg ccagttcttg tggcagcccc 60
attggcctgg agacatggtt ttttgtggtt gcagctgcag ctgtcccccc gtcttttaac 120
tcgacatcaa aagcctctct cctgccagtg ccataggttt gttagagcta ctgttttgta 180
acagctgctc aggtgtcccc aaactcctgg agttttccac cctgagctgt taaaaacctg 240
ccctgcctgt cacccatttc tgtgccacca gcccaccccc tgcctccact ctcctccctg 300
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<210> 332
<211> 1311
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1280)
<223> n equals a,t,g, or c

<400> 332
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gcagtatgct tgcccctgga ggaacgcgca tagatgatgg tgacaagacc aagatgacca 420
accactgtgt gttttcagca aatgaagatc atgaaaccat ccgaaactat gctcaggtct 480
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gctcagaaca tcagctttan tcgtgccgat tcggcacgag cggcacgagc c 1311

<210> 333
<211> 1444
<212> DNA
<213> Homo sapiens

<400> 333
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tgtccttggg gctgtaattg gccccagctg agcagggcaa acactgaggt caactacaag 120
ccacaggccc cttccccagc ctcagttcac agctgccctg ttgcagggag gcggtggccc 180
ttctgttgct agaccgagcc tgtgggatat accaaggcag aggagcccat agccatgagg 240
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ccaacgccgc ccgacaacat ccaagtgcag gaaaacttca atatctctcg gatctatggg 360
aagtggtaca acctggccat cggttccacc tgcccctggc tgaagaagat catggacagg 420
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agcactcgtt ggcggaaagg tgtctgtgag gagacgtctg gagcttatga gaaaacagat 540
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gtccacacca actatgatga gtatgccatt ttcctgacca agaaattcag ccgccatcat 660
ggacccacca ttactgccaa gctctacggg cgggcgccgc agctgaggga aactctcctg 720
caggacttca gagtggttgc ccagggtgtg ggcatccctg aggactccat cttcaccatg 780
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gaagtcacca agaaagaaga ttcctgccag ctgggctact cggccggtcc ctgcatggga 960
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tggccagtgt ctgtcccggg gtcctgtggc aggcagcgcc aagcaacctg ggtccaaata 1380
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aagg 1444

<210> 334
<211> 1030
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (59)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (989)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1006)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1023)
<223> n equals a,t,g, or c

<400> 334
tagaattcgg agaagctgaa gcttagtgtt ctaaacggtg gttgggaagg gggaaggang 60
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gctgtcctga ccacacccac tccttgctgc agccrtgkag tcttccactt tcgccttggt 180
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tcctgttgcc atcagtgccc agcacctgtg ctacagccat gtcactcctg gcgaccctgg 300
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agggcgggct tccagtgggg ggagagcccc tggcaggtga tggcttctct gactggatga 480
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tcccccaacc ttccccaacc ccacctgacc tggaagctat ggcctccctc ctcaagaagg 600
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cgccactacc accaccacca ctaccaccag ccccctccct ccccctgtcc ctcccctcct 720
ttgacctccc ccagccccct gtcttggata ctctggactt gctggccatc tactgccgca 780
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ggggaccgca agcaaaagaa gagagaccag aacaagtcgg cggytytgag gtaccgccag 960
cggaaggggg caggaggggt tgagggcynk gggaagggga agttgncagg gggttgggaa 1020
ggnaagggaa 1030

<210> 335
<211> 2127
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (72)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2098)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (2114)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2117)
<223> n equals a,t,g, or c

<400> 335
ggatctgagg aaagggaggg cttttctgat ctctcccaat tagaggatta ggcaattggc 60
agcgcagtgc gntaactctg ggcggggctg ggctccaggg ctggacagca cagtccctct 120
gaactgcaca gagacctcgc agccccgaga actgtcgccc ttccacgatg tggctccgtg 180
cctttatcct ggccactctc tctgcttccg cggcttgggc agggcatccg tcctcgccac 240
ctgtggtgga caccgtgcat ggcaaagtgc tggggaagtt cgtcagctta gaaggatttg 300
cacagcctgt ggccattttc ctgggaatcc cttttgccaa gccgcctctt ggacccctga 360
ggtttactcc accgcagcct gcagaaccat ggagctttgt gaagaatgcc acctcgtacc 420
ctcctatgtg cacccaagat cccaaggcgg ggcagttact ctcagagcta tttacaaacc 480
gaaaggagaa cattcctctc aagctttctg aagactgtct ttacctcaat atttacactc 540
ctgctgactt gaccaagaaa aacaggctgc cggtgatggt gtggatccac ggagggggc 600
tgatggtggg tgcggcatca acctatgatg ggctggccct tgctgcccat gaaaacgtgg 660
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acattgccag ctttggaggg aacccaggct ctgtgaccat ctttggagag tcagcgggag 840
gagaaagtgt ctctgttctt gttttgtctc cattggccaa gaacctcttc caccgggcca 900
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tatctctgga cttacaggga gaccccagag agagtcaacc ccttctgggc actgtgattg 1140
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cctacatgta tgagtttcag taccgtccaa gcttctcatc agacatgaaa cccaagacgg 1560
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gtgcctcaga agaggagatc agacttagca agatggtgat gaaattctgg gccaactttg 1680
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tagctttctg gaccaacctc tttgccaaga aggcagtgga gaagccaccc cagacagaac 1860
acatagagct gtgaatgaag atccagccgg ccttgggagc ctggaggagc aaagactggg 1920
gtcttttgcg aaagggattg caggttcaga aggcatctta ccatggctgg ggaattgtct 1980
ggtggtgggg ggcaggggac agaggccatg aaggagcaag ttttgtattt gtgacctcag 2040
ctttgggaat aaaggatctt ttgaaggcca aaaaaaaaaa aaaagggcgc ccttttangg 2100
gttcccaatt tacnaanggg tgcttgg 2127

<210> 336
<211> 847
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (291)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (334)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (829)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (847)
<223> n equals a,t,g, or c

<400> 336
ccgccatgcc gttcctggag ctggacacga atttgcccgc caaccgagtg cccgcggggc 60
tggagaaacg actctgcgcc gccgctgcct ccatcctggg caaacctgcg gacggaccac 120
tccccactcc tttcctcacg ccaagctctg actttccgtg ctccacgatc ccgcggctcc 180
ccctccgcac gtctttccct tgtcgccctc cccagtcatg acccgggcgt gaccttcagg 240
gaccgcggcc cgtatcggga tccctgcccc gcgaacactg cgcgtttcgg ntttcgcgcg 300
ctcgggtccc gtccccagag gtagcccggc cggntccaac ttcgggcaaa attttcatgt 360
ccccctgcgg accgcgtgaa cgtgacggta cggccgggcc tggccatggc gctgagcggg 420
tccaccgagc cctgcgcgca gctgtccatc tcctccatcg gcgtagtggg caccgccgag 480
gacaaccgca gccacagcgc ccacttcttt gagtttctca ccaaggagct agccctgggc 540
caggaccgga tacttatccg ctttttcccc ttggagtcct ggcagattgg caagataggg 600
acggtcatga ctttttttatg attgggcacg gagggatcca gggcatctgt gaactggctg 660
cttcttccag agagatctct tggcagagtg agggcctgga gataaccagc tttggattat 720
cccgcatgca acattcctgt gatcacataa tcctcttctt catcctcata tgaaataaat 780
gaagagagct tcctcattca aaaaaaaaaa aaaaaaaccc cggggggggnc cggtaaccca 840
ttggccn 847

<210> 337
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (21)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (150)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (669)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (679)
<223> n equals a,t,g, or c

<400> 337
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ccgcctcttc cgctgcgtgc cggaccatgg cgcaggggca gcgcaagttt caggcgcaca 120
aacccgcaaa gagtaagacg gcagcggcan cctctgaaaa gaatcggggc ccaagaaaag 180
gcggtcgtgt tatcgctccc argaaggcgc gcgtcgtgca gcagcaaaag ctcaagaaga 240
acctagaagt cggaatccgg aagaagatcg aacatgacgt ggtgatgaaa gccagcagca 300
gcctgcccaa gaagctggca ctgctgaagg ccccagccaa gaagaaaggg gcagctgccg 360
ccacctcctc caagacacct tcctgaggac gctggcccca gtgcaggcca acatcccacc 420
ccctacctcc atatgggacc ttgcaagtca tcccacaggc tgcactgtca ggaagaggac 480
cctgtccccc agcactgggc ttcacctaga acttcagtgg gggccaaggg tgctgagaac 540
ccagcaatga ccaggaagat acagtcacta acttcatctg tccccgtgcc ccttcccagg 600
tcctgcctcc acaggtttaa cccagaacaa taaacctggc tttgtcaama aaaaaaaaaa 660
agggccggnc gttttagang atccagctta cgtaccgtgc tt 702

<210> 338
<211> 875
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (791)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (813)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (830)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (861)
<223> n equals a,t,g, or c

<400> 338

taagatagca aaccagttcg ttttaagtaa gctaacttgt tcattagtat ctgtggctta 60
aaatggcaaa aaagaaaata tccttgagtt tgtaatctag ttacagaagt aaggcataca 120
cacacacaaa gataacagta cctagagaga gagtgtgtgt gagtgtgcgt gtctctgtgt 180
gtgcacgtgc acgctcatgg ccaaatgtgc gcactctaca taaaggaggc aggagttcct 240
ataggctatt taatgtaaga gaaactattt ttctcctgtt ccagctgtat cagatactcg 300
ttccgcaaca cagaaatgac tcagaatctc agacaaaatg tattatttgt tcaattttaa 360
ttttgctact acattcataa ctcttaaatt gttaggctgt ttcatttaca tcaaagttat 420
ctcacaaaag agaaggcagg aaacgttttg tgagtgccta ttctatgtca aacactgtgt 480
tggcaccata ttttacaagt ttttttcctc ttctcacagt gatcttgtga gttagttact 540
tatattttta ttagaactca ttattctggg taccctccaa tgagaattag agaggttaaa 600
taccttttcc tagattccca cagcaggaag gtgggcatag ctgttttgtc tgacaccaga 660
acccatctca ccacactgct ttacagtctt cctgaaggga catttgaggg tgggggggg 720
ccttcaaagc tcagaggact gggtttkgaa tgggtttaat ttttgcaagg gatccatgtc 780
catgccaggg ngtttacaat tctttaactt ccntcccaaa ttcgtgtgtn ccattaggga 840
catttgggtt acatccgggc nggggagggt caggg 875

<210> 339
<211> 1448
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1427)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1432)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1440)
<223> n equals a,t,g, or c

<400> 339
cagcgccact agcctcattg tgcccaggag ttctccaaac ccgcgctgcg gagtgagtga 60
ccaagttccg gccagttcga cctcgaggat ccagaggtgg agacggtact acctcccagc 120
tctgttttcc atccccttca ggtccttcct cgggaggcgg cgaaggcggt ccaccctgcg 180
cgtgatcctt yatgcccggc ccctgcccct ccctccgggt ggaacttccc cctcaccgcc 240
agacttaagc tgaggatcgt tggatctctg gcggggtgca gaactgagcc caggccacag 300
taccctattc acgctctgtg cttgtgccaa gggggcaatg gcggcttcct gtgttctact 360
gcacactggg cagaagatgc ctctgattgg tctgggtacc tggaagagtg agcctggtca 420
ggtaaaagca gctgttaagt atgcccttag cgtaggctac cgccacattg attgtgctgc 480
tatctacggc aatgagcctg agattgggga ggccctgaag gaggacgtgg gaccaggcaa 540
ggcggtgcct cgggaggagc tgtttgtgac atccaagctg tggaacacca agcaccaccc 600
cgaggatgtg gagcctgccc tccggaagac tctggctgac ctccagctgg agtatctgga 660
cctgtacctg atgcactggc cttatgcctt tgagcgggga gacaacccct tccccaagaa 720
tgctgatggg actatatgct acgactccac ccactacaag gagacttgga aggctctgga 780
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gctaaatgcc ctgaacaaaa attggagata tattgtgcct atgcttacgg tggatgggaa 1260
gagagtccca agggatgcag ggcatcctct gtaccccttt aatgacccgt actgagacca 1320
cagcttcttg gcctcccttc cagctctgca gctaatgagg tcctgccaca acggaaagag 1380
ggagttaata aagccattgg agcatccaaa aaaaaaaaaa aaaaaanayc tngsggccgn 1440
caagggaa 1448

<210> 340
<211> 843
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (812)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (822)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (829)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (838)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (841)
<223> n equals a,t,g, or c

<400> 340
aattcggcac gagctggcct gagaagccaa ctcagactca gccaacagag attgttgatt 60
tgcctcttaa gcaagagatt cattgcagct cagcatggct cagaccagct catacttcat 120
gctgatctcc tgcctgatgt ttctgtctca gagccaaggc caagaggccc agacagagtt 180
gccccaggcc cggatcagct gcccagaagg caccaatgcc tatcgctcct actgctacta 240
ctttaatgaa gaccgtgaga cctgggttga tgcagatctc tattgccaga acatgaattc 300
gggcaacctg gtgtctgtgc tcacccaggc cgagggtgcc tttgtggcct cactgattaa 360
ggagagtggc actgatgact tcaatgtctg gattggcctc catgacccca aaaagaaccg 420
ccgctggcac tggagcagtg ggtccctggt ctcctacaag tcctggggca ttggagcccc 480

aagcagtgtt aatcctggct actgtgtgag cctgacctca agcacaggat tccagaaatg 540
gaaggatgtg ccttgtgaag acaagttctc ctttgtctgc aagttcaaaa actagaggca 600
gctggaaaat acatgtctag aactgatcca gcaattacaa cggagtcaaa aattaaaccg 660
gaccatctct ccaactcaac tcaacctgga cactctcttc tctgctgagt ttgccttgtt 720
aatcttcaat agttttacct accccagtct ttggaaccyt aaataataaa aataaacatg 780
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naa 843

<210> 341
<211> 1293
<212> DNA
<213> Homo sapiens

<400> 341
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acggatatcc tctgttgggg gagaagcaac attttgtgat tttccaaaaa taaaccatgg 180
aattctatat gatgaagaaa aatataagcc attttcccag gttcctacag gggaagtttt 240
ctattactcc tgtgaatata attttgtgtc tccttcaaaa tcattttgga ctcgcataac 300
atgcacagaa gaaggatggt caccaacacc aaagtgtctc agactgtgtt tctttccttt 360
tgtggaaaat ggtcattctg aatcttcagg acaaacacat ctggaaggtg atactgtgca 420
aattatttgc aacacaggat acagacttca aaacaatgag aacaacattt catgtgtaga 480
acggggctgg tccacccctc ccaaatgcag gtccactgac acttcctgtg tgaatccgcc 540
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gaatcaatca taaartgcac acctttattc agaactttag tattaaatca gttctyaatt 1140
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tgaaaatgta attataagct gagaccggtg gctctcttct taaaagcacc atattaaatc 1260
ctggaaaact aaaaaaaaaa aaaaaaaact cgc 1293

<210> 342
<211> 1273
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (483)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1247)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1262)
<223> n equals a,t,g, or c

<400> 342
gcccangcgg ccgcgaggcg ccgccgccgc cgccgcagcc gccggagccg caatgcctaa 60
aggaggaaga aagggaggcc acaaaggccg ggcgaggcag tatacaagcc ctgaggagat 120
cgacgcgcag ctgcaggctg agaagcagaa ggccagggaa gaagaggagc aaaaagaagg 180
tggagatggg gctgcaggtg accccaaaaa ggagaagaaa tctctagact cagatgagag 240
tgaggatgaa gaagatgact accagcaaaa gcgcaaaggc gttgaagggc tcatcgacat 300
cgagaacccc aaccgggtgg cacagacaac caaaaaggtc acacaactgg atctggacgg 360
gccaaaggag ctttcgagga gagaacgaga agagattgag aagcagaagg caaaagagcg 420
ttacatgaaa atgcacttgg ccgggaagac agagcaagcc aaggctgacc tggcccggct 480
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gcgacccgtg ggaggagatg ccggggacct gggccgcgct gccaggacct ctgctgtgtc 660
tcgcccaccc tgtgccctgg cgccgctgca acagcccctc atggccagga gccccccatg 720
gcctggggcc tcctcttcat cttggcacag aaattgtttg ggggatgggg ggggggactg 780
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cacacagccc cggactgtgt tgcctgggtg ctcattcaga gaggggctat catctgggag 960
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ctcagggcct cacctctctg cccttccctg cccggttcct actcacctgg ctagggccag 1080
tgcccatttt cagccctacc cattgatcat ttcaagaaac ctctgtttac tgtgtggcac 1140
ccaggcaaaa catgctccac aaattcaact tgtatatttg gcagattaaa cttgacatta 1200
tcgtaaaaaa aaaaaaaaaa atttgggggg gggcccggta cccattnggg cccttagggg 1260
gnggtttaaa tta 1273

<210> 343
<211> 1793
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1251)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1267)
<223> n equals a,t,g, or c

<400> 343

gcccacgcgt ccgcccacgc gtccggcatg gacctcagtc ttctctgggt acttctgccc 60
ctagtcacca tggcctgggg ccagtatggc gattatggat acccatacca gcagtatcat 120
gactacagcg atgatgggtg ggtgaatttg aaccggcaag gcttcagcta ccagtgtccc 180
caggggcagg tgatagtggc cgtgaggagc atcttcagca agaaggaagg ttctgacaga 240
caatggaact acgcctgcat gcccacrcca cagagcctcg gggaacccac ggagtgctgg 300
tgggaggaga tcaacagggc tggcatggaa tggtaccaga cgtgctccaa caatgggctg 360
gtggcaggat tccagagccg ctacttcgag tcagtgctgg atcgggagtg gcagttttac 420
tgttgtcgct acagcaagag gtgcccatat tcctgctggc taacaacaga atatccaggt 480
cactatggtg aggaaatgga catgatttcc tacaattatg attactatat ccgaggagca 540
acaaccactt tctctgcagt ggaaagggat cgccagtgga agttcataat gtgccggatg 600
actgaatacg actgtgaatt tgcaaatgtt tagatttgcc acataccaaa tctgggtgaa 660
aggaaagggg ccaggggaca ggagggtgtc cacatatgtt aacatcagtt ggatctccta 720
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tgggcctttc tgactagtat cacacttcta ataaaatcca caattaaacc atgtttctca 840
cttttcacat gtttcatagc aactgcttta tatgactgat gatggcttcc ttgcacacca 900
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gctttttact gcagaatgaa ctgcaagttc agcatagtgg aggggagagg cagaactgga 1020
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accaaaagca ggctttctgc cctgagggac atcttcccac tcccctgctc cacatgagcc 1140
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tgaaatgggg aaatggaagg gtttggaggc agagctgaaa acagggttgg naagggattt 1260
cctgaantta raagacaaac gttagcatac ccagtaagga aaatgagtgc aggggccagg 1320
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gaatgggatt cagattggga acttgtgggg atgagagtga ccaggttgaa ctgggaagtg 1440
gaaaaaggag tttgagtcac tggcacctag aagcctgccc acgattccta ggaaggctgg 1500
cagacaccct ggaaccctgg ggagctactg gcaaactctc ctggattggg cctgattttt 1560
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ctgcagagat ggcgctatct ttcctcctcc tgtgatgtcc tgctcccaac catttgtact 1680
cttcattaca aaagaaataa aaatattaac gttcamwawg ctgaaaaaaa aaaaaaaaaa 1740
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1793

<210> 344
<211> 1672
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (95)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1667)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1668)
<223> n equals a,t,g, or c

<400> 344
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agaaaccatc tcctctggcg ggggtagggg cggantggcg tccgaccaca ccggaagagg 120
aagtctaagc gccggaagtg gtgggcattc tgggtaacga gctatttact tcctgcgggt 180
gcacaggctg tggtcgtcta tctccctgtt gttcttccca tcggcgaaga tggccctgga 240
gacggtgccg aaggacctgc ggcatctgcg ggcctgtttg ctgtgttcgc tggtcaagac 300
tatagaccag tttgaatatg atggttgtga caattgtgat gcatatctac aaatgaaggg 360
taaccgagag atggtatatg actgcactag ctcttccttt gatggaatca ttgcgatgat 420
gagtccagag gacagctggg tctccaagtg gcagcgagtc agtaacttta agccaggtgt 480
atatgcggtg tcagtcactg gtcgcctgcc ccaaggaatc gtgcgggagc tgaaaagtcg 540
aggagtggcc tacaaatcca gagacacagc tataaagacc tagcaagatg caaggctgcc 600
agcatctttg ctctccacct cctgcctctg cttatttctt gttctggaac taaatgaaca 660
gaacttcaaa tacttcctac cctccaattc agactcagct gactgttgag agagcagcac 720
atcattttat cattttatct tctttggact acaggtgggg tgggagggat ttgggttggt 780
ggattaacag atggaattga ggagagagta ggatgctgat tttcctaccc gtggcccagg 840
tctgtgcctt ccccatgcca aggactctag gtcaaatgtc aataaatatg aacctcgaga 900
aagttctgaa ggccatgaca cctgccttgc ctccctcttc cattctctta ggcacagtaa 960
tagcttattt gccctataag aaccttccca gagcagcaga ggcccttcta ctccctcttg 1020
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gtgctgatcc agaggctcag taaccccatc aacttggtgg ccctggtgtc tcacacttgt 1140
atccttctgc cctcgagacc tggcacagca gtatcccttg aagaaatcct gaggctttgt 1200
agagtgctcc ttgaccatgt ttaataattc ttccctcccc tgcttgtcta ttttcttctc 1260
ttcacggctc ttcctatacc ttaggccagt ctcaagcact cactggagac ccttgggcct 1320
tgggcgacca ttgagtccta gtctcccttg tttgtgcccc tgtaggaggt aggtcctttt 1380
ctctccggcc tagtagggga ccttgggtaa catcccattt ttcggccaag gtgagttgtt 1440
ttaggataaa aaaatttacc acaaattctc atttaaattt ccacagaaat cctgttcgta 1500
tccccatttt gatttcccta agttccttgt tctccctcta aaaagagaat gattgcaccc 1560
tgcctgttta cctcaggatt gttgtgattg tagaaacgaa gctatgtgaa aattatataa 1620
gtattataaa ggtgaaatac ttttgctctc aaaaaaaaaa aaaaaanntt aa 1672

<210> 345
<211> 2109
<212> DNA
<213> Homo sapiens

<400> 345
agcactagct ttgacatcca cggtgagctg cagggaagca tcacacacca gccagcatgt 60
gagcagaggg aggcagttgg ggttgaactt cggaactagg ccgggtctyc tgacagatca 120
caagacaccc cagaggatct tcagcagtcc tacttcccat tctctataga gctttgaagc 180
ttggaaccct tccagggtaa acattttctc ttgtgctgct yaggacatyt ggggcctagc 240
tcctgggttc ctgtctccaa gaagcaatga ccttaaactc tgagccatac tctgtcctca 300
ccagcggctc ccatgttttt ctgtgtcagg ttattaagta cctagtcctt gttttctgtc 360
tctstcctaa gctacctctc tgggtccaca gaagacttgg tagtatagtg agaatggcta 420
tacgtgagta caaacrtgga ttttccaagg gcttgggaam tgattcttga gcccagaaga 480
gccamgcctg ctttgaggtc ttttggagtg gagatgcagc cctgggaaat ttggggagtc 540
agcaggccag tgtgaagcwa ttggtcctag gagtatatga gcttgctgtt tctttgatgg 600
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atctatccaa cttctttact gagtgatgta ttccatgggg ttaccttttt cagattattg 720
agttgctctg taagcactaa aactttttaa tcatttttaa gaaacttttt agattgtatt 780
acaaatttgc cttaacagta attagatgtt gaatataatt ttaacatttt attaatgact 840
tgggtcatca gttaatacca gtactaaaac catacgaatt attggtttat tccagaaaat 900

acagtatttg ttctattttt aggtagacaa tcatttggga tcagagtaca ttagcatagt 960
aatgctcagt cagacctgtt caagtagtag agcttggaga atgccatgaa atacttatat 1020
aattaatttg attgcatgaa ctaagcaatt ttactaatga aaaggttgta tatgtgcaag 1080
tcactttttt aaaaaccaag aaaaaacttt aatagaggaa atcttattca ttaatttatt 1140
tttctgagta aaaaaacgaa acccaaatct cattttattt caactgttaa acattttgat 1200
ctgttgaccc ataggatcag gatttgggaa ccactttact aggaaagagc agatcagtac 1260
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gcttggttgt gggcacttct acagcaagga ccatatcata ttcatctttg catccctggc 1380
acatgcatga gacataagta cttaataaat gcagttgaat ggataatgat tagtgttatt 1440
tatggattag aaaaagcatg tttctattta agtaagctgt aaaaagtatt attgaatatt 1500
tactgtaaat atatgttcac ataaaaaaat aacttggagg gtctttgtgt ccctggcata 1560
ttatcatctt catggaaaga atccactgtg gtttctgtag agtgattgga aaaatggatt 1620
attttgagga ttgaagaaag tgttctttct gcgttgtcac tttgttcaac agtaaaactt 1680
tattctcagt gttcctactc tgcattgttt acattttgga cagttttttt tratcaccta 1740
caatctgtaa agaatgtata tattcttttc agcatctcag tttgaaaaga catgcagtta 1800
aacttgacct tttgataatc gctcttacag gtcattgtct gttctaacag caaattgtaa 1860
acatgtgctt catagatatt gtggctctca gtcatcactt tgtcctatgg tatttattga 1920
atgttcacat actaatggtg cacaggtgtt tttttctata aatcttctga ctgtcctgta 1980
attcattctt aagctttaac ttgaaggtat cgtaattgcc ggcatttgat gtttagcaat 2040
aaaagaataa atgtgtacca gcattttatg tttaaaaaaa aaaaaaaaaa actcgagact 2100
agtctctct 2109

<210> 346
<211> 1714
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (21)
<223> n equals a,t,g, or c

<400> 346
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gatttcattc tctacattta aaggacatcc tttctgagct gctgtgaata aatttggaat 120
ggtactgtat attttcatct aatggagaac tagctgtact ttgaataagg attgctgcac 180
tggacgactt tagaacatcc ctcacaatgt cgtcaacccg gagccagaac ccccacggcc 240
tgaagcagat tggcctggac cagatctggg acgacctcag agccggcatc cagcaggtgt 300
acacacggca gagcatggcc aagtccagat atatggagct ctacactcat gtttataact 360
actgtactag tgttcaccag tcaaaccaag cacgaggagc tggagttcct ccttctaagt 420
cgaaaaaggg gcagacacct ggaggagctc agtttgttgg cctggaatta tataaacgac 480
ttaaggaatt tttgaagaat tacttgacaa atcttcttaa ggatggagaa gatttgatgg 540
atgagagtgt actgaaattc tacactcaac aatgggaaga ttatcgattt tcaagcaaag 600
tgctgaatgg aatttgtgcc tacctcaata gacattgggt tcgccgtgaa tgtgacgaag 660
gacgaaaagg aatatatgaa atctattcgc ttgcattggt gacttggaga gactgtctgt 720
tcaggccact gaataaacag gtaacaaatg ctgttttaaa gctgattgaa aaggaaagga 780
atggtgaaac catcaataca agattgatta gtggagttgt acagtcttac gtggaattgg 840
ggctgaatga agatgatgca tttgcaaagg gccctacgtt aacagtgtat aaagaatcct 900
ttgaatctca atttttggct gacacagaga gattttatac cagagagagt actgaattct 960
tgcagcagaa cccagttact gaatatatga aaaaggcaga ggctcgtctg cttgaggaac 1020
aacgaagagt tcaggtttac cttcatgaaa gcacacaaga tgaattagca aggaaatgtg 1080

aacaagtcct cattgaaaaa cacttggaaa ttttccacac agaatttcag aatttattgg 1140
atgctgacaa aaatgaagat ttgggacgca tgtataatct tgtatctaga atccaggatg 1200
gcctaggaga attgaaaaaa ctgttggaga cacacattca taatcagggt cttgcagcca 1260
ttgaaaagtg tggagaagct gctttaaatg accccaaaat gtatgtacag acagtgcttg 1320
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tggctgctct tgataaggct tgtggtcgct tcataaacaa caacgcggtt accaagatgg 1440
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aaagttccaa gaacccagag gaggcagaac tagaagacac actcaatcaa gtgatggttg 1560
tcttcaagta catagaagac aaagacgtat ttcagaagtt ctatgcgaag atgctcgcca 1620
agaggctcgt ccaccagaac agtgcaagtg acgatgccga agccagcatg atctccaagt 1680
taaagcaagc ttgcgggttc gagtacacct ctaa 1714

<210> 347
<211> 1672
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1667)
<223> n equals a,t,g, or c

<400> 347
cgatgtctta ttgtgatgag tctcgactgt caaatcttct tcggaggatc acccgggaar 60
acgacmgaga cygaagattg gyyactgtaa agcagttgaa agaatttatt cagcaaccag 120
aaaataagct ggtactagtt aaacaattgg atatcttggc tgctgyacat gatgtgctta 180
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tttgtgcttc tctgagctat gaggctgaga agatcttcaa gtggattttt agcaaattta 300
gctcatctgc aaaagatgaa gttaaactcc tctacttatg tgccacctac aaagcactag 360
agactgtagg agaaaagaaa gccttttcat ctgtaatgca gcttgtaatg accagcctgc 420
agtcaattct tgaaaatgtg gatacaccag aattgctttg caaatgtgtt aagtgcattc 480
ttttggtggc tcgatgttac cctcatattt tcagcrctaa ttttagggat acagttgata 540
tattagttgg atggcataga gatcatactc agaaaccttc gctcacgcag caggtatctg 600
ggtggttgca gagtttggag ccattttggg tagctgatct tgcatttcct acgactcttc 660
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ggagactgcc tataagttaa tattgggaga aatgacttgt gccctaaaca acctcctgca 1320
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gttcaatgta gacaatgcaa aatttgtagt taaatttgac ctcagtgccc tgactacaay 1440
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cttttctcat tacatattta tgtatttcac tgtcatgtca acatgtctgc agaatcactg 1560
tatgtaacaa acagccatat ttaagacatg cctggataaa taaaattggt aggaatgttt 1620
tcttgccatt ataaaaaaaa aaaaaaaaaa aaaaaaaagg ggggccnccc tt 1672

<210> 348
<211> 1483
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (19)
<223> n equals a,t,g, or c

<400> 348
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gcgcgtggtg cccgggacct gaacccgcgg cgggacatct cctcctggct ggcccagtgg 120
ttccctagaa ccccagccag gtccgtggtg gccctgaaga cccccatcaa ggtggagctg 180
gtggcaggga aaacctacag gtggtgtgtg tgtggccgca gcaagaagca gcccttctgt 240
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aaaggaaaca ggtgctgagc ccaagagact ctggtaccca ctgctggctc atgaaggaag 540
aattattcct tataacctaa aagtctccag tctggggcag gcgggagtgg gccctggttc 600
aatgtttgct gatggggaag atggcaaaaa caagcctgcc caaccagact ggtagtcctg 660
cagtcactgc tatgaggccc atgtgctgcc tcctgctcca gattttaacc tctctgtggg 720
ctgggggcac ctgaccagcc acaggagagg gcagttcaga ttcattctgt atggggtccc 780
caagccaggc taaacccaga gatgagaggc acccttccct tcttccctcc accccaaaga 840
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gcccatcagg gggctcccaa ccccacacac ctacgctatg atggaatctc gagtctcgac 1020
tcccgactcc tctcagatct atgcacactt gaggaaatct cggtgggcag cgacctgcca 1080
gggtctgtcc ctaaggaggt ggtccgctga cctctcaagg ggtgggggtg gggtcagagc 1140
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gggcctcagc tgggggtgga ggggcaattg gaaggctgtt tgcctctggc aaagtctggg 1260
atctgtgctt gtgtgaggtt aacccacccc cacttccact ctaggcccca ggtgagactc 1320
caccaccagt cctgctagtg agggttcccc ggtgagggta aggttggtgg gggtgcagcg 1380
cttcacaatg ctaaagcctt agccctcctc caagagctga gacctctcag ggcctgaatc 1440
ttcttttcca caagataaat gatgcaaagg ccacacacac agg 1483

<210> 349
<211> 1842
<212> DNA
<213> Homo sapiens

<400> 349
aatatwtgta ttttttgatc ctwtgaacct gaaaagggtc agaaggatgc ccagacatca 60
gcctccttct ttcacccctt accccaaaga gaaagagttt gaaactcgag accataaaga 120
tattctttag tggaggctgg atgtgcatta gcctggatcc tcagttctca aatgtgtgtg 180
gcagccagga tgactagatc ctgggtttcc atccttgaga ttctgaagta tgaagtctga 240
gggaaaccag agtctgtatt tttctaaact ccctggctgt tctgatcggc cagttttcgg 300
aaacactgac ttaggtttca ggaagttgcc atgggaaaca aataatttga actttggaac 360
agggttggaa ttcaaccacg caggaagcct actatttaaa tccttggctt caggttagtg 420

acatttaatg ccatctagct agcaattgcg accttaattt aactttccag tcttagctga 480
ggctgagaaa gctaaagttt ggttttgaca ggttttccaa aagtaaagat gctacttccc 540
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cgccaaggaa aggcatgtac aaaaattatg caattcagtg ttccaagtct ctgtgtaacc 660
agctcagtgt tttggtggaa aaaacatttt aagttttact gataatttga ggttagatgg 720
gaggatgaat tgtcacatct atccacactg tcaaacaggt tggtgtgggt tcattggcat 780
tctttgcaat actgcttaat tgctgatacc atatgaatga aacatgggct gtgattactg 840
caatcactgt gctatcggca gatgatgctt tggaagatgc agaagcaata ataaagtact 900
tgactaccta ctggtgtaat ctcaatgcaa gccccaactt tcttatccaa ctttttcata 960
gtaagtgcga agactgagcc agattggcca attaaaaacg aaaacctgac taggttctgt 1020
agagccaatt agacttgaaa tacgtttgtg tttctagaat cacagctcaa gcattctgtt 1080
tatcgctcac tctcccttgt acagccttat tttgttggtg ctttgcattt tgatattgct 1140
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cagcaaattc cagatttgtt tccttttggc ctcctgcaaa gtctccagaa gaaaatttgc 1320
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tgtgactttt taaacgatta gtgatgtcct taaaatgtgg tctgccaatc tgtacaaaat 1440
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atgtatttct atatagactt ggagaatact gccaaaacat ttatgacaag ctgtatcact 1560
gccttcgttt atattttttt aactgtgata atccccacag gcacattaac tgttgcactt 1620
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aaacaatggt gtggtgaatg tgtgagaaaa actaacttga tagggtctac caatacaaaa 1740
tgtattacga atgcccctgt tcatgttttt gttttaaaac gtgtaaatga agatctttat 1800
atttcaataa atgatatata atttaaagtt aaaaaaaaaa ga 1842

<210> 350
<211> 3008
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (59)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (65)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1307)
<223> n equals a,t,g, or c

<400> 350

acagcatcnt taggaaacct aaggtagaga atccccccag agagcctggc aagggaatnt 60
cgagncacga agagtttctc caacccaagg aggccagaca gagggacgtg gtcactctct 120
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<210> 351
<211> 2756
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1597)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2540)
<223> n equals a,t,g, or c

<400> 351
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<210> 352
<211> 1645
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (97)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1574)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1596)
<223> n equals a,t,g, or c

<400> 352
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tactatattt caatttcttt ataaatttaa gtgcatntta actcataatt gtacactata 120
atataagcct aagtttttat tcataagttt tattgaagtt ctgatcggtc cccttcagaa 180
atttttttat attattcttc aagttacttt cttatttata ttgtatgtgc attttatcca 240
ttaatgtttc atactttctg agagtataat accctttttaa aagatatttg gtataccaat 300
acttttcctg gattgaaaac ttttttttaaa ctttttaaaa tttgggccac tctgtatgca 360
tatgtttggt cttgttaaag aggaagaaag gatgtgtgtt atactgtacc tgtgaatgtt 420
gatacagtta caatttattt gacaaggttg taattctaga atatgcttaa taaaatgaaa 480
actggccatg actacagcca gaactgttat gagattaaca tttctattga gaagcttttg 540
agtaaagtac tgtatttgtt catgaagatg actgagatgg taacacttcg tgtagcttaa 600
ggaaatgggc agaatttcgt aaatgctgtt gtgcagatgt gttttccctg aatgctttcg 660
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gttaaaggac tctgtgccat cttacaacct tggatgaatt atcctgccaa cgtgaaaacc 780
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<210> 353
<211> 1637
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (738)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (771)
<223> n equals a,t,g, or c

<400> 353
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gttctccggt cccgccgctc ccgcagcagc catgtcgttc ttcccggagc tttactttaa 120
cgtggacaat ggctacttgg agggactggt gcgcggcctg aaggccgggg tgctcagcca 180
ggccgactac ctcaacctgg tgcagtgcga gacgctagag gacttgaaac tgcatctgca 240
gagcactgat tatggtaact tcctggccaa cgaggcatca cctctgacgg tgtcagtcat 300
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aaaaaaaaaa aaaaaaa 1637

<210> 354
<211> 1119
<212> DNA
<213> Homo sapiens

<400> 354
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ccctgcgggg agtcggcccc cgaccttgcc ggcttcaccc tcctaatgcc agcagtatct 180
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<210> 355
<211> 738
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (654)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (689)
<223> n equals a,t,g, or c

<400> 355
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gagatgaagc tagtgcagat gaagtggcat gaggcctgtc tcagcatctc agccgccatc 420
ttggaaatcc tcaatgcctg ggagaatggg gtcctggcct tcgagtccat ccagaaaatc 480
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gcccacgtcc ggatgctggg gctggatgag cgtgagaagt cgctgcagat gatccgccag 600
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ttcaagtttc cctccaac 738

<210> 356
<211> 1966
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (56)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (788)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1753)
<223> n equals a,t,g, or c

<400> 356
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acgcttcagt tctgctctgc aaggatatat aataactgat tggtgtgccc gtttaataaa 180
agaatatgga aactgaacag ccagaagaaa ccttccctaa cactgaaacc aatggtgaat 240
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<210> 357
<211> 1562
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (16)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (18)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (260)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (262)
<223> n equals a,t,g, or c

<400> 357
taccccgccg cctgcngnac cggtccggaa ttcccgggtc gacccacgcg tccgcatgaa 60
atggaccaat actggggaat tggcagtctg gccagtggga taaatttgtt cacaaacagt 120
tttgagggcc cagttcttga tcacaggtat tatgcaggtg gatgctcccc gcattacatc 180
ctgaacacga ggtttaggaa gccctacaat gtggaaagct acacgccaca gacccaaggc 240
aaatacgaat tcatattaan anagtatgaa tcatactcag attttgaacg caatgtcaca 300
gagaaaatgg caagcaagtc tggtttcagt tttggtttta aaatacctgg aatatttgaa 360
cttggcatca gtagtcaaag tgatcgaggc aaacactata ttaggagaac caaacgattc 420
tctcatacta aaagcgtatt tctgcatgca cgctctgacc ttgaagtagc acattacaag 480
ctgaaaccca gaagcctcat gctccattac gagttccttc agagagttaa gcggctgccc 540
ctggagtaca gctacgggga atacagagat ctcttccgtg attttgggac ccactacatc 600

acagaggctg tgcttggggg catttatgaa tacaccctcg ttatgaacaa agaggccatg 660
gagagaggag attatactct taacaacgtc catgcctgtg ccaaaaatga ttttaaaatt 720
ggtggtgcca ttgaagaggt ctacgtcagt ctgggtgtgt ctgtaggcaa atgcagaggt 780
attctgaatg aaataaaaga cagaaacaag agggacacca tggtggagga cttggtggtc 840
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gcggacctga tgcaggagtg ggagacgct gtgcagtaca acccagccat catcaaagtt 960
aaggtggagc ctctgtatga actagtgaca gccacagatt ttgcctattc cagcacagtg 1020
aggcagaaca tgaagcaggc actggaggag ttccagaagg aagttagttc ctgccactgt 1080
gctccctgcc aaggaaatgg agtccctgtc ctgaaaggat cacgctgtga ctgcatctgt 1140
cctgttggat cccaaggcct agcctgtgag gtctcctatc ggaagaatac cccattgat 1200
gggaagtgga attgctggtc aaattggtct tcatgctctg gaagacgtaa gacaagacaa 1260
aggcagtgta acaatccacc tcctcaaaat gggggtagcc cctgttcagg ccctgcttca 1320
gaaacacttg actgctccta gcagatgata cagcagtggg ctacatacaa tgagagccct 1380
gagccctcaa gaactcaygc cagctcagcc ctacaccagt ttccacctgg agttcatgca 1440
agggcaaaag gcagtgccat gcaagctgtt taaaataaag atgttacctt gtaaaatgca 1500
agttgattta aataaatact gagttaaagg ctttaaaaaa aaaaaaaaaa aaaggggggg 1560
cg 1562

<210> 358
<211> 1931
<212> DNA
<213> Homo sapiens

<400> 358
ctcgggagct cggactccta cgcatcaccg ggaagggccg ccgccccgcc cgcggctgct 60
ggcccgggtg acacttccgc ctgctataag agcagcggcc ctcggtgcct ccttcctgac 120
ctcgcaccca gctcggagcc cggagcgtgc ctcggcggcc tgtcggtttt caccatggag 180
cagctgagct cagcaaacac ccgcttcgcc ttggacctgt tcctggcgtt gagtgagaac 240
aatccggctg gaaacatctt catctctccc ttcagcattt catctgctat ggccatggtt 300
tttctgggga ccagaggtaa cacggcagca cagctgtcca agactttcca tttcaacacg 360
gttgaagagg ttcattcaag attccagagt ctgaatgctg atatcaacaa acgtggagcg 420
tcttatattc tgaaacttgc taatagatta tatggagaga aaacttacaa tttccttcct 480
gagttcttgg tttcgactca gaaaacatat ggtgctgacc tggccagtgt ggattttcag 540
catgcctctg aagatgcaag gaagaccata aaccagtggg tcaaaggaca gacagaagga 600
aaaattccgg aactgttggc ttcgggcatg gttgataaca tgaccaaact tgtgctagta 660
aatgccatct atttcaaggg aaactggaag gataaattca tgaaagaagc cacgacgaat 720
gcaccattca gattgaataa gaaagacaga aaaactgtga aatgatgta tcagaagaaa 780
aaatttgcat atggctacat cgaggacctt aagtgccgtg tgctggaact gccttaccaa 840
ggcgaggagc tcagcatggt catcctgctg ccggatgaca ttgaggacga gtccacgggc 900
ctgaagaaga ttgaggaaca gttgactttg gaaaagttgc atgagtggac taaacctgag 960
aatctcgatt tcattgaagt taatgtcagc ttgcccaggt tcaaactgga agagagttac 1020
actctcaact ccgacctcgc ccgcctaggt gtgcaggatc tctttaacag tagcaaggct 1080
gatctgtctg gcatgtcagg agccagagat atttttatat caaaaattgt ccacaagtca 1140
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ttctgcatgt tgatgcccga agaaaatttc actgccgacc atccattcct tttcttattt 1260
cggcataatt cctcaggtag catcctattc ttggggagat ttcttcccc ttagaagaaa 1320
gagactgtag caatacaaaa atcaagctta gtgctttatt acctgagttt ttaatagagc 1380
caatatgtct tatatcttta ccaataaaac cactgtccag aaacaagtct ttcattttct 1440
ttgtaagttt ggctctgttg gctgtttaca cccatgaatt ttggcatggg tatctatttt 1500
yctttttttac attgaaaaaa atccagtggt tgcttttgaa tgcatcaagt aaagaagaag 1560
aaaagaatac atccgatgcg tagattcttg accatgtagt aatctataaa attgctatat 1620

cctcctgata gccatgggaa aacatgataa gatggtcatt tattttgcag ttagaatttt 1680
ggaagccaca aaatagacag acaccctgac tgttgaaggg aggtttaaaa acagatattc 1740
aattgaaatg taagagagca ccccaattga gagcccaggt tacgaagaca agcttgcctc 1800
gcctgacttt tctgtccctt gttctgcagg attagtattc tgttacagac ctctagtttt 1860
tagactcttc aattaaaggg ccaatggtta taacctgcaa aaaaaaaaaa aaaaaaaaaa 1920
aaaaaaaaaa a 1931

<210> 359
<211> 869
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (869)
<223> n equals a,t,g, or c

<400> 359
gctctggcgg gcataccagc gggccctggc cgctcacccg tggaaagtac aggtyctgac 60
agctgggccc tgtggtagga ggctggtaca aggttttgga tcggttcatc cctggcacca 120
ccaaagtgga tgcactgaag aagatgttgt tggatcaggg gggctttgcc ccgtgttttc 180
taggctgctt tctcccactg gtaggggcac ttaatggact gtcagcccag gacaactggc 240
caaactacag cgggattatc ctgatgccct tatcaccaac tactatctat ggcctgctgt 300
gcakttagcc aacttctacc tggtccccct tcattacagg ttggccgttg tccaatgtgt 360
tgctgttatc tggaactcct acctgtcctg gaaggcacat cggctctaag cctgcctcac 420
tccatcgttt ccaccttgca gtgatgcagc ttgaccctgg aacggtcaga caacctcctc 480
aaagtgggca taccagtttc cacggggttg ggttgccggt cagagcttaa gaggactagc 540
accctgcaat gcccctcttc actctaaaat gtacactgac tgctttagag cccttgataa 600
tagtcttatt cccaccacat actaggcact ccataaatat ctgttgaacc ttcatgacct 660
tatcaacttt acacccatat cccagcaaat gccactcatc cccactcttc atagacacat 720
ttgttactct aaccctgcct aggcttcttg tagctccagc tctttagaga ctcccggaac 780
cctttatatg gtgcctcagt aaatatgtta ttaaatatgt aatccggaaa aaaaaaaaaa 840
aaaaaaaaaa aaaaaaaaaa aaaaaaaan 869

<210> 360
<211> 561
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (521)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (525)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (560)
<223> n equals a,t,g, or c

<400> 360
ggcacgagag actccagccg ccaggggagc gcgtgccgtt cttgcctctc tggcctgcgc 60
ctcctgagcc gagtagatat cccggagttc cgcgcggcgc cagcccttcc gccacggccg 120
tctctggaga gcagcagcca tggccctacg ctaccctatg gccgtgggcc tcaacaaggg 180
ccacaaagtg accaagaacg tgagcaagcc caggcacagc cgacgccgcg ggcgtctgac 240
caaacacacc aagttcgtgc gggacatgat tcgggaggtg tgtggctttg ccccgtacga 300
gcggcgcgcc atggagttac tgaaggtctc caaggacaaa cgggccctca aatttatcaa 360
gaaaagggtg gggacgcaca tccgcgccaa gaggaagcgg gaggagctga gcaacgtact 420
ggccgccatg aggaaagctg ctgccaagaa agactgagcc cctcccctgc cctctccctg 480
aaataaagaa cagcttgaca gaaaaaaaaa aaaaaaaaaa ntcgnggggg ggcccggtac 540
ccattcgccc tawagggggn g 561

<210> 361
<211> 1680
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c

<400> 361
gagtttacac tgaccatggt ggaatgttaa ggngaacccc acccсttctt acagatggtg 60
acccagagcc tgctcttggg aacagccaga gtaagattgg aacccagact tgcaagccag 120
cgctgtttgc attaaaaggg tgggtgagtc aggacccctg gctcargagc cgyctctcct 180
aaaagagggt ttcaaggcca aatgggtttg tcaacggtgc tgtctccctt tcttggagat 240
gctcattagc ttatcaaaga ctgagaagtc ccgctgttac agaaataatt tagtttgctg 300
tattaactgc tcctgggcct ggagcagtat tcccacctta agattcccag catccctgtg 360
ctgtcccggc tctcattcat gccgaaggcc caacccattg gctgtgttct gtttgaagat 420
ttgggggcg ccttctcttt cttccccagg gaattctcta gcagagggag gggacccacc 480
ccagtgagga agtagattgc tgcctctagc cagagacctg aactggggaa tttgaacatt 540
cctttacatt gttggagaaa tgaagccaaa gttattcaga tggtttccc aggctaaagg 600
aaagtcacct gcaagagatc ccggcactga tctggagcag ctgacagggt gggtctccct 660
taccaaagag aagaaccact ctctggcgct ggggtgacct gctggctggg cctgtaaggt 720
ttccatgttg ctgaggccat ggagattccc agagctggtc acaccgaccg ctctcagggc 780
ccgctgccct gggctggcaa caccattctg gccttggcct gcagaagctt tcagagtctt 840
cactggcagt agggggagat ggggagagga atgatctctg cccagcccct tcctttccaa 900
accatgcaat ggaagagccc agatgggtga agattgattt tgccttaact caagagaatt 960
cctgttctcc ttgtgctatg atttggacac aagattctgg atacctggaa cttagctgtg 1020
tactcctgta ccctaaacag tggatttgag ttccagcgtt tattcttttt tcctttttc 1080
agatcaccat ctaagttaca tctttagctc aggtccatcc ttctcaagat ctccttctta 1140
gcccccccagc ccctggtgct gtctgtggtc aggtgacctt actcaggagc agatatctcc 1200
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gggtggccac ccgacctgcc cccagaactt ttggatactg gaggcagttg cataggtctc 1440
cctctctggg caccaggact cagtccagcc caagactact ctgggcagct cccatcccag 1500

tctggggcca tttgcagact caggaaagga tttctacagt gttctataaa agccaaaaga 1560
gagagtgggt ttgggaagag tgagggtggt tggggagagg ggaccgatgt gcctcattgt 1620
ttagtggtga ttacaaatat gcttttctgg ataaagtttg gttgtttgct cttggaaaaa 1680

<210> 362
<211> 740
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (591)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (709)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (718)
<223> n equals a,t,g, or c

<400> 362
cagaaacaaa caaaaaggca gctgggttgt cactgatggg cagcatttga gcctgccaca 60
ctggcctgga agtttccctt ccagtctgga ttttgtctgc tccttccttc cccctcaccc 120
cgttacctct tcacctccca tctcatttca ctgtgtagct cagtctctcc cacgcacata 180
attggggaca gtgggggctc tcttaccagc ctcctcagca acgcacgtcc atcaggcctg 240
gcctcagtgg ccagccacat tgatgtcaca ctggaattgt taccccagag agggcgaaga 300
gataggctat ctccccacct cccaccctac tccccactat attcccgttt tgaccacctc 360
agcccctcag ctgccccctc tcactttggc caatcccagg caccaatcag acttcctcct 420
ccacctggag cccctagcat ttccttgtcc cctcttcccc aaaacctctg taaagggtac 480
gagagggacc ccctgccgag ccgcccgcca ctcagggcag tccgatctaa gaagcagaag 540
ctggttggag gctggctggg cctctgtcca gtccccagat gggataaact ngccttttct 600
camatcccct cttgggtgcc tkgatctttc tytgcccccg gggccaggac ccactgtgct 660
gttttcttgt tcagttttgt ggggaaagga accaaggttt ttgccaagna accagttnct 720
tgaaaggggt tagggaaggg 740

<210> 363
<211> 1324
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (385)
<223> n equals a,t,g, or c

<400> 363
cgctgcctgg tgccgtggcc gcctcctcgg gcagcccccc gggctcggcg ctggcggcag 60

tggcgagcgg cggagacctc ttcccggggc agccggtgtc cgaactgatc gcgcagctgc 120
tgcgcgctga gccctaccct gcggcggccg gacgcttcgg cgcagggggc ggcgcggcgg 180
gcgcggtgct gggcatcgac aacgtgtgcg agctggcggc gcggctgctc ttcagcaccg 240
tggagtgggc gcgccacgcg cccttcttcc ccgagctgcc ggtggccgac caggtggcgc 300
tgctgcgcct gagctggagc gagctcttcg tgctgaacgc ggcgcaggcg gcgctgcccc 360
tgcacacggc gccgctactg gccgncgccg gcctccacgc cgcgcctatg gccgccgagc 420
gcgccgtggc tttcatggac caggtgcgcg ccttccagga gcaggtggac aagctgggcc 480
gcctgcaggt cgactcggcc gagtatggct gcctcaaggc catcgcgctc ttcacgcccg 540
acgcctgtgg cctctcagac ccggcccacg ttgagagcct gcaggagaag gcgcaggtgg 600
ccctcaccga gtatgtgcgg gcgcagtacc cgtcccagcc ccagcgcttc gggcgcctgc 660
tgctgcggct ccccgccctg cgcgcggtcc ctgcctccct catctcccag ctgttcttca 720
tgcgcctggt ggggaagacg cccattgaga cactgatcag agacatgctg ctgtcgggga 780
gtaccttcaa ctggccctac ggctcgggcc agtgaccatg acggggccac gtgtgctgtg 840
gccaggcctg cagacagacc tcaagggaca gggaatgctg aggcctcgag gggcctcccg 900
gggcccagga ctctggcttc tctcctcaga cttctatttt ttaaagactg tgaaatgttt 960
gtcttttctg tttttaaat gatcatgaaa ccaaaaagag actgatcatc caggcctcag 1020
cctcatcctc cccaggaccc ctgtccagga tggagggtcc aatcctagga cagccttgtt 1080
cctcagcacc cctagcatga acttgtggga tggtggggtt ggcttccctg gcatgatgga 1140
caaaggcctg gcgtcggcca gaggggctgc tccagtgggc aggggtagct agcgtgtgcc 1200
aggcagatcc tctggacacg taacctatgt cagacactac atgatgactc aaggccaata 1260
ataaagacat ttcctacctg caaaaaaaaa aaaaaagggt ggccgctcgc gatctagaac 1320
tagt 1324

<210> 364
<211> 2853
<212> DNA
<213> Homo sapiens

<400> 364
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tagaattgaa gatgggaaat tttgttttat taaaaaggtg ctagaagatg tttcaaagac 120
aatattctta ttttaatacg ctgtagaagg taggtgtgga acctccatgc taccatgtgc 180
acaaacctaa ttatgctttg ggtcacttgt cagttcagta aatctgcctt cctcttctcc 240
caaatcatgt catctttagg ttgttcacct gcagctgctt taaatgaatt agtatctttc 300
agatagataa ccttacaagg agaatgtttg ttttgagcag ctgaccaaaa atatatcaaa 360
caggattatg gccaaaaagt cactcaaatt tctagagatt cctttaaaag atgtatgttg 420
atgaaattgc ccctttataa gaaaaacaac agcaagtctt ttagtagaaa tttgaaagaa 480
gtgtttgcta ccattttgac ccattattcc cttacctatc agatgaattt gccattcact 540
ggatagaaac cattcttgga tttggtaaga ggtgagcaag acaaatcttg taccatactc 600
ttatgtacca gcacttctga tggagaagca gtgaagttca gaacgktctt cacatagtcc 660
agatactgkt tagagtcagg caaatcagca aagcctttgg tatggagatg mcccatgatg 720
gctgcagttg taagtgggca tacatgttct atcattttga aggagaaaga aaaccgttct 780
cacatgtcgc aaatatgtga atcatactat attcccctaa agtaaaacca gtgacttagt 840
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cttatcctta agggaaaagt tctaaatttt taaatttatt tttaattccc tagtctgagg 960
gaaatgtctt tattgtccat tacataaaaa tgttgactcc agtaatttat ttttctctat 1020
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gaaatgttaa ccaattagct caacttttct ctacctttgt tgagtcttaa tcttttagaa 1140
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gtctgcttct tagtaaatgt taagtctgra atggaagtga ggatgtaact ctactgaata 1320

atcaaagatc atcttagatt tggcttgatc tgtgtttatt gcttctatta atgtaaatca 1380
actctgtgcc aaatcctcct ccacaaacca tttattgtct tagttctagt ggtatcaatg 1440
aagatagtta cagtatatga attctaagtc ctgaggaaga aattttatgg ggtttgttaa 1500
gtttcacatt cgtgaaagag gaaattagta gagtattcag actttgatat ttggctgtta 1560
atgggatgca tatcaaattt ttaaaagaag gcttggccta aggagtttat tggtacaggt 1620
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actgagacca tctaacattt ttcttttgga gtctcatttt tatttgtgca atattttcag 1740
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aagtaaaaat ctgaatatga aagaaaatat cagatttgca ctttaaatga gcttaattgc 1860
ttgaagttgt gcctgaaata tcgaattgcc tcctattggg tgtggctttg ttgaaataaa 1920
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atgttcctgt agcataaatg gtgttacaga cactgaggtg cactcttggt ttctgagcag 2160
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caggcttgca attaagatca ataaggctgc agcaccattt caatttactt tccatcttac 2280
ccagtagttt ttgtgttttt aaattcgttt gggtggttat gtttgcatgc ttaagcacac 2340
atttgaaaat taattatagc tgtactaccc gatgtttttc cttggggatg atggccttgt 2400
tcctttttaa attctgatgc ttgaattcta ttttctagtg atttttcaca tctcccttta 2460
agtttttgct gcagcaattt gagagagtac ttttgattaa atgattctga tggtgggcac 2520
caatctacaa ctatgtcatt aactgaagat acatgtttta atcttgttgg gaataagctt 2580
acccactttc tccttggtaa agcgtttact taacaaaata atacccgaga atgtaaggtc 2640
tctaagtcat tactaacaaa gagcaaaaat aatatctgca gtattgtttt tcccattgat 2700
tttaagtcag tttagagtac aaactgtata ttagaatttg cctgtaaaat gaattctaaa 2760
aagcagatgt aaagtctctc ctgaaaatgt tggcatagta aataaaaata aagttcataa 2820
ttataaaaaa aaaaaaaaaa aaaaaaatta ctg 2853

<210> 365
<211> 1837
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (136)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (749)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1816)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1829)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1832)
<223> n equals a,t,g, or c

<400> 365
nnnttttttt tttttcacgt gtgtggtcaa gatgctrgag ctcggcttat atttcggacc 60
acatgaaggt gcacagccag ggtcctcacc atgtctgtga gctctgcaac aaaggtacat 120
gccgagggct gccggnaggg ccaggggcag agggtgggcg cctggccaga cgccttgcca 180
cggatacggg ttaagggtgc tgtagccaag agctcgtggc gtctagattc ctacaagagg 240
tcaagggagc agcgggggga cacctgaatg aacatcatta gactctaaga agtcctggtt 300
ggaagagatg atctgccaga gaggttgaac ctcctggtaa tgtgtgggga aagcgggagt 360
ggaacttggc tgctctgggg aaggagtagt caagaaagcc agttccaggg gtcacaaggc 420
aaggtttccg ctgcgcagcc acaaggtctt gtctccagct cctggggcag gtggagtaca 480
cgggccgggc tttaccagca cgcaccctgc gcatccacgc ggtgaaggac cacgggctcc 540
aggccccgcg gctgaccgca tcctgtgcaa gctgtgcagc gtgcactgca agacccctgc 600
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aaaaaaaaaa aaaacncgag gggggccng gnaccca 1837

<210> 366
<211> 1823
<212> DNA
<213> Homo sapiens

<400> 366
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tgccaaagca ggagtcatct ttcccgtggg gcggatgctg cggtacatca agaaaggcca 180
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gaagcgggga tccaaaggaa agttggaagc catcatcaca ccaccccccag ccaaaaaggc 480
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<210> 367
<211> 898
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (17)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<400> 367
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cacagcccca caactggatg atgaggagat gtactcagcc cacatgcccg ctcacctgcg 240
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caaacttcat acctcaaact ctgggggcg gcgggagctg agcgagttgg tctacacgga 360
tgtcctggac cggagctgct cccggaactg gcaggactac ggagttcgag aagtggacca 420
agtgaaacgt ctcacaggcc caggacttag cgaggggcca gagccaagca tcagcgtgat 480
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gtttggagaa gaccagatct atgaagccca ccaacaaggc cgaggggctc tggaggcatt 600
gctatgtggg ggaccccagg gggcctgctc agagaaggtg tcagccacaa gagaagagct 660
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aaataaaacc cagtgacctc aaaaaaaaa aaaaaaaaaa aaaaaaaaa aaactcga 898

<210> 368
<211> 1117
<212> DNA
<213> Homo sapiens

<400> 368
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aagctcacca ctgctcagga ggtgctggcc cgggcccgca acctgatttc acccaggatg 180
gagaaggcct tgagtcaatt ggccctgcgy tctgctgcgc ccagcagccc cgggtctccc 240
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cgcaccgaca cctacgtcaa gctggacaag gccgcggacc tsgcccacat cactgcacgc 660
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tgaatatggg accttccaca gcaaagggtg acttttg 1117

<210> 369
<211> 2226
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (35)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c

<400> 369
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tttgcatttt gtttttttata actcttactc ccttttcccc tcaaaggaga actgtgttta 180
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tcttggtgaa atgaaaagtg gagtaccagt gttggcagta tccttagcat tggaggggaa 360
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aaaaaa 2226

<210> 370
<211> 3636
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1937)
<223> n equals a,t,g, or c

<400> 370
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caatctcggt cagaatttgt gggggcccca cagatatggg tgcctggcgg gggtccgggt 180
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atggggcagc tgggccttgg caaccagaca gacgctgttc ccagccccgc gcagataatg 480
tacaacggcc agccaattac caaaatggcc tgtgggsstg aattcagtat gataatggac 540
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aaacaacatt gtctactgtc aaaaaaaaaa aaaaaa 3636

<210> 371
<211> 4039
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1085)
<223> n equals a,t,g, or c

<400> 371
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atatcttatt tagataatct cagtaccttt tctggcattt ttgccctgta taggttgact 180
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<210> 372
<211> 1599
<212> DNA
<213> Homo sapiens

<400> 372
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<210> 373
<211> 464
<212> DNA
<213> Homo sapiens

<400> 373

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actggagaga ttctctgaat gccttaagaa tttggttaat atggagaccc ttcccagggg 420
aaccagaagg aggatcgtga aaacctgttg actacttaga tgat 464

<210> 374
<211> 890
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (886)
<223> n equals a,t,g, or c

<400> 374
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gagcaacatg cccaagtttt attgtgacta ctgcgataca tacctcaccc atgactctcc 180
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tcagaaatgg atggaagagc aggctcagag cctgattgac aaaacaacgg ctgcatttca 300
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaanaaaa 890

<210> 375
<211> 1874
<212> DNA
<213> Homo sapiens

<400> 375
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aaaaaaaaaa aagc 1874

<210> 376
<211> 2018
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1997)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2012)
<223> n equals a,t,g, or c

<400> 376
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gccctgaacc cagtgcctgc agccatggct cccggccagc tcgccttatt tagtgtctct 120
gacaaaaccg gccttgtgga atttgcaaga aacctgaccg ctcttggttt gaatctggtc 180
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<210> 377
<211> 818
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (818)
<223> n equals a,t,g, or c

<400> 377
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ctctggcgat cgaggggtcc tagtacaccg caatcatgtc tattatgtcc tataacggag 120
gggccgtcat ggccatgaag gggaagaact gtgtggccat cgctgcagac aggcgcttcg 180
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<210> 378

<211> 2565
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1508)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2565)
<223> n equals a,t,g, or c

<400> 378
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<210> 379
<211> 1680
<212> DNA
<213> Homo sapiens

<400> 379
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aatagttaca cacaagaggg aaactggaag ccaaacactg tacagtattg tgtagaaagt 180
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aagggctact gttaattgca cataaacatg aaatgtgttt tcccctgtgt actaacacat 960
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ctaaaattgt ttttctacca tatcaaatta aacaattcat gcctttatag ggtcaggcct 1140
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acatttcggg ggcattaggg tagggagatg aatcaaaaaa tacccctagt aatgctttat 1260
attttaatac tgcaaaagct ttacaaatgg aaaccatgca attacctgcc ttagttcttt 1320
tgtcataaaa acaatcactt ggttggttgt attgtagcta ttacttatac agcaacattt 1380
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tgactgtatt aatattttag tgctataaaa tactatgtga atctcttaaa aatctgacat 1500
tttacagtct gtattagaca tactgttttt ataatgtttt acttctgcct taagatttag 1560
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<210> 380
<211> 1267
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (214)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1165)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1255)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1262)
<223> n equals a,t,g, or c

<400> 380
aagnaagaaa accacaacta aaactggaaa tgtatatttt gtatatttga gaaaacaggg 60
aatacattgt attaatacca aagtgtttgg tcattttaag aatctggaat gcttgctgta 120
atgtatatgg ctttactcaa gcaratctca tctcatgaca ggcagccacg tctcaacatg 180
ggtaaggggt gggggtggag gggaatgtgt gcancgtttt tacctaggca ccatcattta 240
atgtgacagt gttcartaaa caaatcagtt ggcaggcacc agaagaagaa tggattgtat 300
gtcaagattt tacttggcat tgagtagttt ttttcaatag taggtaattc cttagagata 360
cagtatacct ggcaattcac aaatagccat tgaacaaatg tgtgggtttt taaaaattat 420
atacatatat gagttgccta tatttgctat tcaaaatttt gtaaatatgc aaatcagctt 480
tataggttta ttacaagttt tttaggattc ttttggggaa gagtcataat tcttttgaaa 540
ataaccatga atacacttac agttaggatt tgtggtaagg tacctctcaa cattaccaaa 600
atcatttctt tagagggaag gaataatcat tcaaatgaac tttaaaaaag caaatttcat 660
gcactgatta aaataggatt attttaarta caaaaggcat tttatatgaa ttataaactg 720
aagagcttaa agatagttac aaaatacaaa agttcaacct cttacaataa gctaaacgca 780
atgtcatttt taaaaagaag gacttagggt gtcgttttca catatgacaa tgttgcattt 840
atgatgcagt ttcaagtacc aaaacgttga attgatgatg cagttttcat atatcgagat 900
gttcgctcgt gcagtactgt tggttaaatg acaatttatg tggattttgc atgtaataca 960
cagtgagaca cagtaatttt atctaaatta cagtgcagtt tagttaatct attaatactg 1020
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anaaatt 1267

<210> 381
<211> 1031
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1015)
<223> n equals a,t,g, or c

<400> 381
ggtccaggat tctagcagtc ctggggcact gacctttgcc agctacctgg gggagggctt 60
gccactggaa aacctttcag gccgccccca tcagtgggct ccaaagtaaa tggctgaaaa 120
caaaaatgtt tcacttccta acagttttcc tttttccact gtgtgactga aagctcctat 180
atcattttat atttctgaat ctataaaaca aaacaaacaa gcctgamagt gtctggarga 240
rccaaaggtg gcctccctgt ccccaaatat attggctata tgagagtaat tttacccctc 300
tacgtaccta aaggcaccca gttcactagt ctgtggggtc ctggagcctg tctcttcttt 360
ctggaggttc aaactgaata gcaataatta cgttacccaa agcatgtgga ggaaaagtga 420
aaccagccac ggagacgctg gcccacgggc tcggcctgcg gtgtggcctg ctttgctcac 480
cagcgtcagc cgctcatttc cttctcatga agtcccatct ggtcatgggg acgagggccg 540
ggagggcacc gggtagcctt ttcacacttg ggattagggg gagtgagaaa agatttgggc 600
catgcatgca aagtcaaagt ttaaaatttt atccttttca aatagatgat ataatatacc 660
tatacatgat ataatatttg tatatatgaa atctctctat atttgtttaw tttgagccat 720
tcaatctaaa ccaatgtaca ggtgtacaat gaaaaattta aatgcttagt tatttttccc 780
aacacagtgt aaagtcaccc tcctctgaga gtgggatgtg cagagttttg atgttgcagc 840
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gggtggggt tgaaagttgt tatctttaaa tacatgtaca aatcgttgtc aaaagtaacg 960
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gggggggccc c 1031

<210> 382
<211> 1597
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1577)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1579)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1597)
<223> n equals a,t,g, or c

<400> 382
atcacgtgga cgctactcgc tatccccggc ctgttggctt cttccgcgct ggagtatcca 60
gataggcgac acgccgrcgg gcggctgagg cgggaatggc tgctgtactg cagcgcgtcg 120
agcggctgtc caatcgagtc gtgcgtgtgt tgggctgtaa cccgggtccc atgaccctcc 180
aaggcaccaa cacctaccta gtggggaccg gccccaggag aatcctcatt gacactggag 240
aaccagcaat tccagaatac atcagctgtt taaagcaggc tctaactgaa tttaacacag 300

caatccagga aattgtagtg actcactggc accgagatca ttctggaggc ataggagata 360
tttgtaaaag catcaataat gacactacct attgcattaa aaaactccca cggaatcctc 420
agagagaaga aattatagga aatggagagc aacaatatgt ttatctgaaa gatggagatg 480
tgattaagac tgagggagcc actctaagag ttctatatac ccctggccac actgatgatc 540
acatggctct actcttagaa gaggaaaatg ctatcttttc tggagattgc atcctagggg 600
aaggaacaac ggtatttgaa gacctctatg attatatgaa ctctttaaaa gagttattga 660
aaatcaaagc tgatattata tatccaggac atggcccagt aattcataat gctgaagcta 720
aaattcaaca atacatttct cacagaaata ttcgagagca gcaaattctt acattatttc 780
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attcatgcaa atgaattttt ggtgattgaa aaatattaaa ttcccaattt aaagtaaaaa 1560
aaaaaaaaaa aaaaaangnc cccggggggg ggccggn 1597

<210> 383
<211> 175
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (95)
<223> n equals a,t,g, or c

<400> 383
gtgagtggtg actatgggca tcctgtgtat atcgtgcagg atgggccccc ccagagccct 60
ccaaacatct actacaaggt atgagggctc ctctnacgtg gctatcctga atccagccct 120
tcttggggtg ctcctccagt ttaaattcct ggtttraggg acamctstaa catct 175

<210> 384
<211> 2171
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2166)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2170)

<223> n equals a,t,g, or c

<400> 384
agaacaagag ctggacacat taaaaagaaa gagtccatca gatttgtgga aagaagactt 60
ggctacattt attgaagaat tggaggctgt tgaagccaag gaaaaacaag atgaacaagt 120
cggacttcct gggaaagtgg ggaaggccaa ggggaaaaaa acacaaatgg ctgaagtttt 180
gccttctccg cgtggtcaaa gagtcattcc acgaataacc atagaaatga aagcagaggc 240
agaaaagaaa aataaaaaga aaattaagaa tgaaaatact gaaggaagcc ctcaagaaga 300
tggtgtggaa ctagaaggcc taaaacaaag attagaaaag aaacagaaaa gagaaccagg 360
tacaaagaca aagaaacaaa ctacattggc atttaagcca atcaaaaaag gaaagaagag 420
aaatccctgg tctgattcag aatcagatag gagcagtgac gaaagtaatt ttgatgtccc 480
tccacgagaa acagagccac ggagagcagc aacaaaaaca aaattcacaa tggatttgga 540
ttcagatgaa gatttctcag attttgatga aaaaactgat gatgaagatt ttgtcccatc 600
agatgctagt ccacctaaga ccaaaacttc cccaaaactt agtaacaaag aactgaaacc 660
acagaaaagt gtcgtgtcag accttgaagc tgatgatgtt aagggcagtg taccactgtc 720
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aatgttatat tgataaccat gctcagcaat gagctattag attcattttg ggaaatctcc 1980
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caattttgta ctttaataaa atgttctaaa cattgcaaaa aaaaaaaaaa aaaccccggg 2160
gggggncccn g 2171

<210> 385
<211> 2364
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (19)
<223> n equals a,t,g, or c

<400> 385
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accgttggcc tcataaacct gttttgcaga actcatttat tcagcaaata tttattgagt 120
gcctaccaga tgccagtcac cgcacaaggc actgggtata tggtatcccc aaacaagaga 180
cataatcccg gtccttaggt agtgctagtg tggtctgtaa tatcttacta aggcctttgg 240
tatacgaccc agagataaca cgatgcgtat tttagttttg caaagaaggg gtttggtctc 300
tgtgccagct ctataattgt tttgctacga ttccactgaa actcttcgat caagctactt 360
tatgtaaatc acttcattgt tttaaaggaa taaacttgat tatattgttt ttttatttgg 420
cataactgtg attcttttgg gacaattact gtacacatta aggtgtatgt cagatattca 480
tattgaccca aatgtgtaat attccagttt tctctgcata agtaattaaa atatacttaa 540
aaattaatag ttttatctgg gtacaaataa acaggtgcct gaactagttc acagacaagg 600
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gaacactgtt taggtagggt gttaagactt acacagtacc tcgtttctac acagagaaag 720
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gtttaacaaa agatttgttt ttgtagagat tttaaagggg gagaattcta gaaataaatg 900
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taacttttaa atgtttatag gagtatgtgc tgtgaagtga tctaaaattt gtaatatttt 2040
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tataagccat agacactata gtataccagt gaatctttta tgcagcttgt tagaagtatc 2220
ctttatttct aaaaggtgct gtggatatta tgtaaaggcg tgtttgctta aacttaaaac 2280
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atttatttat ttccttttat caaa 2364

<210> 386
<211> 2864
<212> DNA
<213> Homo sapiens

<400> 386
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ccggtaacaa agaacgaacg gcaggtgatg aagccactat acgacaggta ccggctggtc 120
aaacagatcc tctcccgagc taacaccata cccatcattg gttccccctc cagcaagcgg 180

agaagccctt tgctgcagcc aattatcgag ggcgaaactg cttccttctt caaggagata 240
aaggaagaag aggaggggtc agaagacgat agcaatgtga agccagactt catggtcact 300
ctgaaaaccg atttcagtgc acgatgcttt ctggaycaat tcgaagatga cgctgatgga 360
tttatttccc caatggatga taaaatacca tcaaaatgca gccaggacac agggctttca 420
aatmtccatg ctgcctcaat acctgaactc ctggaacacc tccaggaaat gagagaagaa 480
aagaaaagga ttcgaaagaa acttcgggat tttgaagaca actttttcag acagaatgga 540
agaaatgtcc agaaggaaga ccgcactcct atggctgaag aatacagtga atataagcac 600
ataaaggcga aactgaggct cctggaggtg ctcatcagca agagagacac tgattccaag 660
tccatgtgag gggcatggcc aagcacaggg ggcyggcagc tgcggtgaga gtttactgtc 720
cccagagaaa gtgcagctct ggaaggcagc cttggggctg gccctgcaaa gcatgcagcc 780
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attaactaaa gatttattca ggaatcccca tttgaatttg tatgattcaa taaaagaaaa 2820
caccaagtaa gttatataaa ataaaaaaaa aaaaaaaaac tcga 2864

<210> 387
<211> 2683
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2649)
<223> n equals a,t,g, or c

<400> 387
acgccttccc cgaggtgtac gacaagatct gcaaggccgn cagactgags ctggagcccg 60
cctggagaga cagacacgtg tgagtggtca ggcatcttcc cttcactcaa gcttggctgc 120
tttcctagat ccacactttc aaagagaaac ccctccagaa ctcccaccct gacagcccaa 180
caccaccttc ctcctggctt ccagggggca gcccagtgga atggaaagaa tgtgggattt 240
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gtgagtccct taacccctct gagcccgggt ctcttcatta gttgaaaggg atagtaatac 360
ctacttgcag gtygttgtca tctgagttga gcactggtca cattgaaggt gctgggtaag 420
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<210> 388
<211> 1446
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (35)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (37)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (57)
<223> n equals a,t,g, or c

<400> 388
aagaactaaa acgactcact atagggaaaa actananacg cctgacagga aaccggnccg 60
gaattcccgg gtcgacccac gcgtccgaar argaggtgga ggargagggt gatgttgata 120
gtgatgaaga agaggaggaa gatgaggaga gctcctcgga gggcttggag gctgaggact 180
gggcccaggg agtagtggag gccggtggca gcttcggggc ttatggtgcc caggaggaag 240
cccagtgccc tactctgcat ttcctggaag gtggggagga ctctgattca gacagtgagg 300
aagaggacga tgaggaagag gatgatgaag atgaagacga cgatgatgat gaggaggatg 360
gtgatgaggt gcctgtaccc agctttgggg aggccatggc ttactttgcc atggtcaaga 420
ggtacctgac ctccttcccc attgatgacc gcgtgcagag ccacatcctc cacttggaac 480
acgatctggt tcatgtgacc aggaagaacc acgccaggca ggcgggagtt cgaggtcttg 540
gacatcaaag ctgagtcact ggacctagct gtgcccccaa cctagattgg cagcaccacc 600
ccagggcaga ggactctctg ggcacccgct gtgcatggag ccagagtgca gagccccaga 660
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gctgaggtca gcctcactgc ctgcttattg cctctttctc agaatcctct ttcctcccca 780
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cctgcttctg cctgctttcc acctccccag tccctttctc tggccctgtc catgtgactt 1140
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ccaagggcgc ttccttgtgg gcagctgcag gccccatgcc tctcctccct ctctggcagg 1260
gccccatcct gggcagaggg gcctggggct gggcccagag tccagccgtc cagctgctcc 1320
tttcccagtt tgatttcaat aaatctgtcc actccccttt tgtgggggtg aacgttttaa 1380
cagccaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1440

aaaaaa 1446

<210> 389
<211> 723
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (705)
<223> n equals a,t,g, or c

<400> 389
gggcaagacc tcatgcctaa aaaataaaga gaaagcagag taaaactgga ctctgagata 60
ygactaaagt tctgtgtgat acgtgtgcct tatttagctc aagacattcc tggagcacct 120
ataaaaactg acttgtaatc caggctatgt ctctttttag cttcgtaatc tttggcaagg 180
ccattggatt cttcagctgt acaattagga gactcgatca ggtgattgcc tttctcagct 240
gtcagttctc taatttcagg cttggtagct tgtaggaact gaaattgcaa ttaaaacctt 300
tataaactca aactaaatca tgaattacag aaaaagtcca ttcttccaaa acttgatgtt 360
accacactta caagtttaaa atatgaagtc gactgtttaa aggattctgc atatattcta 420
gtgtgcacat tcagaaacat ttttcttgga aaaagtaccc aacatttttt ataactgcac 480
atattaattt attgccagaa taaattgcat tgcatgctaa ataaagtcag ataattcaaa 540
tccatttgct tttatgtagt ttttcttcta aatgtcaaca ttttggaatt aaaatgttta 600
tggttttata tgagggtagg aaatcttaac tgctttgggg ggtattgttt ataggctttt 660
tgttatgggg ccggtagttt tttaataggg ggattgccca tttcnaccgt ttgggggccc 720
ggg 723

<210> 390
<211> 1046
<212> DNA
<213> Homo sapiens

<400> 390
cgggtcgacc cacgcgtccg gtccaccaca ggcaccgcag ctcatctacc aggaatatgt 60
gaaccagcca gatgttcggc cccagccccc ttcgccccga gagggccctc tgcctgctgc 120
ccgacctgct ggtgccactc tggaaagggc caagactctc tccccaggga agaatggggt 180
cgtcaaagac gtttttgcct ttgggggtgc cgtggagaac cccgagtact tgacacccca 240
gggaggagct gcccctcagc cccaccctcc tcctgccttc agcccagcct tcgacaacct 300
ctattactgg gaccaggacc caccagagcg gggggctcca cccagcacct tcaaagggac 360
acctacggca gagaacccag agtacctggg tctggacgtg ccagtgtgaa ccagaaggcc 420
aagtccgcag aagccctgat gtgtcctcag ggagcaggga aggcctgact tctgctggca 480
tcaagaggtg ggagggccct ccgaccactt ccaggggaac ctgccatgcc aggaacctgt 540
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agggtccagt ggatgccaca gcccagcttg gccctttcct tccagatcct gggtactgaa 720
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gcgacccatt cagagactgt ccctgaaacc tagtactgcc ccccatgagg aaggaacagc 840
aatggtgtca gtatccaggc tttgtacaga gtgcttttct gtttagtttt tacttttttt 900
gttttgtttt tttaaagatg aaataaagac ccagggggag aatgggtgtt gtatggggag 960
gcaagtgtgg ggggtccttc tccacaccca ctttgtccat ttgcaaatat atttggaaa 1020
acaaaaaaaa aaaaaaaaaa aaaaaa 1046

<210> 391
<211> 699
<212> DNA
<213> Homo sapiens

<400> 391
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tcttcgcctt agtactcgtg tgaagttggc ggggacggtt cctgtcatct tcttgggctt 120
atttggtgtg ctgttgaagg ggggagacta gagaaatggc agggaacctc ttatccgggg 180
caggtaggcg cctgtgggac tgggtgcctc tggcgtgcag aagcttctct cttggtgtgc 240
ctagattgat cggtataagg ctcactctcc cgccccccaa agtggttgat cgttggaacg 300
agaaaagggc catgttcgga gtgtatgaca acatcgggat cctgggaaac tttgaaaagc 360
accccaaaga actgatcagg gggcccatat ggcttcgagg ttggaaaggg aatgaattgc 420
aacgttgtat ccgaaagagg aaaatggttg gaagtagaat gttcgctgat gacctgcaca 480
accttaataa acgcatccgc tatctctaca aacactttaa ccgacatggg aagtttcgat 540
agaagagaaa gctgagaact tcggaaaagg ctcatctgtc accctggaga agggaaactg 600
tacttttccc tgtgaggaaa cggctttgta ttttctctgt aataaaatgg ggcttctttg 660
gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aagtcgacc 699

<210> 392
<211> 1545
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (54)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (58)
<223> n equals a,t,g, or c

<400> 392
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ccggactcgg acgcgtggta gccccaggat gggtgagttc aacgagaaga agacaacatg 120
tggcaccgtt tgcctcaagt acctgctgtt tacctacaat tgctgcttct ggctggctgg 180
cctggctgtc atggcagtgg gcatctggac gctggccctc aagagtgact acatcagcct 240
gctggcctca ggcacctacc tggccacagc ctacatcctg gtggtggcgg gcactgtcgt 300

catggtgact ggggtcttgg gctgctgcgc caccttcaag gagcgtcgga acctgctgcg 360
cctgtacttc atcctgctcc tcatcatctt tctgctggag atcatcgctg gtatcctcgc 420
ctacgcctac taccagcagc tgaacacgga gctcaaggag aacctgaagg acaccatgac 480
caagcgctac caccagccgg gccatgaggc tgtgaccagc gctgtggacc agctgcagca 540
ggagttccac tgctgtggca gcaacaactc acaggactgg cgagacagtg agtggatccg 600
ctcacaggag gccggtggcc gtgtggtccc agacagctgc tgcaagacgg tggtggctct 660
ttgtggacag cgagaccatg cctccaacat ctacaaggtg gagggcggct gcatcaccaa 720
gttggagacc ttcatccagg agcacctgag ggtcattggg gctgtgggga tcggcattgc 780
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catgtgcctc tgcggggcag ggccttcctg gttttgtaca ctgctgtacc cagatgccta 1440
caaccatccc tgccacatac aggtgctcaa taaacacttg tagagcagaa aaaaaaaaaa 1500
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 1545

<210> 393
<211> 749
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (490)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (748)
<223> n equals a,t,g, or c

<400> 393
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ttyggcatca atatggtgac ctcccgggag cggrggacca ccaggttgcc taaggagggg 120
tgaaccggyc caggtcggaa acggagcagt tttccttgag cggagattca ggtttttcag 180
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ctgaatggcc acccttagac cctgtgatcc atcctctctc ctagctgagt aaatccgggt 480
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gactgcctcg ctgccccacc tcccgctcct tggcctgtcc ccagattcct tccctggttg 600
acttgactca tgcttgtttc actttcacat ggaatttccc agttatgaaa ttaataaaaa 660
tcaatggttt ccacaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 720
aaaaaaaaaa aaaaaaaaaa aaaaaaana 749

<210> 394
<211> 611
<212> DNA
<213> Homo sapiens

<400> 394
gcgcggcggc ggcggggtgg ctgggccggc ggcggcggcg gtacgaggcg cgcgctcggg 60
gtcccggtcg cgaggaggag gaggatgtgg cgcgcggagg ggaaatggct gccgaaaaca 120
agccggaaga gcgtttccca aagtgtattc tgcggaacta gcacctactg tgttctcaac 180
accgtgccac ctatagaaga tgatcatggg aacagcaata gtagtcatgt aaaaatcttt 240
ttaccgaaaa agctgcttga atgtctgccg aaatgttcaa gtttaccaaa agagaggcac 300
cgctggaaca ctaatgagag atcatgatgc agccgtcctt ttggatttct ttttaataat 360
gtgtgaccct tcacctttga tcccctgacc tgcattacct tggtaaccat ttcatttttt 420
aatttaattt catttttaa ttttggtgta caagctgtaa catttcatct ttcaaagtgt 480
aacacgctga tttcctcaaa tagagatacc cctttgagtg ataaatttgc aaaatgctgt 540
cttcattttc tgtattaaaa ttcatttcag ttttaaaata aagtgtaatc tgtgttttca 600
tccttttaaa a 611

<210> 395
<211> 1856
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1851)
<223> n equals a,t,g, or c

<400> 395
gttggcgcgc ggtgcgcggt gcgtagtctg gagctatggt ggtggtggca gccgcgccga 60
acccggccga cgggacccct aaagttctgc ttctgtcggg gcagcccgcc tccgccgccg 120
gagccccggc cggccaggcc ctgccgctca tggtgccagc ccagagaggg gccagcccgg 180
aggcagcgag cggggggctg ccccaggcgc gcaagcgaca gcgcctcacg cacctgagcc 240
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accaaaaact tttgctagaa aatcagcttt tacgagagaa aactcatggc cttgtagttg 420
agaaccagga gttaagacag cgcttgggga tggatgccct ggttgctgaa gaggaggcgg 480
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<210> 396
<211> 2651
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2642)
<223> n equals a,t,g, or c

<400> 396
gtcacgagcg agggggtgcg tgtgaggtca tcgcgcgggc gggcntncgg ggtctggcgg 60
tttgaacgag acgaagacgg aaccggagcc ggttgcgggc agtggacgcg gttctgccga 120
gagccgaaga tggcagtgaa cgtatactca acgtcagtga ccagtgataa cctaagtcga 180
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ggtgtggtgc gaaagaaccc tggtgtgggc aacggagacg acgaggcagc tgagttgatg 720
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ttcggaaagc tacggaacat tgaattgatt tgccaggaga acgaggggga aaacgaccct 840
gtattgcaga ggattgtaga cattctgtat gccacagatg aaggctttgt gatacctgat 900
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<222> (1471)
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gtttaataga atataaacct cttgataaaa aatgcacaaa aaatcacttt gtatatgtga 1260
gtttcactgc attgtatatt ttttcatttg gtacacaaag aatgtattct tcataggttt 1320
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<210> 403
<211> 1750
<212> DNA
<213> Homo sapiens

<220>
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<222> (2)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (70)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (107)
<223> n equals a,t,g, or c

<400> 403
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aatccgcaga agatgtcgag tttcaaaagg aggtggcgca ggttcgcaag cgcataaccc 180
agcgaaaaaa acaagaacaa cttactcctg gagtagtcta tgtgcgccac ctacctaacc 240
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aattagctaa aaaaggaatt gactatgatt ttccttcttt gattttacag aaaacggaaa 660
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aacttttttc tacaatgtat ttgtttgcga gtaggacttg ggagtcattg ggaaaaaaaa 1680

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aaaaataaaa 1750

<210> 404
<211> 1339
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (150)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1330)
<223> n equals a,t,g, or c

<400> 404
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gagagtgaaa ttatgtgata cactgaaatn acttttgttt ttcttctaac tcatacaaaa 180
ctggtttgga aagtctttgc tttggaagcg tcagacatta gaacaggcca aactggactg 240
tctgttcata gcgtgcctga ataagaaggc ctcttaggga gccagaggga gcagagtggt 300
cgtgtcctgc gtgctcttca ccctctgggg cgcccctgct gcggctggca ggtgcagaca 360
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cactgtgagg ctgtgagaga tttgtggcag gaactgttta tgaggctcta gttgttgctg 480
ttgtggcggg aaagttaaga aacatagccc ttaaggaaac cacctttatg tattttctta 540
aagcacgcct ttaaataagc aaaaacttta aaaggcagga aagagaattc ttaggcaaat 600
tcagagaaat aagtgctagt taatactaat cacctcctcc tctgtctctc atcctccttt 660
ctcccatcaa agcaaaatat ggcctcacca ccagccccaa atcagtgctc agaccctctc 720
tgtgtctgtg tgccctcctg ggagtcagtc agcgctcagg ccaggactgt gcagggccag 780
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tcatcggtaç tctttctgca tttccctcgt gctgtgtccc gctcgggttc caatggacag 1260
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gattgttaan ctgcctctt 1339

<210> 405
<211> 482
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (440)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (469)
<223> n equals a,t,g, or c

<400> 405
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ttcactggct gtgggcctta tggcacagtc agtcaccagg ttagagacat gcttcacatt 120
cacctaccca caaactagtg gatgataaat tttggctatt cagaagacgt ttattatagg 180
agtatgtaga ttttccatag agtgctgtta tgtgacttga attttagtct cggccctgcc 240
tctgacattg tcggtggttt atcctggttc caggaaataa gactagcctt ttcctcatga 300
tagtctttgg tggtttttaa aacagttgtt taagtcaaca gatgtatcat atgcctgaca 360
ctgctctaca ccagtgaata atttacactc taatagggg tggtaactat aaagatgata 420
aacatagcat cttaattggn gtgtgtatga aggtggttgt tacctcttnc tagccaccca 480
gg 482

<210> 406
<211> 1413
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

<400> 406
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ggaattcggc acgaggtttg gtggggttac acgcgggttc aacatgcgta tcgaaaagtg 120
ttatttctgt tcggggccca tctatcctgg acacggcatg atgttcgtcc gcaacgattg 180
caaggtgttc agattttgca aatctaaatg tcataaaaac tttaaaaaga agcgcaatcc 240
tcgcaaagtt aggtggacca aagcattccg gaaagcagct ggtaaagagc ttacagtgga 300
taattcattt gaatttgaaa aacgtagaaa tgaacctatc aaataccagc gagagctatg 360
gaataaaact attgatgcga tgaagagagt tgaagaaatc aaacagaagc gccaagctaa 420
atttataatg aacagattga agaaaaataa agagctacag aaagttcagg atatcaaaga 480
agtcaagcaa aacatccatc ttatccgagc ccctcttgca ggcaaaggga aacagttgga 540
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aactaatggc aaaaattcat ggctagtgat gtataaaata aaatattctt tgcagtaaaa 960
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ggtacctcgg ccgcgaccac gctaagccga att 1413

<210> 407
<211> 1693
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1548)
<223> n equals a,t,g, or c

<400> 407
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gccctcgcat gcgcctggtg gtcaccgcgg acgactttgg ttactgcccg cgacgcgatg 120
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acgccaacct gtccgagggc cgccccgtgg gtccggcccg ccgtggcgcc tcatcgctgc 300
tcggccccgga argcttcttc cttggcaaga tgggattccg ggaggcggtg gcggccggag 360
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gagctccgcc cggaggtact gtgaggccgt tagagctggc ggtggatgac ttccgcattc 480
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cgcagagcat ttggtgcccc tccatgttgc aatgcaaaca ccttcaccac tggggcagtg 1620
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tcgagacagt tct 1693

<210> 408
<211> 1342

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (107)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1332)
<223> n equals a,t,g, or c

<400> 408
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aaaaaaaaaa anaaaaaaac ca 1342

<210> 409
<211> 2417
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (107)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (680)

<223> n equals a,t,g, or c

<400> 409
aaaaaaaaaa aaaaaaacca aacacaaaga gagcaatttt gggccaacag ttaccattca 60
agcctggccc tttaggccag cccagtccac gggctctgag tgtggangct gcgtagcacc 120
aggaagcggc tctgctgagg ttcaaggggc cccagcacag tgtggcatcc gttcagcttt 180
tggttggtcc aggatggtgg ggagccaggc ctcggggcct cggagcaacc acccgagcag 240
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<210> 410
<211> 1401
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (1394)
<223> n equals a,t,g, or c

<400> 410
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aaccaacaaa tgtgccagcc aggcaggtat gacagcttac gggactagga ggcatcttta 120
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<210> 411
<211> 3016
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (399)
<223> n equals a,t,g, or c

<400> 411
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agatccaggg acagagtctc agcctcgccg ctgctgccgc cgccgccgcc cagagactgc 180
tgagcccgtc cgtccgccgc caccacccac tccggacaca gaacatccag tcatggataa 240
aaatgagctg gttcagaagg ccaaactggc cgagcaggct gagcgatatg atgacatggc 300
agcctgcatg aagtctgtaa ctgagcaagg agctgaatta tccaatgagg agaggaatct 360
tctctcagtt gcttataaaa atgttgtagg agcccgtang tcatcttgga gggtcgtctc 420
aagtattgaa caaaagacgg aaggtgctga gaaaaaacag cagatggctc gagaatacag 480
agagaaaatt gagacggagc taagagatat ctgcaatgat gtactgtctc ttttggaaaa 540
gttcttgatc cccaatgctt cacaagcaga gagcaaagtc ttctatttga aaatgaaagg 600

agattactac cgttacttgg ctgaggttgc cgctggtgat gacaagaaag ggattgtcga 660
tcagtcacaa caagcatacc aagaagcttt tgaaatcagc aaaaaggaaa tgcaaccaac 720
acatcctatc agactgggtc tggcccttaa cttctctgtg ttctattatg agattctgaa 780
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ctctcgtgcc gaattc 3016

<210> 412
<211> 958
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (930)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (934)
<223> n equals a,t,g, or c

<400> 412
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caaccctagt cccccgcgcg gccccttatt cgctccgaca agatgaaaga aacaatcatg 120
aaccaggaaa aactcgccaa actgcaggca caagtgcgca ttggtgggaa aggaactgct 180
cgcagaaaga agaaggtggt tcatagaaca gccacagcag atgacaaaaa acttcagttc 240
tccttaaaga agttaggggt aaacaatatc tctggtattg aagaggtgaa tatgtttaca 300
aaccaaggaa cagtgatcca ctttaacaac cctaaagttc aggcatctct ggcagcgaac 360
actttcacca ttacaggcca tgctgagaca aagcagctga cagaaatgct acccagcatc 420
ttaaaccagc ttggtgcgga tagtctgact agtttaagga gactggccga agctctgccc 480
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ccagatcttg tggagaattt tgatgaggct tccaagaatg aggcaaactg aattgagtca 600
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ttttaagaaa tttttgttta tggatctgat aaaatctaga tctctaatat ttttaagccc 720
aagccccttg gacactgcag ctcttttcag tttttgctta tacacaattc attctttgca 780
gctaattaag ccgaagaagc ctgggaatca agtttgaaac aaagattaat aaagttcttt 840
gcctagtaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900
aaaaaaaaaa aaaaaaaaaa aaaaaaaaan gggnggccgt tttaaaggaa ccaggttt 958

<210> 413
<211> 500
<212> DNA
<213> Homo sapiens

<400> 413
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atgcaaagag gttggatcaa gtttaaatga ctgtgctgcc cctttcacat caaagaacta 180
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gtgaaatcta gagtaaaacc aagctggccc aaggtgtcct gcaggctgta atgcagttta 360
atcagagtgc cattttttttt tttgttcaaa tgattttaat tattggaatg cacaattttt 420
ttaatatgca aataaaaagt ttaaaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 480
gcggccgctc gaattaagcc 500

<210> 414
<211> 3397
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3081)
<223> n equals a,t,g, or c

<400> 414
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gctgaagcgg gacccggagc ccgagcagcc gccgccatgg caatcaaatt tctggaagtc 180
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aaggagaaag tgctgtggac cgctatcacc ctctttatct tcttagtgtg ctgccagatt 300
cccctgtttg ggatcatgtc ttcagattca gctgaccctt tctattggat gagagtgatt 360
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cgagctctct tcaacggagc ccaaaagtta tttggcatga tcattactat cggccagtct 540
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 3397

<210> 415
<211> 2880
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (5)
<223> n equals a,t,g, or c

<400> 415
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tagccccaac gcaatggcca aggttcagat ttttgaatat aatgaaaaca ccaggaaata 120
tgcaaaagct gaaactctta tgacagtcac tgatcctgtt catgatattg cattcgctcc 180
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attaaagcct gtgaggaaag aactgacttc ctctggtggg ccaacaaagt ttgaaatcca 300
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<210> 416
<211> 1616
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1610)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1611)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1616)
<223> n equals a,t,g, or c

<400> 416
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gcacactgac catcaaagag agcgactggc tcagccagag catgttcacc tgccgcgtgg 660
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaagggggggn nccccn 1616

<210> 417
<211> 1815
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (270)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1184)
<223> n equals a,t,g, or c

<400> 417
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tacccacata gtcacagtct ggccaccatc ggtgcttcag tgggcatgca tgccgcactg 120
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<211> 1966
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<400> 418
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<210> 419
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<212> DNA
<213> Homo sapiens

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<222> (2838)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (2843)
<223> n equals a,t,g, or c

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<210> 420
<211> 2705
<212> DNA
<213> Homo sapiens

<400> 420
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<210> 421
<211> 1901
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1828)
<223> n equals a,t,g, or c

<400> 421
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<212> DNA
<213> Homo sapiens

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atgatatttt gcttcctgta atactattat aaaataaagt ttgtttattc tctaaaaaaa 2460
aaaaaaaaaa actcgag 2477

<210> 423
<211> 777
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (759)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (764)
<223> n equals a,t,g, or c

<400> 423
ttcctcgcgg aagtggggag gaggcggttg cggttagtgg accgggaccg gtaggggtgc 60
tgttgccatc atggctgacc ccgacccccg gtaccctcgc tcctcgatcg aggacgactt 120
caactatggc agcagcgtgg cctccgccac cgtgcacatc cgaatggcct ttctgagaaa 180

agtctacagc attctttctc tgcaggttct cttaactaca gtgacttcaa cagtttttt 240
atactttgag tctgtacgga catttgtaca tgagagtcct gccttaattt tgctgtttgc 300
cctcggatct ctgggtttga tttttgcgtt gaytttaaac agacataagt atccccttaa 360
cctgtaccta ctttttggat ttacgctgtt ggaagctctg actgtggcag ttgttgttac 420
tttctatgat gtatatatta ttctgcaagc tttcatactg actactacag tattttttgg 480
tttgactgtg tatactctac aatctaagaa ggatttcagc aaatttggag cagggctgtt 540
tgctcttttg tggatattgt gcctgtcagg attcttgaag ttttttttt atagtgagat 600
aatggagttg gtcttagccg ctgcaggagc ccttcttttc tgggggattc atcatctatg 660
acacacacta ctgatgcata aactgtcacc tgaagagtac gtattagctg gcatcaagcc 720
tctacttgga tatcatcaat ctattcctgg acctgtacng gttnttggga acaagtt 777

<210> 424
<211> 1649
<212> DNA
<213> Homo sapiens

<400> 424
ggccctttgc gcctgcgccc agctcgccct gcctagccag gagcgccccg cccccctgcct 60
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gcgcgttggg aggtgtagcg cggctctgaa cgcgctgagg gccgttgagt gtcgcaggcg 180
gcgagggcgc gagtgaggag cagacccagg catcgcgcgc cgagaaggcc gggcgtcccc 240
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ggcgcagctg tgcgggctga ggcggagccg ggcgtttctc gccctgctgg gatcgctgct 480
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gaaggtggtg ggcagatgcc gggcctccat gcctaggtgg tggtacaatg tcactgacgg 600
atcctgccag ctgtttgtgt atgggggctg tgacggaaac agcaataatt acctgaccaa 660
ggaggagtgc ctcaagaaat gtgccactgt cacagagaat gccacgggtg acctggccac 720
cagcaggaat gcagcggatt cctctgtccc aagtgctccc agaaggcagg attctgaaga 780
ccactccagc gatatgttca actatgaaga atactgcacc gccaacgcag tcactgggcc 840
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1649

<210> 425
<211> 1608
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1598)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1600)
<223> n equals a,t,g, or c

<400> 425
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agtgcagctc ttcgagatca gcctgagcca cggccgcgtc gtctacagcc ccggggagcc 120
gttggctggg accgtgcgcg tgcgcctggg ggcaccgctg ccgttccgag ccatccgggt 180
gacctgcata ggttcctgcg ggtctccaa caaggctaat gacacagcgt gggtagtgga 240
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tttcgggaag atcgtgcacc aggtgagggc cgccatccac acgccacggt tttccaagga 420
tcacaagtgc agcctcgtgt tctatatctt gagccccttg aacctgaaca gcatcccaga 480
cattgagcaa cccaacgtgg cctctgccac caagaagttc tcctacaagc tggtgaagac 540
gggcagcgtg gtcctcacag ccagcactga tctccgcggc tatgtggtgg ggcaggcact 600
gcagctgcat gccgacgttg agaaccagtc aggcaaggac accagccctg tggtggccag 660
tctgctgcag aaagtgtcct ataaggccaa gcgctggatc cacgacgtac ggaccattgc 720
ggaggtggag ggtgcgggcg tcaaggcctg gcggcgggcg cagtggcacg agcagatcct 780
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gcccactcag gacctgccca gcctctgcca gctcctctgc atccgccctc ttctccctgg 1500
ggctggggtg ggggtggcag ggagctggga cctggagaga caactcctgt aaataaaaca 1560
ctttatttgt agaaaaaaaa aaaaaaaaaa aaaaaaantn gggggggg 1608

<210> 426
<211> 1794
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1789)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (1790)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1793)
<223> n equals a,t,g, or c

<400> 426
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ctacggggac atacctatcc ccaactatcc taggcccgag aaccagccct tgccttcgcg 180
taacaggcgg agactcgctg aggcgagttg cacttctaat tgggcgtgag gtcttgtcaa 240
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tgaaacagcc gtttgagttt ggctgcgggt ggagaacgtt tgtcaggggc ccggccaaga 480
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tcctttttaa ctgcactttc tttatataat cgtttgcatt ttgttacttg ctaccctgag 1560
tactttcagg aagactgact taaatattcg gggtgagtaa gtagttgggt ataagatctg 1620
aacttttcat ctgcagaggc aagaaaaata tttgacattg tgacttgact gtggaagatg 1680
atggttgcat gtttctagtt tgtatatgtt tccatctttg tgataagatg atttaataaa 1740
tctctttaaa tactaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaann aana 1794

<210> 427
<211> 770
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (14)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (97)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (618)
<223> n equals a,t,g, or c

<400> 427
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ggagttgggg acccggctgg gccaccatag ccagggnccc tgtctatttt tttaaaaaag 120
taaaaaatag aaattatctc actacttaaa tcccattttt ttcacttcat atgaaagaac 180
atattgatag tatattctat attatttcat agatctgtct gaaagagatt gggaacaaaa 240
atatctaatt gagatattct ttaatttttt acatagcagc tttatttttt ttattctgta 300
gtatcagcga aatcagtcat gtttatacct tgaatataaa tatcaggaat catgcaatta 360
tttctactat gtatttagta gtatcttata tttgtataac attattacat tttgcaaatt 420
agtatcacaa ctgctaagta gatgtttctg agtattagaa aaatcagtgt tattacctgc 480
aggatattaa aaaacatttg aaaaagagaa aaagaaaaat cagtgtttag aaatgttgat 540
agttattgaa tctttgaatt gaattttaaa aatccattct agtaatcaga gtatactttt 600
tttatagaac aaggtggnca ggtggggagc cctttaccct tctggtgaag ttaaaccata 660
ggaagtttac aatttgcctt tcacaaacat tagcagtccg gggcatggtg gctgragcct 720
gtgratyccc agcatgttgg ggaggcccga gttggggagg gttgcctgag 770

<210> 428
<211> 512
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (18)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (484)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (491)
<223> n equals a,t,g, or c

<400> 428
tggatccccc gggactgnca gaattccggn cacgaggnaa gagacttgct ttgacaagta 60
cactgggaac acttaccgag tgggtgacac ttatgagcgt cctaaagact ccatgatctg 120
ggactgtacc tgcatcgggg ctgggcgagg gagaataagc tgtaccatcg caaaccgctg 180
ccatgaaggg ggtcagtcct acaagattgg tgacacctgg aggagaccac atgagactgg 240
tggttacatg ttagagtgtg tgtgtcttgg taatggaaaa ggagaatgga cctgcaagcc 300
catagctgag aagtgttttg atcatgctgc tgggacttcc tatgtggtcg gagaaacgtg 360
ggagaagccc taccaaggct ggatgatggt agattgtact tgcctgggag aargcagcgg 420
acgcatcact tgcacttcta gaaatagatg caacgwtcag gacacaagga catctataga 480
attngagaca ncttgagcaa gaaggataat cg 512

<210> 429
<211> 1470
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1346)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1347)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1357)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1387)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1415)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (1454)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1462)
<223> n equals a,t,g, or c

<400> 429
gtggacacgg aagtggtcgt cgtcgcggca ccggtgggag ctaggcgcga ggctcggagt 60
gcggccagcg ggcggaggcg gtctcgcatc ggcggcgacg gagggctcag gcgtcgtcgt 120
ttgggtgggg ggccgctgaa ctgacaagcg acatttcagc tcctttcacc cgccggaacc 180
ccggagccgg ggcccgctca gccggcgtta ccatgaccaa ggccggtagc aagggcggga 240
acctccgcga caagctggac ggcaacgaac tggacctgag cctcagcgac ctgaatgagg 300
tcccggtgaa ggagctggct gcccttccaa aggccaccat cctggatctg tcttgtaata 360
aactgactac tctaccgtcg gatttctgtg gcctcacaca cctggtgaag ctagacctga 420
gtaagaacaa gctgcagcag ctgccagcag actttggccg tctggtcaac ctccagcacc 480
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gctcccgtcc ccgcaagcca ccaccccgga agcacactcg ttcctgggct gtgctgaagc 960
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gtctacgccg ccatgagatc ctccagtggg tcctccagac cgactctcag cagtgagctt 1140
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aggcaaggtt ggtntactaa anggcagttg 1470

<210> 430
<211> 434
<212> DNA
<213> Homo sapiens

<400> 430
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atgcacccgt gggagctctt tgtaaagtac taccatgcta agaacggccg tgcttatgtg 120
gaatccccag cccggaagct ctcccagtcc ttcgcccttc ctgttacggg aggcactgtt 180
gtcaccccca aacagagcct actgacagcc atccacatgg tgctgacaga gcatgaccct 240
tttaagcgca gtgcagactc agaattgaag gccttggtgt gcatggcact gaatgagcca 300
gcgtctggtg tcctgggtga acctcatctg caaktccggg tcactsatcg agcctcacta 360
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gcctcaacaa cctc 434

<210> 431

<211> 1823
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1804)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1805)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1815)
<223> n equals a,t,g, or c

<400> 431
ggcacgagcc ccgccccgcc cgcgccgcgc cggccgctgt cagctccctc agcgtccggc 60
cgaggcgcgg tgtatgctga gccgctgccg cagcsggctg ctccacgtcc tgggccttag 120
cttcctgctg cagacccgcc ggccgattct cctctgctct ccacgtctca tgaagccgct 180
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cgagaaatat ggctacacac acctttctgc aggagagctg cttcgtgatg aaaggaagaa 300
cccagattca cagtatggtg aacttattga aaagtacatt aaagaaggaa agattgtacc 360
agttgagata accatcagtt tattaaagag ggaaatggat cagacaatgg ctgccaatgc 420
tcagaagaat aaattcttga ttgatgggtt tccaagaaat caagacaacc ttcaaggatg 480
gaacaagacc atggatggga aggcagatgt atctttcgtt ctctttttg actgtaataa 540
tgagatttgt attgaacgat gtcttgagag gggaaagagt agtggtagga gtgatgacaa 600
cagagagagc ttggaaaaga gaattcagac ctaccttcag tcaacaaagc caattattga 660
cttatatgaa gaaatgggga aagtcaagaa aatagatgct tctaaatctg ttgatgaagt 720
ttttgatgaa gttgtgcaga tttttgacaa ggaaggctaa ttctaaacct gaaagcatcc 780
ttgaaatcat gcttgaatat tgctttgata gctgctatca tgacccettt ttaaggcaat 840
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aattttttta tgttcttttt tttggtcaca ggagtagaca gtgaattcag gtttaacttc 960
accttagtta tggtgctcac caaacgaagg gtatcagcta ttttttttta aattcaaaaa 1020
gaatatccct tttatagttt gtgccttctg tgagcaaaac tttttagtac gcgtatatat 1080
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atttcccatt tgtattttat tttcttgaat actttttca tagttatttg tttaaaaaga 1740
tttaaaaatc attgcacttt ggtcagaaaa ataataaata tatcttataa ggggggggccc 1800
ggannccaat tcggnctgga gga 1823

<210> 432
<211> 3391
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (68)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (99)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (114)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3293)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3391)
<223> n equals a,t,g, or c

<400> 432
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<222> (2516)
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<213> Homo sapiens

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<211> 1822
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<213> Homo sapiens

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<213> Homo sapiens

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<221> misc feature
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<213> Homo sapiens

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<223> n equals a,t,g, or c

<400> 438
actcgtgccg aattcggcac gagcggncac gagcaagccc catctcatcc tggcacgccc 60
tactccactg ccctggcagc agcaggtgtg gccaatggag gggggtgctg gcccccagga 120
ttcccccagc caaactgtct ttgtcaccac gtggggctca cttttcatcc ttccccaact 180
tccctagtcc ccgtactagg ttggacagcc cccttcggct acaggaaggc aggaggggtg 240
agtcccctac tccctcttca ctgtggccac agccccettg ccctccgcct gggatctgag 300
tacatattgt ggtgatggag atgcagtcac ttattgtcca ggtgaggccc aagagccctg 360
tggccgccac ctgaggtggg ctggggctgc tcccctaacc ctactttgct tccgccactc 420
agccatttcc ccctcctcag atggggcacc aataacaagg agctcaccct gcccgctccc 480
aacccccctc ctgctcctcc ctgcccccca aggttctggt tccatttttc ctctgttcac 540
aaactacctc tggacagttg tgttgttttt tgttcaatgt tccattcttc gacatccgtc 600
attgctgctg ctaccagcgc caaatgttca tcctcattgc ctcctgttct gcccacgatc 660
ccctccccca agatactctt tgtggggaag aggggctggg gcatggcagg ctgggtgacc 720
gactacccca gtcccaggga aggtggggcc ctgcccctag gatgctgcag cagagtgagc 780
aagggggccc gaatcgacca taaagggtgt aggggccacc tcctccccct gttctgttgg 840
ggaggggtag ccatgatttg tcccagcctg ggctccctc tctggtttcc tatttgcagt 900
tacttgaata aaaaaaatat ccttttctgg aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 960
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aannnggggg gggccccccc ccccca 1016

<210> 439
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (476)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (519)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (530)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (531)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (539)
<223> n equals a,t,g, or c

<400> 439
ttgaaaaacg ggtcgactgg cmcgwccsgc ccggagccag cggttctcca agcacccagc 60
atcctgctag acgcgccgcg caccgacgga ggggacatgg gcagagcaat ggtggccagg 120
ctcgggctgg ggctgctgct gctggcactg ctcctaccca cgcagattta ttccagtgaa 180
acaacaactg gaacttcaag taactcctcc cagagtactt ccaactctgg gttggcccca 240
aatccaacta atgccaccac caaggyggct ggtggtgccc tgcagtcaac agccagtctc 300
ttcgtggtct cactctctct tctgcatctc tactcttaag agactcaggc caagaaacgt 360
cttctaaatt tccccatctt ctaaacccaa tccaaatggc gtctggaagt ccaatgtggc 420
aaggaaaaac aggtcttcat cgaatctact aattccacac cttttaaaaa tttttnggga 480
acccaaccca aagggtaaaa aaaaaaaaaa atttggggnt ttttttgggn naaaggggna 540
aaaaaaattt ttcccccccc ccccaaaaaa aaaaaaaaat tttttttttt tttt 594

<210> 440
<211> 1580
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (873)
<223> n equals a,t,g, or c

<400> 440
gcccacgcgt tcgcaaggct gccccatctg gcgctgatta tcctgctgct gccgccaccg 60
ctgctgctgc tctgcaaaat tcagctgctg cctctgtctt gaggacccca gcgcctttcc 120
cccggggcca tgctgcctgc agccacagcc tccctcctgg ggcccctcct cactgcctgc 180
gccctgctgc cttttgccca gggccagacc cccaactaca ccagacccgt gttcctgtgc 240
ggaggggatg tgaaggggga atcaggttac gtggcaagtg aggggttccc caacctctac 300
ccccctaata aggagtgcat ctggaccata acggtccccg agggccagac tgtgtccctc 360
tcattccgag tcttcgacct ggagctgcac cccgcctgcc gctacgatgc tctggaggtc 420
ttcgctgggt ctgggacttc cggccagcgg ctcggacgct tttgtgggac cttccggcct 480
gcgcccctag tcgcccccgg caaccaggtg accctgagga tgacgacgga tgagggcaca 540
ggaggacgag gcttcctgct ctggtacagc gggcgggcca cctcgggcac tgagcaccaa 600
ttttgcgggg ggcggctgga gaaggcccag ggaaccctga ccacgcccaa ctggcccgag 660
tccgattacc ccccgggcat cagctgttcc tggcacatca tcgcgccccc ggaccaggtc 720
atcgcgctga ccttcgagaa gtttgacctg gagccggaca cctactgccg ctatgactcg 780
gtcagcgtgt tcaacggagc cgtgagcgac gactcccgga ggctggggaa gttctgcggc 840
gacgcaktcc cgggctccat ctcctccgaa ggnaatgaac tcctcgtcca gttcgtctca 900
gatctcagtg tcaccgctga tggcttctca gcctcctaca agaccctgcc gcggggcact 960
gccaaagaag ggcaagggcc cggccccaaa cggggaactg agcctaaagt caagctgccc 1020
cccaagtccc aacctccgga gaaaacagag gaatctcctt cagcccctga tgcacccacc 1080
tgcccaaagc agtgccgccg gacaggcacc ttgcagagca acttctgtgc cagcagcctt 1140
gtggtgactg cgacagtgaa gtccatggtt cgggagccag gggagggcct tgccgtgact 1200
gtcagtctta ttggtgctta taaaactgga ggactggacc tgccttctcc acccactggt 1260
gcctccctga agttttacgt gccttgcaag cagtgccccc ccatgaagaa aggagtcagt 1320
tatctgctga tgggccaggt agaagagaac agaggccccg tccttcctcc agagagcttt 1380
gtggttctcc accggcccaa ccaggaccag atcctcacca acctaagcaa gaggaagtgc 1440

ccctctcaac ctgtgcgggc tgctgcgtcc caggactgag acgcaggcca gccccggccc 1500
ctagccctca ggccttcttt cttatccaaa taaatgtttc ttaatgagga atgggtcaga 1560
tctccatgct tatggtaaaa 1580

<210> 441
<211> 1082
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (136)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (462)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (465)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1074)
<223> n equals a,t,g, or c

<400> 441
ctgccgagcg cctcttggag ctgggctttc ccccgcggtg cggcgccagg agccgccttt 60
tccgctgggt gtcactcggg ggtggggaag atggcccatt caaaagcgcc gcgagggggc 120
ccggccagtg cccttnagtg agcgctcgca agaggacggc agaggcccgg cagctcggag 180
ctccgggacc ttgtggcgca tcaggacgcg gctgtccctc tgccgggacc cagagccgcc 240
gccgccgctc tgcctcctgc gtgttagcct cctctgcgcg ctccgggcag gcggccgtgg 300
gagccgctgg ggcgaggacg gcgcgaggct gctgctgctg cccccggccc gcgcggctgg 360
aaacggagag gccgagccaa gcggcggccc ctcttatgct gggaggatgc tggagagtag 420
cggctgcaaa gcgctgaagg agggcgtgct ggagaagcgc anacngggtt gttgcagctc 480
tggaagaaaa agtgttgcat cctcaccgag gaagggctgc tgcttatccc gcccaagcag 540
ctgcaacacc agcagcagca gcaacagcag cagcagcagc agcaacaaca gcccgggcag 600
gggccggccg agccgtccca acccagtggc cccgctgtcg ccagcctcga gccgccggtc 660
aagctcaagg aactgcactt ctccaacatg aagaccgtgg actgtgtgga gcgcaagggc 720
aagtacatgt acttcactgt ggtgatggca gagggcaagg agatcgactt tcggtgcccg 780
caagaccagg gctggaacgc cgagatcacg ctgcagatgg tgcagtacaa gaatcgtcag 840
gccatcctgg cggtcaaatc cacgcggcag aagcagcagc acctggtcca gcagcagccc 900
ccctcgcagc cgcagccgca gccgcagctc cagccccaac cccagcctca gcctcagccg 960
caaccccagc cccaatcaca accccagcct cagccccaac ccaagcctca gccccagcag 1020
ctccamccgt atycgcatyc amattcamat ycamaatctt atccttmatt tggnaaccaa 1080
aa 1082

<210> 442

<211> 1241
<212> DNA
<213> Homo sapiens

<400> 442
agacgagcgt ggcggccgcg gctgctcggg gccgcgctgg ttgcccattg acagcggcgt 60
ctgcagctcg cttcaagatg gccgcttgct cgcattcatt ttctgctgaa cgacttttaa 120
ctttcattgt cttttccgcc cgcttcgatc gcctcgsgcc ggctgctctt tccgggattt 180
tttatcaagc agaaatgcat cgaacaacga gaatcaagat cactgagcta aatccccacc 240
tgatgtgtgt gctttgtgga gggtacttca ttgatgccac aaccataata gaatgtctac 300
attccttctg taaaacgtgt attgttcgtt acctggagac cagcaagtat tgtcctattt 360
gtgatgtcca agttcacaag accagaccac tactgaatat aaggtcagat aaaactctcc 420
aagatattgt atacaaatta gttccagggc ttttcaaaaa tgaaatgaag agaagaaggg 480
atttttatgc agctcatcct tctgctgatg ctgccaatgg ctctaatgaa gatagaggag 540
aggttgcaga tgaagataag agaattataa ctgatgatga gataataagc ttatccattg 600
aattctttga ccagaacaga ttggatcgga aagtaaacaa agacaaagag aaatctaagg 660
aggaggtgaa tgataaaaga tacttacgat gcccagcagc aatgactgtg atgcacttaa 720
gaaagtttct cagaagtaaa atggacatac ctaatacttt ccagattgat gtcatgtatg 780
aggaggaacc tttaaaggat tattatacac taatggatat tgcctacatt tatacctgga 840
gaaggaatgg tccacttcca ttgaaataca gagttcgacc tacttgtaaa agaatgaaga 900
tcagtcacca gagagatgga ctgacaaatg ctggagaact ggaaagtgac tctgggagtg 960
acaaggccaa cagcccagca ggaggtattc cctccacctc ttcttgtttg cctagcccca 1020
gtactccagt gcagtctcct catccacagt ttcctcacat ttccagtact atgaatggaa 1080
ccagcaacag ccccagcggt aaccaccaat cttcttttgc caatagacct cgaaaatcat 1140
cagtaaatgg gtcatcagca acttcttctg gttgatacct gagactgtta aggaaaaaaa 1200
aaaaaaaaaa accccggccg ctcccacttc agattggtaa c 1241

<210> 443
<211> 968
<212> DNA
<213> Homo sapiens

<400> 443
cccacgcgtc cgcaggaagc caactatttg aaatgcacga gaaactaagt tgtatggcaa 60
actctgtaat aaaaaatcta cagtcacgtt ggagatcacc atcccatgaa aattctattt 120
agtattttca gagaaaattg aaggtttttt taaacatcac tggatttctt gattgaggaa 180
acaagttctg aaataatagc acaatttcaa agaagagact ctttgcaaag ttgataacat 240
ttcaaaccct gaaggacagt gacttattat gtwagttcaa tkttgtaagt ycattatgtw 300
agatcctttt tttttttcat aatatgtatt cttggctgct atgcgtggtt tttcaggaaa 360
tttaattatc ttactgagat gtgaaagcaa aactagtaac agaacttaca ttttatttca 420
tgctttctta aacccgtgca tattctggtg aaacatgtaa aatactttaa gtaaaattga 480
acatttttat ttgaattttt gctgaactga taaaggtgtt tatatttttg tttgttkgtt 540
tgtttaattc atgtttgttg ggactgaggt ttaggaagtt tgttactggt taaaaacctc 600
aaatgaaatg cgaaagaatt tgaatttttc ctgcatatgt caactttgga cagctttcaa 660
gaaaaatgag aaaagtttca acttctggcg gttaaaatat taatgcagaa tttactaaga 720
ttttattcat ttgcattagc aaatattcat gcagcagcag ttgactgaaa atttattctt 780
atgagacgta tagtattcat ttttaaatgc atgattgtac attatgtata gacgacaatg 840
tttttaattt ataaatttca ttctttgtta attgcatggg tttttctgca gcttattgtg 900
aataccttgg ttctgttcaa tagaaacatt ttgtatatat traatactga aatatcaaaa 960
aaaaaaaa 968

<210> 444
<211> 1360
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (114)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (302)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (330)
<223> n equals a,t,g, or c

<400> 444
cgccggagcg tcatctgcga ctccaatgcc actgcactgg agcttcccgg ccttcctctt 60
tccctgcccc agcccagcat ccccgcggct gtcccgcaga gtgctccacc gganccccac 120
cgggaagaga ccgtgaccgc caccgccact tcccaggtag cccagcagcc tccagccgct 180
gccgcccctg ggaacaggc cgtcgcgggc cctgcccctc gactgtcccc agcagtacca 240
gcaaagaccg cccagtgtcc cagcctagcc ttgtggggag caaagaggag ccgccgccgg 300
angaaagtgg cagcggcggc gcaagcgcmn aaggagccac aggaggaacg gagccagcag 360
caggatgata tcgaagagct ggagaccaag gccgtgggaa tgtctaacga tggccgcttt 420
ctcaagtttg acatcgaaat cggcagaggc tcctttaaga cggtctacaa aggtctggac 480
actgaaacca ccgtggaagt cgcctggtgt gaactgcagg atcgaaaatt aacaaagtct 540
gagaggcaga gatttaaaga agaagctgaa atgttaaaag gtcttcagca tcccaatatt 600
gttagatttt atgattcctg ggaatccaca gtaaaaggaa agaagtgcat tgttttggtg 660
actgaactta tgacgtctgg aacacttaaa acgtatctga aaaggtttaa agtgatgaag 720
atcaaagttc taagaagctg gtgccgtcag atccttaaag gtcttcagtt tcttcatact 780
cgaactccac ctatcattca ccgcgatctt aaatgtgaca acatctttat caccggccct 840
actggctcag tcaagrttgg agacctcggt ctggcaaccc tgaagcgggc ttcttttgcc 900
aagagtgtga taggtacccc agagttcatg gcccctgaga tgtatgagga gaaatatgat 960
gaatccgttg acgtttatgc ttttgggatg tgcatgcttg agatggctac atctgaatat 1020
ccttactcgg agtgccaaaa tgctgcgcag atctaccgtc gcgtgaccag tggggtgaag 1080
ccagccagtt ttgacaaagt agcaattcct gaagtgaagg aaattattga aggatgcata 1140
cgacaaaaca aagatgaaag atattccatc aaagaccttt tgaaccatgc cttcttccaa 1200
gaggaaacag gagtacgggt agaattagca gaagaagatg atggagaaaa aatagccata 1260
aaattatggc tacgtattga agatattaag aaattaaagg gaaaatacaa agataaaaaa 1320
aaaaaaaaaa aaaaaaaaaa aaaaaacacc caccgtgccg 1360

<210> 445
<211> 1835
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (326)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1229)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1738)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1747)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1758)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1801)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1806)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1831)
<223> n equals a,t,g, or c

<400> 445
tcgacccacg cgtccgggat gaggcccggc ctctcatttc tcctagccct tctgttcttc 60
cttggccaag ctgcagggga tttgggggat gtgggacctc caattcccag ccccggcttc 120
agctctttcc caggtgttga ctccagctcc agcttcagct ccagctccag gtcgggctcc 180
agctccagcc gcagcttagg cagcggaggt tctgtgtccc agttgttttc caatttcacc 240
ggctccgtgg atgaccgtgg gacctgccag tgctctgttt ccctgccaga caccamcttt 300
cccgtggaca gagtggaacg yttggnaatt cacagctcat gttctttctc agaagtttga 360
gaaagaactt tccaaagtga gggaatatgt ccaattaatt agtgtgtatg aaaagaaact 420
gttaaaccta actgtccgaa ttgacatcat ggagaaggat accatttctt acactgaact 480
ggacttcgag ctgatcaagg tagaagtgaa ggagatggaa aaactggtca tacagctgaa 540
ggagmstttt ggtggaagct cagaaattgt tgaccagctg gaggtggaga taagaaatat 600
gactctcttg gtagagaagc ttgagacact agacaaaaac aatgtccttg ccattcgccg 660

agaaatcgtg gctctgaaga ccaagctgaa agagtgtgag gcctctaaag atcaaaacac 720
ccctgtcgtc caccctcctc ccactccagg gagctgtggt catggtggtg tggtgwacat 780
cagcaaaccg tctgtggttc agctcaactg gagagggttt tcttatctat atggtgcttg 840
gggtagggat tactctcccc agcatccaaa caaaggactg tattgggtgg cgccattgaa 900
tacagatggg agactgttgg agtattatag actgtacaac acactggatg atttgctatt 960
gtatataaat gctcgagagt tgcggatcac ctatggccaa ggtagtggta cagcagttta 1020
caacaacaac atgtacgtca acatgtacaa caccgggaat attgccagag ttaacctgac 1080
caccaacacg attgctgtga ctcaaactct ccctaatgct gcctataata accgcttttm 1140
atatgctaat gttgcttggc aagatattga ctttsctgtg gatgagaatg gattgtgggt 1200
tatttattca actgaagcca gcactggtna catggtgatt agtaaactca atgacaccac 1260
acttcaggtg ctaaacactt ggtataccaa gcagtataaa ccatctgctt ctaacgcctt 1320
catggtatgt ggggttctgt atgccacccg tactatgaac accagaacag aagagatttt 1380
ttactattat gacacaaaca cagggaaaga gggcaaacta gacattgtaa tgcataagat 1440
gcaggaaaaa gtgcagagca ttaactataa ccctttttgac cagaaacttt atgtctataa 1500
cgatggttac cttctgaatt atgatctttc tgtcttgcag aagccccagt aagctgttta 1560
ggagttaggg tgaaagagaa aatgtttgtt gaaaaaatag tcttctccac ttacttagat 1620
atctgcaggg gtgtctaaaa gtgtgttcat tttgcagcaa tgtttargtg catagttcta 1680
ccacactaga gatctaggac atttgtcttg atttggtgag tctcttgggg atcatctngc 1740
ytttcangcg cmttttgnca taaagtcygt cyagggtggg attgtcagag gtctaggggc 1800
ncttgngggc ctaatggaac ccttctgtga ngaag 1835

<210> 446
<211> 1355
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<400> 446
ggcacgagcg cgtcgcacgg gaagtcgaag cggagatccc ggggtcgcgc gaganccgca 60
agcggagttg gtgggcgcta tgctatcacc cgaggcagag cgagtgctgc ggtaccttgt 120
agaagtggag gagctcgccg aggaggtgct ggcggacaag cggcagattg tggacctgga 180
cactaaaagg aatcagaatc gagagggcct gagggccctg cagaaggatc tcagcctctc 240
tgaagatgtg atggtttgct tcgggaacat gtttatcaag atgcctcacc ctgagacaaa 300
ggaaatgatt gaaaaagatc aagatcatct ggataaagaa atagaaaaac tgcggaagca 360
acttaaagtg aaggtcaacc gcctttttga ggcccaaggc aaaccggagc tgaagggttt 420
taacttgaac cccctcaacc aggatgagct taaagctctc aaggtcatct tgaaaggatg 480
agactcaaga accaagatgg gggaccagca accccccagg gtcatggagg acccaggacc 540
ctccaacctt gacacctgta aggacaggat ctgccctgta agggccagcc gtcaggaatc 600
tggccatgaa aacctctttg tagtgcttgg ctactctgtg atggcaggag ggaaccttca 660
gcctgtctgg ctgctggacc tggacaccag ggctcggtgg acacaagatc tattgacggg 720
ccttggtagc caccagtggg tgtgtggggc agtggctgtg gggtgtaag aatgactgca 780
acaggcactt cccaacaatg gcctgctgtt cacatggacc ctgagcaagg aaggagggag 840
ggaggggcag agtggagtgt cattccagca ttcctctcag aagggagaga ggttttcagg 900
ctggtgccat gcgattggaa taaagcagga ggctcatggg tggttgctga atgaagaaca 960
gaatcttggt gctttgtggc tcaccacagc catctgtggg gcaggcacac acacctcccg 1020
ccagctccaa ttttgcactt tttccctgct tgattccaag agtaggtgct gcctagcagc 1080
ccttcgtggc cactctttac tcaggagggc cttgcagagt cctgcaccag gcctgggtga 1140

gtggatgcgc ctcttaccat atgacacgtg tcaagatgcc cttccgcccc ctctgaaagt 1200
ggggcccggc cagcactgct cgttactgtc tgccttcagt ggtctgaggt cccagtatga 1260
actgccgtga agtcaaaact cttatgtgtt cattaagggc tcaataaatg ttagctgaat 1320
gaawaaaaaa aaaaaaaaaa amawaaaaaa aaaaa 1355

<210> 447
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (153)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (313)
<223> n equals a,t,g, or c

<400> 447
tgcctctgtg tgtgtgcaag acagagagat aggctatttg tcaagtcagc tagttgccta 60
ggtatctttg tctcacatct ggctgtttcc tcctagagaa ccatccagtt ggctttccag 120
gtctggaggt gagctaatgg atgagtgaat atnagcagtg ggtgttcctc atctctttga 180
ggatttgcct cagagttcac taccaaggga tttctggaac taggwgccat tctttacatc 240
agttcttgag ggttctttga tatcaggggc aaaatgatcc cttctctttt ctttcttata 300
tcctgtgctt tgnctcctgg gtgatttctc ttcaagtcag ttgtgggagg tgcctaggaa 360
caacgctaac acggg 375

<210> 448
<211> 1393
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1360)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1383)
<223> n equals a,t,g, or c

<400> 448
tcttttacat gtttaaattt aaaccattct tcgtgacccc ttttcttggg agattcatgg 60
caagaacgag aagaatgatg gtgcttgtta ggggatgtcc tgtctctctg aactttgggg 120
tcctatgcat taaataattt tcctgacgag ctcaagtgct ccctctggtc tacaatccct 180
ggcggctggc cttcatccct tgggcaagca ttgcatacag ctcatggccc tccctctacc 240
ataccctcca cccccgttcg cctaagctcc cttctccggg aatttcatca tttcctagaa 300
cagccagaac atttgtggtc tatttctctg ttagtgttta accaaccatc tgttctaaaa 360

gaagggctga actgatggaa ggaatgctgt tagcctgaga ctcaggaaga caacttctgc 420
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<211> 1663
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (57)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (180)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (621)
<223> n equals a,t,g, or c

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<211> 1380
<212> DNA
<213> Homo sapiens

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<210> 451
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<212> DNA

<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (865)
<223> n equals a,t,g, or c

<400> 451
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<210> 452
<211> 1642
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (147)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (150)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1608)
<223> n equals a,t,g, or c

<400> 452

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<211> 2254
<212> DNA
<213> Homo sapiens

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gagtttgatt ataaaaaaaa aaaaaaaaaa aaaa 2254

<210> 454
<211> 1931
<212> DNA
<213> Homo sapiens

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aaaaaaaaaa a 1931

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<211> 771
<212> DNA
<213> Homo sapiens

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<210> 456
<211> 1169
<212> DNA
<213> Homo sapiens

<220>
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<222> (1164)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1167)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1169)
<223> n equals a,t,g, or c

<400> 456
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<211> 3249
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3234)
<223> n equals a,t,g, or c

<400> 457
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gaggggccgc gatactggtt gcccgcggtg taagcagaat tcgacgtgta tcgctgccgt 180
caagatggag gggcctttgt ccgtgttcgg tgaccgcagc actggggaaa cgatccgctc 240
ccaaaacgtt atggctgcag cttcgattgc caatattgta aaaagttctc ttggtccagt 300
tggcttggat aaaatgttgg tggatgatat tggtgatgta accattacta acgatggtgc 360
aaccatcctg aagttactgg aggtagaaca tcctgcagct aaagttcttt gtgagctggc 420
tgatctgcaa gacaaagaag ttggagatgg aactacttca gtggttatta ttgcagcaga 480
actcctaaaa aatgcagatg aattagtcaa acagaaaatt catcccacat cagttattag 540
tggctatcga cttgcttgca aggcaagcag tgcgttatat caatgaaaac ctaattgtta 600
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aaatcattgg aataaatggt gatttctttg ctaacatggt agtagatgct gtacttgcta 720
ttaaatacac agacataaga ggccagccac gctatccagt caactctgtt aatattttga 780
aagcccatgg gagaagtcaa atggagagta tgctcatcag tggctatgca ctcaactgtg 840
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tccacaact 3249

<210> 458
<211> 1916
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1895)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (1902)
<223> n equals a,t,g, or c

<400> 458
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aaaatgacaa tttctttatt gctacagagt atcctctata agttattaaa cgagtgtaat 360
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gttacagatg gcgtagaagt cacaagtctg ttaattggac tgttgcttct ttgcctgttc 600
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aatgcaacac aaaaacatga agtgactgcc cagaggtaga gttagtgttt aggtggaaag 960
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attttacttt aaaatgagaa tctggtgtta ctgtatttta tcgttttcaa taaaacttct 1860
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<210> 459
<211> 2773
<212> DNA
<213> Homo sapiens

<400> 459
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aaggtatata ccctctcagt gtctggagac cggctgattg tgggaacagc aggccgcaga 660
gtgttggtgt gggacttacg gaacatgggt tacgtgcagc agcgcaggga gtccagcctg 720
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cgcgatctag aac 2773

<210> 460
<211> 2031
<212> DNA
<213> Homo sapiens

<400> 460
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tttcttcaat cacatctgaa taaatcactt gaagaaagct tatagcttca ttgcaccatg 180
tgtggcattt gggcgctgtt tggcagtgat gattgccttt ctgttcagtg tctgagtgct 240
atgaagattg cacacagagg tccagatgca ttccgttttg agaatgtcaa tggatacacc 300

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aactgctgct ttggatttca ccggttggcg gtagttgacc cgctgtttgg aatgcagcca 360
attcgagtga agaaatatcc gtatttgtgg ctctgttaca atggtgaaat ctacaaccat 420
aagaagatgc aacagcattt tgaatttgaa taccagacca aagtggatgg tgagataatc 480
cttcatcttt atgacaaagg aggaattgag caaacaattt gtatgttgga tggtgtgttt 540
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<210> 461
<211> 1839
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1496)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1832)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1839)
<223> n equals a,t,g, or c

<400> 461

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gcccaggccg agcacgatgc cccctaaaaa gggaggtgat ggaattaaac cacccccaat 180
cattggaaga tttggaacct cactgaaaat tggtattgtt ggattgccaa atgttgggaa 240
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<210> 462
<211> 779
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (26)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (731)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (737)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (759)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (762)
<223> n equals a,t,g, or c

<400> 462
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gaggcaggga agacaagcca ggcacgatgg ccaccttccc accagcaacc agcgcccccc 180
agcagccccc aggcccggag gacgaggact ccagcctgga tgaatctgac ctctatagcc 240
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<210> 463
<211> 1717
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (27)
<223> n equals a,t,g, or c

<400> 463
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<210> 464
<211> 828
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (787)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (819)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (827)
<223> n equals a,t,g, or c

<400> 464
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gaagccggta caggtgccct gcggacacgt cttttgctct gcatgcctgc aggaatgtct 180
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tttcttcctg tccaagatcc ggtcccacgt ggctacttgt tccaaatacc agaattacat 360
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gaatcaggtg ttgcagcgct ccatcatcga ccagtgagca gagtccgtgc ttgctatctg 720
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<210> 465
<211> 1173
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (137)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1166)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1168)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1171)
<223> n equals a,t,g, or c

<400> 465
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gcgtttcagg cccttgntca ctcaatgacc tccagttctt tagatacaac agtaaagaca 180
ggaagtctca gcccatggga ctctggagac aggtggaagg aatggaggat tggaagcagg 240
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agaataacag aagcagcgga cattctggaa atattactat gatggaaagg actacattga 420
attcaacaaa gaaatcccag cctgggtccc cttcgaccca gcagcccaga taaccaagca 480
gaagtgggag gcagaaccag tctacgtgca gcgggccaag gcttacctgg aggaggagtg 540
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tccttgccta gcaaaaaaaa aaaaangngg ngg 1173

<210> 466
<211> 521
<212> DNA
<213> Homo sapiens

<400> 466
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tgctggacat gtcctacgag cagctgatgc agctgtacag tgcgcgccag gcggcggctg 180
aaccggggcc tgcggcggaa gcagcactcc ctgctgaagc gcctgcgcaa ggccaagaag 240
gaggcgccgc ccatggagaa gccggaagtg gtgaagacgc acctgcggga catgatcatc 300
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taatggctca gytaataaag gcgsacatga ctccaaaaaa a 521

<210> 467
<211> 1428
<212> DNA
<213> Homo sapiens

<400> 467
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tgagcaccct tacctgaccc catcccccga atcccctgag cactgggcca gcccctcacc 180
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<210> 468
<211> 3463

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1187)
<223> n equals a,t,g, or c

<400> 468
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gccctgccgc gccccatccg caacctggag gtcaagttca ccaagatatt tatcaacaat 180
gaatggcacg aatccaagag tgggaaaaag tttgctacat gtaacccttc aactcgggag 240
caaatatgtg aagtggaaga aggagataag cccgacgtgg acaaggctgt ggargctgca 300
caggttgcct tccagagggg ctcgccatgg cgccggctgg atgccctgag tcgtgggcgg 360
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gaatgataaa ataaaattgg atatttgaga aaaaaaaaaa aaa 3463

<210> 469
<211> 621
<212> DNA
<213> Homo sapiens

<400> 469
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ctgggagact gaaaaaatgc agaccgccgg ggcattattc atttctccag ctctgatccg 120
ctgttgtacc aggggtctaa tcaggcctgt gtctgcctcc ttcttgaata gcccagtgaa 180
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gaccagtgtt gtctcccggg acattgacac agcagccaag tttattggtg ctggggcagc 300
cacagttggt gtggctggtt caggggctgg cattggaacc gtgtttggca gcttgatcat 360
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tgccctgtct gaggccatgg ggcttttctg tttgatggtc gccttcctca tcctcttcgc 480
catgtgaggc tccatggggg gtcaccggcc tgttgctact gcaactccac accattcttg 540
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aaaaaaaaaa aaaaaaaaaa a 621

<210> 470
<211> 1833
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (126)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (386)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (524)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1798)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1812)
<223> n equals a,t,g, or c

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tgccggctcc ggtccccggc gcggctgtcc gagcccctgc ggcgggcgga cgatggtgtg 120
gcggancacg cagacgcggg cggcmgcggc ggcgggcatg aaggaggatg gaagggcagg 180
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<210> 471
<211> 3202
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3160)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3180)
<223> n equals a,t,g, or c

<400> 471
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ggctcatagt cgtatcaggg gtcgggacca aggcccaaat gtctgtgccc ttcaacagat 180
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<210> 472
<211> 941
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (927)
<223> n equals a,t,g, or c

<400> 472
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agcaaggctc tattcctagt ctccagccat gcctgtggca acctgagccc gctctcagca 180
cattggaccc aggcagatgy aaaaaattca cagaactatg atttggactc aagggtttgt 240
agatttcctc cttcattcta atttcagtgt ctaaaattct tgcatccrtg aacgagctgg 300
gcatttgatg agacagggcy gaatactgca gttttcctcc tagaaatcmt ctggggcatt 360
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tcttgwaaca gcctgactcc tgccwgccct ayrgaagttc cttttatgca ttggaggaaa 840
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<210> 473
<211> 1279

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1144)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1273)
<223> n equals a,t,g, or c

<400> 473
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ggaatgagtg tgtggttgtc attagggtgg acaaagaaaa aggatatatt gatttgtcaa 120
aaagaagagt ttctccagag gaagcaatca aatgtgaaga caaattcaca aaatccaaaa 180
ctgtttatag cattcttcgt catgttgctg aggtgttaga atacaccaag gatgagcagc 240
tggaaagcct attccagagg actgcctggg tctttgatga caagtacaag agacctggat 300
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atttgaatga agatgaacgg gaagtactca ttaataatat taataggcgc ttgaccccac 420
aggctgtcaa aattcgagca gatattgaag tggcttgtta tggttatgaa ggcattgatg 480
ctgtaaaaga agccctaaga gcaggtttga attgttctac agaaaacatg cccattaaga 540
ttaatctaat agctcctcct cggtatgtaa tgactacgac aaccctggag agaacagaag 600
gcctttctgt cctcagtcaa gctatggctg ttatcaaaga gaagattgag gaaaagaggg 660
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gaaccaagtt tantttggg 1279

<210> 474
<211> 3209
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (427)
<223> n equals a,t,g, or c

<400> 474
caactcccgg gacacatcct tcgagcagca tgtgctgtgg caacgggcgg gaagggcgtt 60
gacctggtct tgaactcctt ggcggaagag aagctgcarg ccagcgtgag gtgcttggct 120
acgcacggtc gcttcctgga aattggcaaa ttcgaccttt ctcagaacca mccgctcggc 180

atggctatct tcctgaagaa cgtgacatcc acggggtcct actggatgcg ttcttcaaac 240
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gtggtacggc ccctcaagtg cacggtgttc catggggccc aggtggagga cgccttccgc 360
tacatggccc aagggaagca cattggcaaa gtcgtcgtgc aggtgcttgc ggaggagccg 420
gasagtngct gaagggggcc aaacccaagc tgatgtcggc catctccaag accttctgcc 480
cggcccacaa gagctacatc atcgctggtg gtctgggtgg cttcggcctg gagttggcgc 540
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aaaaaaaaaa aaaaaaaama mgcgtccgc 3209

<210> 475
<211> 833
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (58)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (73)
<223> n equals a,t,g, or c

<400> 475
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ttcggacacg agncagagat ggctcccaat gcttcctgcc tctgtgtgca tgtccgttcc 120
gaggaatggg atttaatgac ctttgatgcc aacccatatg acagcgtgaa aaaaatcaaa 180
gaacatgtcc ggtctaagac caaggttcct gtgcaggacc aggttctttt gctgggctcc 240
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caccttaccc tgaaagtggt gaagcccagt gatgaggagc tgcccttgtt tcttgtggag 360
tcaggtgatg aggcaaagag gcacctcctc caggtgcgaa ggtccagctc agtggcacaa 420
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aatggaaaga gactggaaga tgggaagatg atggcagatt acggcatcag aaagggcaac 540
ttactcttcc tggcatstta ttgtattgga gggtgaccac cctgggcatg gggtgttggc 600
aggggtcaaa aagcttattt cttttaatct cttactcaac gaacacatct tctgatgatt 660
tcccaaaatt aatgagaatg agatgagtag agtaagattt gggtgggatg ggtaggatga 720
agtatattgc ccaactctat gtttctttga ttctaacaca attaattaag tgacatgatt 780
tttactaatg tattactgag actagtaaat aaatttttaa ggcaaaatag agc 833

<210> 476
<211> 1141
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (11)
<223> n equals a,t,g, or c

<400> 476
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gaggaacaaa gagcttataa atacattagg acctggaatt cagttgtcga gccaggacgg 120
tgacagcgtt taacaaagct tagagaaacc tccaggagac tgctatcatg gcagagaagc 180
ccaagctcca ctacttcaat gcacggggca gaatggagtc cacccggtgg ctcctggctg 240
cagctggagt agagtttgaa gagaaattta taaaatctgc agaagatttg gacaagttaa 300
gaaatgatgg atatttgatg ttccagcaag tgccaatggt tgagattgat gggatgaagc 360
tggtgcagac cagagccatt ctcaactaca ttgccagcaa atacaacctc tatgggaaag 420
acataaagga gagagccctg attgatatgt atatagaagg tatagcagat ttgggtgaaa 480
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aagactacct tgttggcaac aagctgagcc gggctgacat tcatctggtg gaacttctct 660
actacgtcga ggagcttgac tccagtctta tctccagctt ccctctgctg aaggccctga 720
aaaccagaat cagcaacctg cccacagtga agaagtttct acagcctggc agcccaagga 780
agcctcccat ggatgagaaa tctttagaag aagcaaggaa gattttcagg ttttaataac 840
gcagtcatgg aggccaagaa cttgcaatac caatgttcta aagttttgca acaataaagt 900
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gatctgatgt gaattcagat ttccaatctt ctcctagcca accattttcc tggaattaaa 1080
aattcagtaa aaaaggaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaag 1140
g 1141

<210> 477
<211> 1102
<212> DNA
<213> Homo sapiens

<400> 477
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agtccattgg caagtttggc ctggccttag ctgttgcagg aggcgtggtg aactctgcct 180
tatataatgt ggatgctggg cacagagctg tcatctttga ccgattccgt ggagtgcagg 240
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<210> 478
<211> 4201
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4077)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4161)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4186)
<223> n equals a,t,g, or c

<400> 478
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gctccccata ctagtcgccg atatttggag ttcttacaac atggcagaca ttgacaacaa 180
agaacagtct gaacttgatc aagatttgga tgatgttgaa gaagtagaag aagaggaaac 240
tggtgaagaa acaaaactca aagcacgtca gctaactgtt cagatgatgc aaaatcctca 300
gattcttgca gcccttcaag aaagacttga tggtctggta gaaacaccaa caggatacat 360
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c 4201

<210> 479
<211> 787
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (780)
<223> n equals a,t,g, or c

<400> 479
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ccggatgata gtgctcaggt taatgccagt gggagggcgg cgcccaatag taacttcctt 120
tggaggttgt agtaccgccc ccagagccaa ttttccactt ccgcktccgg cgctgcggca 180
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aagtatatgg gaccttaagc tcaccttctt tacttgtatc aaatgatgac tggtatactg 660
gtctcccatc cctttgcttg tggcaggaga tggcttaaat aaataactta aayttaaaaa 720
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaactn 780
ggggccg 787

<210> 480
<211> 731
<212> DNA
<213> Homo sapiens

<400> 480
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tccctgcagt gtcggcattg taaataaagc ctgagcactt gctgatgcga aaaaaaaaaa 720
aaaaaaaaaa a 731

<210> 481
<211> 1119
<212> DNA
<213> Homo sapiens

<400> 481
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ccccagtccc ccccacccgc gcgtggcggc gccggctccc tagccaccgs ggccccaccc 180
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ggaaagactg ttccaaaaac agtggataat tttgtggcct tagctacagg agagaaagga 480
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ataaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaagg 1119

<210> 482
<211> 2056
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (137)
<223> n equals a,t,g, or c

<400> 482
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gcgcccgggc ccgcgacccc cgcacccagc tccgcagacc ggcgggcgcg cgcgggctct 120
ggaggccacg ggcatgnatg cttcgggtcc tggtgggggc tgtcctccct gccatgctac 180
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aaamaggggg gggccc 2056

<210> 483
<211> 887
<212> DNA
<213> Homo sapiens

<400> 483
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attaatttca agaaaaatat cttgagtttt aagaaataaa catctccaga aaaggagaaa 180
gtcgatttta taaaatgtcg caactctcca acatttgggg tagtgactcc ttttttgtta 240
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tttttgatgt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aataaaa 887

<210> 484
<211> 1878
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1446)
<223> n equals a,t,g, or c

<400> 484
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actatgagcc cgaggccttc ccctctccca gagcgcagag gctttgaagg ctacctctgg 120
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aaaaaaaaaa aaaaaaa 1878

<210> 485
<211> 1566
<212> DNA
<213> Homo sapiens

<400> 485
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tagcaaactt caggagagct actttctatc caaataattt aaaaaacact tttcacctac 120
tcctttcatg gttataacac attggcagac tttttgctgg ctctgggagc catgatttta 180
atcacattct gcaaggtgac aaatgtcata cattccacat tgtgtggtag ccatctcttt 240
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ctaaaataac attgtacatc caagagaggg aagaagagta tgtcagtata ttatgcagaa 420
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aaaatt 1566

<210> 486
<211> 3046
<212> DNA
<213> Homo sapiens

<400> 486
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ctatcaggcc agcgttttaa aactagaaaa agagatgaaa aagagaggtt tgaccctact 180
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<210> 487
<211> 1904
<212> DNA
<213> Homo sapiens

<400> 487

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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1904

<210> 488
<211> 827
<212> DNA
<213> Homo sapiens

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<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (826)
<223> n equals a,t,g, or c

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<210> 489
<211> 1926
<212> DNA
<213> Homo sapiens

<400> 489
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<210> 490
<211> 1461
<212> DNA
<213> Homo sapiens

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<222> (1432)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1452)
<223> n equals a,t,g, or c

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<210> 491
<211> 805
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (20)
<223> n equals a,t,g, or c

<400> 491
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aaaaaaaaaa aaaaaaaaaa aaaaa 805

<210> 492
<211> 2269
<212> DNA
<213> Homo sapiens

<400> 492
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<210> 493
<211> 4108
<212> DNA
<213> Homo sapiens

<400> 493
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tcaattttgg agcgcagtag ctatgttaaa gatgaactat ttggtctcat tgaagccaac 3960
acagaacttg ctgctgtgtt ttttcttcag tgataaataa aatacttaca gaatttgttt 4020
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gaggtttttt tttacttgaa tttttaat 4108

<210> 494
<211> 2209
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (352)
<223> n equals a,t,g, or c

<400> 494
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ttcatgggca tcagcccccct cccgggcgga gagcgcttcc cgtacccttc tttccactgg 120
gaccccatcc gggacccctt gagggatcct taccragaac ttgacattca ccggagagac 180
ccgctgggca rggacttcct gctaaggaac gacccgytcc accggctctc gactycccgg 240
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caccaccacc accacccgct gtctgtggac cctcggcggg agcacgagcg gngaggccac 360
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aacaagaccc ctccgacagc agcgctgagc gcacctcccc cgctcatctc cacgctgggg 600
ggccgcccgg tctctcccag aaggacgact cctctgtccg cagagataag ggagaggccc 660
ccttccccaca cgctgaagga tatcgaggcc cgataagccg agaacaggag caagaacgag 720
gaagaagaaa ccctaggcag acaccaggcc aggcttgaga gacagaactc ctgcatggct 780
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gcacattttg aaatgttttg tatattatat gttgagattt ttcagatctt ttagcccagt 900
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gagaagtcca cgccatccat catgcaaaat tctttcagat gaggtgggaa ggccgtgtac 1080
atagttatgt aaaaagagat tgcttcatga gctaatggtt catatatgca aaagggtaag 1140
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gcaaccagtg ccagggaggg tgggatttgc cagatgccaa aatcagggga cgggtggtgg 1620
tgtctgtcag acacacacag gtcgccagtg acttcacaca cacctcatgt gagaaccatg 1680
cctttttttag tgtgtcctat ttcatacctg tacacacttc ctcgttttgt aatgagattt 1740
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ttcactgtat tcaataactg acggatgtaa ggtgcacgtt tcctgatgtg acgcactgta 1860

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tgtaaaatat atgtatgaaa taaaattagt tccatttggt cttctagtat attaaagtgc 2160
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<210> 495
<211> 1677
<212> DNA
<213> Homo sapiens

<400> 495
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aggccaggtc agatggacaa tcggagcaag ctccggaaca tcgtggagct gcgcctggca 120
ggcctggaca tcacagatgc ctccctgcgg ctcatcatcc gccacatgcc cctgctctcc 180
aagctccacc tcagttactg taaccacgtc accgaccagt ctatcaacct gctcactgct 240
gttggcacca ccacccgaga ctccttaacc gagatcaacc tgtctgactg caataaggtc 300
actgatcagt gcctgtcctt cttcaaacgc tgtggaaaca tctgtcatat tgacctgagg 360
tactgcaagc aagtcaccaa ggaaggctgt gagcagttca tagccgagat gtctgtgagt 420
gtccagtttg ggcaagtaga agaaaaactc ctgcaaaaac tgagttagtc caaggataag 480
tatgtaaata cggggcgggc tctgggaggg gagagacttt acaaaaatga gggcttttat 540
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agggagaagc tgttcaacca cccgtttggg ggatgagtga gccgacactt tcctttggtc 660
tttctgaatc gtaactgcac tgctttctgg accatttcta aggcggcctt tacaagaaga 720
cattcctgtc ggagaggagg gtggacttcg gagaaattct catactgaag catgagctta 780
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tgggtgttga cataaagtgg accacacacc acatctgctg ccgtcttgac acttttttt 900
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ggtggtgttt cctagacctt ccctgatgcg attttacctt tgttgaattt gtataaacaa 1560
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tttaagccca gagtcagtaa acactgtttt gaagtccaaa aaaaaaaaaa aaaaaaa 1677

<210> 496
<211> 1702
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1691)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1701)
<223> n equals a,t,g, or c

<400> 496
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cgttttggcg tgcctgcgct ctctgcaggc agaagcgaac aaagacccag caagagaagg 120
cagaggctaa gacccatccc gtatctgctc tcctgaaata attctggagt catgcctgaa 180
atgccagagg acatggagca ggaggaagtt aacatcccta ataggagggt tctggttact 240
ggtgccactg ggcttcttgg cagagctgta cacaaagaat ttcagcagaa taattggcat 300
gcagttggct gtggtttcag aagagcaaga ccaaaatttg aacaggttaa tctgttggat 360
tctaatgcag ttcatcacat cattcatgat tttcagcccc atgttatagt acattgtgca 420
gcagagagaa gaccagatgt tgtagaaaat cagccagatg ctgcctctca acttaatgtg 480
gatgcttctg ggaatttagc aaaggaagca gctgctgttg gagcatttct catctacatt 540
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cccctaaatt tgtatggcaa aacaaaatta gatggagaaa aggctgtcct ggagaacaat 660
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agtgctgtga ctgttatgtt tgataaagtg cagttcagca acaagtcagc aaacatggat 780
cactggcagc agaggttccc cacacatgtc aaagatgtgg ccactgtgtg ccggcagcta 840
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tagtttattt gtgttgggtt cttttttttt tttaaatgaa aagtatagta tgtggcactt 1200
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attatttgct ttgcctgagc tcagatcaaa atgtttgaag aaaggaactt tatttttgca 1620
agttacgtac agtttttatg cttgagatat ttcaacatgt tatgtatatt ggaaaaataa 1680
agttcctttc ntcaaacatt nt 1702

<210> 497
<211> 2376
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2354)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2375)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2376)
<223> n equals a,t,g, or c

<400> 497
ggctcnaaca tccttttgct gtgacgagct acgggaagaa tctgtatttc acagactgga 60
agatgaattc cgtggttgct ctcgatcttg caatttccaa ggagacggat gctttccaac 120
cccacaagca gacccggctg tatggcatca ccacggccct gtctcagtgt ccgcaagcca 180
taactactgc tcagtgaaca atggcggctg cacccaccta tgcttggcca ccccagggag 240
caggacctgc cgttgccctg acaacacctt gggagttgac tgtatcgaac agaaatgaag 300
acaagagtgc cttatttcct ttccaagtat ttcacagcaa caywytactt gaagcaactt 360
ggtccagatt gaaaagtgtc ctctggctga gtggccacta ggcccagacc cagcccagcc 420
tgagccccaa caacttttcc ctcactgttc cccaaaacat gcaccctgga cttctctaat 480
agaaaagtct ccacccctac acaaggacag aaccctccac ccctaccccc aaccctcaga 540
cagacttata cacccctgag tgaggattac atgcccatcc cagtgtccta ggaccttttc 600
ccaatactag ccccccagtg gtgaacagaa cctcccaaat ttgagttgca cccttccctg 660
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ggattttttt gatgtgcctt aaattatacc aaagattact aattattcct ctttgcccaa 1140
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caatttgttt agaaaacatc tcctgaccat atcagtagct cgtgttatct ttttatcaac 1560
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aaccactgaa ggtgcttatt aactgttctc ccagatttgt acaagtattg gatgattcct 2280
tgagtttaca gctgtacaaa tagtgtggaa aataaacttt ttttaaaaaa gaaaaaaaaa 2340

aaaaaaaaaa aaanaaaaaa aaaaaaaaaa aaaann 2376

<210> 498
<211> 840
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (840)
<223> n equals a,t,g, or c

<400> 498
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gaagatggcg gtggagtcgc gcgttaccca ggaggaaatt aagaaggagc cagagaaacc 120
gatcgaccgc gagaagacat gcccactgtt gctacgggtc ttcaccacca ataacggccg 180
ccaccaccga atggacgagt tctcccgggg aaatgtaccg tccagcgagt tgcagatcta 240
cacttggatg gatgcaacyt tgaaagaact gacaagctta gtaaaagaag tctacccaga 300
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tggctatcga gttaaggaga ttggcagcac catgtctggc agaaagggga ctgatgattc 420
catgaccctg cagtcgcaga agttccagat aggagattac ttggacatag caattacccc 480
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ttgttgaatt tatttttccg tcagttatgt aaaataaaca tactcttctt cctcccctga 600
ttattgccat taagccttta aattctaaac aaattataat gcatcatcta tttaggagtt 660
agatttggat gtgctattgt atgattacga atagtctgta tgtttcaagc ccttctgtaa 720
aatatgaaga aaagtgctct tagcattctg tgtaaaactg tactgttaaa tatatgtgtg 780
taatcaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaan 840

<210> 499
<211> 461
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (452)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (455)
<223> n equals a,t,g, or c

<400> 499
ggcacagctt ccctcctctt cctttctccg ccatcgtggt gtgttcttga ctccgctgct 60
cgccatgtct tctcacaaga ctttcaggat taagcgattc ctggccaaga aacaaaagca 120
aaatcgtccc attccccagt ggattcggat gaaaactgga aataaaatca ggtacaactc 180
caaaaggaga cattggagaa gaaccaagct gggtctataa ggaattgcac atgagatggc 240
acacatattt atgctgtctg aaggtcacga tcatgttacc atatcaagct gaaaatgtca 300
ccactatctg gagatttcga cgtgttttcc tctctgaatc tgttatgaac acgttggttg 360
gctggattca gtaataaata tgtaaggcct ttcyttttta aaaaaaaaaa aaaaacyyrr 420

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<210> 500
<211> 2782
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2620)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2641)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2643)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2712)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2742)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2759)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2779)
<223> n equals a,t,g, or c

<400> 500
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aagaagttca agtacggtat tgaagagcat ggtaaggtga aaatgcgagg ggggttgctg 120
cgaacctaca tcatcagtat cctcttcaag tctatctttg aggtggcctt cttgctgatc 180
cagtggtaca tctatggatt cagcttgagt gctgtttaca cttgcaaaag agatccctgc 240
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gcgctgagcc ctgccaaaga ctgtgggtct caaaaatatg cttatttcaa tggctgctcc 480

tcaccaaccg ctcccctctc gcctatgtct cctcctgggt acaagctggt tactggcgac 540
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tacagtgcag aacaaaatcg aatggggcag gcgggaagca ccatctctaa ctcccatgca 660
cagccttttg atttccccga tgataaccag aattctaaaa aactagctgc tggacatgaa 720
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<210> 501
<211> 1249
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c

<400> 501

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cacacaggaa ttctgctgag gtccccccctc cttccggcca atggcagaag tgggggaaaa 240
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gtctcccttt agagccgtct tttgcaggga gcgggaagtg acaagagctc agatctccct 420
cccgatctcc ctccccacct ccgaagtctc ctccgtggac cacaggtgga tctttgtgcg 480
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ctaccctcct tttttttttt gtattttggc tgctagagtg cagcatttgt gacacgtatt 1080
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<210> 502
<211> 1358
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1334)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1347)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1349)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1351)
<223> n equals a,t,g, or c

<400> 502
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tatccacttt tctyggataa tcaggaggtg ccccagtsgt cacagtgtgg cattccgagt 120
tggggcgggt ggtcgggtca agatagcagc agcaggtgtc agggctcaag acaccacccc 180

ctccagcttc tggggcccag gagcctctcc ctgctacagg gggtgggggt cctgctcagc 240
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gaggctggag ggcagggagg gatcactttg gagcccaggg agattggagg gctggcagtg 1260
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<210> 503
<211> 501
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (457)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (492)
<223> n equals a,t,g, or c

<400> 503
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atagcgctca cgcaagcatg gttaacgtcc ctaaaacccg ccggactttc tgtaagaagt 120
gtggcaagca ccaaccccat aaagtgacac agtacaagaa gggcaaggat tctctgtacg 180
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gagataagaa gagaaagggc caagtgatcc agttctaagt gtcatctttt attatgaaga 420
caataaaatc ttgagtttat gttcaaaaaa aaaaaanggg gggggcccgg tacccawtcg 480
cctatagggg gncgtttaaa a 501

<210> 504
<211> 2011
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1941)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1961)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1974)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1976)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2002)
<223> n equals a,t,g, or c

<400> 504
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agaatcattg agggcttatt ttgtatacca actgctaaac tagatgcttc atacattgtt 180
gtcaatactc atgacagcct tgtaaagtag aaawtaattc ttccagttaa cackaaggct 240
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tcaactttcc tgctgaaaat gcccatttaa ttaaagaagg ttggatagag ctctctatat 600
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gagaaactgt aaatttccac tactaaaaat cacaaaaata acagaaacaa aagaagagat 720
aagaatttgg ggaattgtgc tgaacaattt agtggttaaa aaaaacaact gtgcatgttt 780
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agggatctta tcacttcact tccacactaa aatgtttttc ctgggggaac cacacttcct 1920
tagcaatctg acccatcaga nctttccagg ctgtctcctg nctggttccc taangntccc 1980
agccaacacc ggaattatca tngggcccaa a 2011

<210> 505
<211> 1989
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1917)
<223> n equals a,t,g, or c

<400> 505
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cggccctgag cgggacccgc gtcctggcca gcaagaccgc gaggaggatc ttccaggagc 240
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agaaggcaga ggcttccttt tggaccgccg aggaggtgga cctctccaag gacattcagc 420
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ttacagaagc ccgctgtttc tatggcttcc aaattgccat ggaaaacata cattctgaaa 600
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tcttttccgg ttcttttgcg tcgatattct ggctcaagaa acgaggactg atgcctggcc 840
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tagtcagttg gtgccagata gaagacaggt tgtgttttta tcctgtggct tgtgtantgt 1920
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agggggctt 1989

<210> 506
<211> 1085
<212> DNA
<213> Homo sapiens

<400> 506
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ggaatgacat cttacgcaaa aagggtatct taccccccaa ggaaagtctg aaagaattgg 180
aagaggaggc agaagaggag cagcgcatcc tccagcagtc agtggtgaaa acatatgaag 240
atatgacttt ggaagagctg gaggatcatg aagacgagtt taatgaggag gatgaacgtg 300
ctattgaaat gtacagacgg cggagactgg ctgagtggaa agcaactaaa ctgaagaata 360
aattyggaga agttttggag atctcaggga aggattatgt tcaagaagtt accaaagctg 420
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aaaattaaaa ccagccattt gtatggcaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1080
aaaaa 1085

<210> 507
<211> 1485
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (570)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1475)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1476)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1485)
<223> n equals a,t,g, or c

<400> 507
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cctggcctcg cggtgccatg ctgccccggc ggcggcgctg aaggatggcg acgccgctgc 180
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cagacctgcg gaaaaaaaaa aaaaaaaaaa aaacnngggg ggggn 1485

<210> 508
<211> 1930
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<400> 508
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ttatttgtaa aaagatgagg acacacatta artgawgtca gcattttagt aaacttttag 120
acaaaatttg ttagggtcat tcatgaaaac tttaatacta aaagcacttt ccattatata 180
ctttttaaag gtctagataa ttttgaacca atttattatt gtgtactgag gagaaataat 240
gtatagtaga ggacagcctt ggtttgtaaa gctcagttcc actagttcat ggttttgtgc 300
aacttctgag cctcagtttt ctcctttgca aattaataat tacatacctt tatagatttt 360
gaaattaatt taaatattag tatttggtac atgaaggctt aatgttaagt ttcctttaat 420

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gatccacaat aatccctttg atcacgttaa tctaaatcta gatgtctttg tctaattttt 480
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<210> 509
<211> 1134
<212> DNA
<213> Homo sapiens

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<222> (895)
<223> n equals a,t,g, or c

<220>
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<222> (1041)
<223> n equals a,t,g, or c

<220>
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<222> (1064)
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<223> n equals a,t,g, or c

<220>
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<222> (1106)
<223> n equals a,t,g, or c

<400> 509
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attatccaaa ggaagaaaga atttcggaac cctagcatct acgagaagct gatccagttc 540
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tctgaggact cctactatga ggcattagcc aaggcccaga aaattgagat ggacaaattg 660
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<211> 1382
<212> DNA
<213> Homo sapiens

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cc 1382

<210> 511
<211> 1741
<212> DNA
<213> Homo sapiens

<220>
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<222> (1696)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1710)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1715)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1717)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1720)
<223> n equals a,t,g, or c

<400> 511
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tgtacttgct cagctcaact gcatttcagt tgtattatag tccagttctt atcaacatta 180
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<210> 512
<211> 1530
<212> DNA
<213> Homo sapiens

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<222> (1342)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1444)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1488)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1508)
<223> n equals a,t,g, or c

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<210> 513
<211> 2999
<212> DNA
<213> Homo sapiens

<220>
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<222> (243)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2606)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2996)
<223> n equals a,t,g, or c

<400> 513
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<210> 514
<211> 2048
<212> DNA
<213> Homo sapiens

<400> 514
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ggactttata tgttcaagtg caggaattgg aaagttggac ttgttttcta tgatccaaaa 180
cagccctata agaaggttgg aaaaggagga actatatagc agcctttgct attttctgct 240

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<210> 515
<211> 3300
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (126)
<223> n equals a,t,g, or c

<400> 515
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tatcangtat gcaggaagta tatccttctc caaaatatca tacttgcatc accaggtaga 180
cacatttcct tctacacaga attatcttca gagcttctta aagcaaataa agcctgcttc 240
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<210> 516
<211> 3425
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (402)
<223> n equals a,t,g, or c

<400> 516
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ggggc 3425

<210> 517
<211> 1358
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1346)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1356)
<223> n equals a,t,g, or c

<400> 517
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tttacagcca atacaggttt aatcgatgtt caatattggt ttaggaaatt taaggccttc 180
taaatcataa tagctctttc atgtctaaaa ccattttatg atattgccaa aatgtgatag 240
gaaacctact cattaaattg ttaaactttt taatgactat gtgaagatat gaattgtttc 300
ctgaagataa tactcttaat tgagttgtat tgtacttctt aggcaaagca gtgtaaaact 360
gtatcaatta aggcttgtga gtagtgattt ccactggggc atcagagtct tggctgggct 420
gaatctgctg cttgttggtt cagtgtttct tatgaacaag agccacagta cagagcttca 480
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tttgtaaact aataaactta taaagtgatt ggcacaaaga ctccttgagc aaaagctgtg 600
cagttaagta caaaaagata cttaatttgg agactcttac agtaattttt gccatgtcaa 660
aacaatggct tttacattga aagattaata gaaactctac atatgttaat ttttttatag 720
aacctgactc aaatcaaggt actctccatt ttattgcctt acctgaatca gtcctttttg 780
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taaaaaaaaa aaaaaaaaaa aaaagnagga aagaanag 1358

<210> 518
<211> 1368
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1225)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1311)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1333)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1335)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1347)
<223> n equals a,t,g, or c

<400> 518
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ccgccgccgc ggagccgccg ccggggagga gcagccgctg ccgcccagga ctgggccctt 120
agggaggagg aggcgagaag atggcggacg accccagtgc tgccgacagg aacgtggaga 180
tctggaagat caagaagctc attaagagct tggaggcggc ccgcggcaat ggcaccagca 240
tgatatcatt gatcattcct cccaaagacc agatttcacg agtggcaaaa atgttagcgg 300

atgagtttgg aactgcatct aacattaagt cacgagtaaa ccgcctttca gtcctgggag 360
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<210> 519
<211> 933
<212> DNA
<213> Homo sapiens

<400> 519
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ctctactgga aaagaaacag taaatgccac cttcccggta gctatagtaa tgctgcgggc 120
cattagagat ttcttctgga aaactggaaa caagataggg tttaaaccag caggaggcat 180
ccgcagtgca aaggattccc ttgcttggct ctctcttgta aaggaggagc ttggagatga 240
gtggctgaag ccagaactct ttcgaatagg tgccagtact ctgctctcgg acattgagag 300
gcagatttac catcatgtga ctggaagata tgcagcttat catgatcttc caatgtctta 360
aatcagtcac cagttccaga aaagttcttt acgacaatgt ttaaaaatta tttttctacg 420
taattgctaa aattatttaa ttaaaaaatt gggcagtagg taactggcat tcctctcttt 480
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aaaaaaaaaa aaaaaactcg aggggggccc cgg 933

<210> 520
<211> 1430
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (104)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (105)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1428)
<223> n equals a,t,g, or c

<400> 520
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ctgtctcagg agatgaattg atgaccctgg ctcataaaca catnntcaag actgtggatt 120
tcacgcagga tagtaattat ttgttaaccg ggggacagga taaactgtta cgcatatatg 180
acttgaacaa acctgaagca gaacctaagg aaattagtgg tcatacttct ggtataaaaa 240
aagctctgtg gtgcagtgag gataaacaga ttctttctgc tgatgacaaa actgttcgac 300
tttgggatca tgctactatg acagaagtga aatctctaaa ttttaatatg tctgttagta 360
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ctgcatctct tcatcctgag aaagaatttc ttgttgcagg cggtgaagat tttaaacttt 540
ataagtatga ttataatagt ggagaagaat tagaatccta caagggacac tttggtccta 600
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<210> 521
<211> 1169
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1159)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1166)
<223> n equals a,t,g, or c

<400> 521
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acaaaccagg gctcgccatg aagccaggat tcagtccccg tgggggtggc tttggcggcc 120
gagggggctt tggtgaccgt ggtggtcgtg gaggccgagg gggctttggc gggggccgag 180
gtcgaggcgg aggctttaga ggtcgtggac gaggaggagg tggaggcggc ggcggcggtg 240
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atactgttgc acgtgtgttt ttctattaaa agactcatcc gtcaaaaaaa aaaaaaaaaa 1140
argggggccc gctaggggnt ccaagntta 1169

<210> 522
<211> 2162
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (169)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2133)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2136)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2139)
<223> n equals a,t,g, or c

<400> 522
gccgggcgcg gagaagtcgg ggcgggcggc agagaggccg ggacgcggac cgggccgggg 60
cgcccacagc cgcccgacgg cgcccagaga gcgcgcgccc cgcagccccg cgcctagccc 120

gccgggcatg gggcgcgcgg cagccgctga agccccggcc tggcccggnc gcacccggcc 180
ggaggcggag ggcagagcgc gcgcccagtt gcccgggcac caaatcggag cgcggcgtgc 240
gggagggccc agagcaggac tggaaatgtc ctggccgcgc cgcctcctgc tcagatacct 300
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tt 2162

<210> 523
<211> 799
<212> DNA
<213> Homo sapiens

<220>
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<222> (443)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (758)
<223> n equals a,t,g, or c

<400> 523
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ctttgtaaag tcctgtaaga tcctgtctcc tttgccatga cgctgcaagg tcataaagta 180
gataaaacct aagttgcaat tccggttttc ctcaagatct aagacatgtt acaaatggtt 240
aattgccttt gtttctcgct ttggtaacat cttcccgcct caggtatttc ccgccttgaa 300
gagtttaaaa ggcaatccta taatctaact ctggctaccc attctggacc ccctccatgc 360
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tccatgtctc tttcactcac tgnggtcagc ttccacacca tttctttggt gtggcttggc 480
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aggacaccaa actgcagggc cccttyttca cccctaacca gcaggaagta gccagaacgg 720
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<210> 524
<211> 1722
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (13)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<400> 524
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yacagatggg accatgaact ccggacacag cttcagccag acccccctcgg cctccttcca 180
tggcgccgga ggtggctggg gccggcccag gagcttcccc agggctccca ccgtccatgg 240
cggtgcgggg ggagcccgca tctccctgtc cttcaccacg cggagctgcc cacccccctgg 300
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caacatgaag ctggaaagcc gcatcctgaa atggcaccag cagagagatc ctggcagtaa 480
gaaagattat tcccagtatg aggaaaacat cacacacctg caggagcaga tagtggatgg 540
taagatgacc aatgctcaga ttattcttct cattgacaat gccaggatgg cagtggatga 600
yttcaacctc aagtwtgaaa atgaacactc ctttaaaaaa gacttggaaa ttgaagtcsa 660
gggcctccga aggaccttag acaacctgac cattgtcaca acagacctag aacaggaggt 720
ggaaggaatg aggaaagagc tcattctcat gaagaagcac catgagcagg aaatggagaa 780
gcatcatgtg ccaagtgact tcaatgtcaa tgtgaaggtg gatacaggtc ccagggaaga 840

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tccagccact gtgcagagca gacaaggtga catccacgaa ctgaagcgca cattccaggc 1020
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ctttcctact gcagccttca gattctcatc attttgcatc tattttgtag ccaataaaac 1680
tccgcactag caaaaaaaaa aaaaaaaaaa aaaaagttcg ac 1722

<210> 525
<211> 562
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (515)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (526)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (557)
<223> n equals a,t,g, or c

<400> 525
tcccgggccc gagggcatca gacggcggct gattagctcc ggtttgcatc acccggaccg 60
ggggattagc tccggtttgc atcacccgga ccgggggatt agctccggtt tgcatcaccc 120
ggaccggggg ccgggcgcgc acgagactcg cagcggaagt ggaggcggct ccgcgcgcgt 180
ccgctgctag gacccgggca gggctggagc tgggctggga tcccgagctc ggcagcagcg 240
cagcgggccg gcccacctgc tggtgccctg gargctctga gccccggcgg cgcccgggcc 300
cacgcggaac gacggggcga gatgcgagcc acccctctgg ctgctcctgc gggttccctg 360
tccaggaaga agcggttgga gttggatgac aacttagata ccgagcgtcc cgtccagaaa 420
cgagctcgaa gtgggcccca gcccagactg cccccctgcc tgttgcccct gagcccacct 480
actgctccag atcgtgcaac tgctgtggsc actgnctccc gtyttnggsc ctatgtccty 540
ctkgaagccc gaagaanggc gg 562

<210> 526
<211> 2023
<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (12)
<223> n equals a,t,g, or c

<400> 526
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taaatgttaa tgaagttaaa cccataaaca aaggtgaaga acaaattggt tttgagctag 120
tggagaaatt atttcaaggt cagctggtat taaggacgcg ttgcttggaa tgtgaaagtt 180
taacagaaag aagagaagat tttcaagaca tcagtgtgcc agtacaagaa gatgagcttt 240
ccaaagtaga ggagagttct gaaatttctc cagagccaaa aacagaaatg aagaccctga 300
gatgggcaat ttcacaattt gcttcagtag aaaggattgt aggagaagat aaatatttct 360
gtgaaaactg ccatcattat actgaagctg aacgaagtct tttgtttgac aaaatgcctg 420
aagttataac tattcatttg aagtgctttg ctgctagtgg tttggagttt gattgttatg 480
gtggtggact ttccaagatc aacactcctt tattgacacc tcttaaattg tcactagaag 540
aatggagcac aaagccaact aacgacagct atggattatt tgcggttgtg atgcatagtg 600
gcattacaat tagtagtggg cattacactg cttctgttaa agtcactgac cttaacagtt 660
tagaactaga taaaggaaat tttgtggttg accaaatgtg tgaaataggt aagccagaac 720
cattgaatga ggaggaagca aggggtgtgg ttgagaatta taatgatgaa gaagtgtcaa 780
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cacgatctgt atatagtaca tcaaacttag aggtgtgacc ttaaatttaa cttttttaa 1920
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<210> 527
<211> 2847
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (286)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (290)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2842)
<223> n equals a,t,g, or c

<400> 527
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actctttaaa aaggcgctat agaaaaccaa tttctgagta aaccagcaga cagcatgact 120
tgtaaatggt cttttaatta attaaaaaga aattagtcag ctacaagcat gaacatgtgg 180
aacgcttacc tttgtactag gcgtttttgt ttttgtttta atggcttttg gaatattata 240
gtattaacat ctggaaaact aggtaaattt atcttagaat taagtntttn gctccttttt 300
tgcagaaaaa gaacagcaag aagcgattga acacattgat gaagtacaaa atgaaataga 360
cagacttaat gaacaagcca gtgaggagat tttgaaagta gaacagaaat ataacaaact 420
ccgccaacca ttttttcaga agaggtcaga attgatcgcc aaaatcccaa atttttgggt 480
aacaacattt gtcaaccatc cacaagtgtc tgcactgctt ggggaggaag atgaagaggc 540
actgcattat ttgaccagag ttgaagtgac agaatttgaa gatattaaat caggttacag 600
aatagatttt tattttgatg aaaatcctta ctttgaaaat aaagttctct ccaaagaatt 660
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aaaaaaaaaa aaaaaaaaaa anaaaaa 2847

<210> 528
<211> 816
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (8)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (94)
<223> n equals a,t,g, or c

<400> 528
aaaacgantg tgtaattaac anaggctgtg cgcatgaacg ttgccgttat ggttcgcgaa 60
ttttccccgg cgcccaatgc gagggagacg aaantatgta aatgagtgga ttctggctga 120
gctatcctat tggctatcgg gacaaaattt gcttgagcca atccaaagtg ctccgtggac 180
aatcgccgtt ctgtctataa aaaggtgaag cagcggcgtt ttcggcgact ttcccgatcg 240
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gaggcaaggc ccgcgccaag gccaagtcgc gctcgtcccg cgctggcctt cagttcccgg 360
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ccgtctacat ggctgcggtc ctcgagtatc tgaccgccga gatcctggag ctggcgggca 480
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gctggcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 816

<210> 529
<211> 885
<212> DNA
<213> Homo sapiens

<400> 529
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atcgtgcgcc gaggcccgcg aggggtcgcc gcccagatcc caccagccag caagctaaag 180
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gcccgaggtt ccaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaa 885

<210> 530
<211> 742
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (693)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (695)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (715)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (730)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (741)
<223> n equals a,t,g, or c

<400> 530
ggtacctgac agtaccggtc ggaattcccg ggtcgaccca cgcgtccgct gctgctctta 60
aaggtacagg cctcagggtc cctgctgtag acggggcggg ggagagtacg atgggtgggg 120

cgtggtgggt cgtagggcgc tcgagatgga gcccccagct tccttgatgg atcgcggggc 180
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cgcattggaa gaacgcggtg ggcttctggc tgctgggcct ttgcaacaac ttctcttatg 480
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gccatgtgga cccaggccca acgccgatcc cccacaacag ctcatcacga tttgactgca 600
actctgtctc tacggctgct gtgctcctgg cggacatcct ccccacactc gtcatcaaat 660
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<210> 531
<211> 525
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (502)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (510)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (523)
<223> n equals a,t,g, or c

<400> 531
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<210> 532
<211> 1925
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<213> Homo sapiens

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<213> Homo sapiens

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<220>
<221> misc feature
<222> (482)
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<220>
<221> misc feature
<222> (487)
<223> n equals a,t,g, or c

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gnctggnagc cattaattca ag 502

<210> 534
<211> 1800
<212> DNA
<213> Homo sapiens

<400> 534
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<211> 2497

<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2487)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2493)
<223> n equals a,t,g, or c

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<211> 4090
<212> DNA
<213> Homo sapiens

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<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (528)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (535)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2475)
<223> n equals a,t,g, or c

<400> 536
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<210> 537
<211> 586
<212> DNA
<213> Homo sapiens

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<222> (56)
<223> n equals a,t,g, or c

<400> 537
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tgctttcaga tagcagcctt cacctcttcc ttacagagcc atctga 586

<210> 538
<211> 1250
<212> DNA
<213> Homo sapiens

<400> 538
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<220>
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<223> n equals a,t,g, or c

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<211> 2509

<212> DNA
<213> Homo sapiens

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<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (367)
<223> n equals a,t,g, or c

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<212> DNA
<213> Homo sapiens

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ccc 1743

<210> 542
<211> 2210
<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<400> 542
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<211> 1715
<212> DNA
<213> Homo sapiens

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<210> 544
<211> 3109
<212> DNA
<213> Homo sapiens

<220>
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<222> (1011)
<223> n equals a,t,g, or c

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<210> 545
<211> 1176
<212> DNA
<213> Homo sapiens

<400> 545
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<211> 1735
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

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<210> 547
<211> 1048
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1043)
<223> n equals a,t,g, or c

<400> 547

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<211> 736
<212> DNA
<213> Homo sapiens

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<222> (719)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (724)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (727)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (734)
<223> n equals a,t,g, or c

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<210> 549
<211> 2231
<212> DNA
<213> Homo sapiens

<220>
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<222> (2224)
<223> n equals a,t,g, or c

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<211> 1816
<212> DNA
<213> Homo sapiens

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<212> DNA
<213> Homo sapiens

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<210> 552
<211> 4021
<212> DNA
<213> Homo sapiens

<220>
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<222> (4000)
<223> n equals a,t,g, or c

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<222> (3006)
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<213> Homo sapiens

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<221> misc feature
<222> (1980)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1992)
<223> n equals a,t,g, or c

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<222> (906)
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<211> 3484
<212> DNA
<213> Homo sapiens

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aagt 3484

<210> 558
<211> 790
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (788)
<223> n equals a,t,g, or c

<400> 558
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gaaagacttg gccagcgagg ctccctacca ctccgaaaaa agagagtggg ggtcagcagg 180
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tgaaaaaggm aggcattgac ctccctctga ggcagtttcc aggcccaccg tggtgcacgc 720
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ggccctcncg 790

<210> 559
<211> 558
<212> DNA
<213> Homo sapiens

<400> 559
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aaaaaaaagg gsggcccc 558

<210> 560
<211> 534
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (16)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (17)
<223> n equals a,t,g, or c

<400> 560
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caaggaggac gagggccggt tgccgggcgc gggcgagaaa gcctcccagt gcaacgtcag 120
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caatgtggag gcccctccac ccagcagccc cagtgtgctt ccgccactgg tggaggagaa 240
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tggaaagaaa tgtgtggtca ttgatttaga tgaaacattg gtgcacagtt cgtttaagcc 360
tattagtaat gctgatttta ttgttccggt tgaaatcgat ggaactatac atcaggtgta 420
tgtgctgaag cggccacatg tggacgagtt cctccagagg atggggcagc ttttgaatgt 480
gtgcwcttta ctgccgcwtg gccaagtatg cagacctgtg gctgacctcc taga 534

<210> 561
<211> 3043
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3038)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (3039)
<223> n equals a,t,g, or c

<400> 561
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tggaagtcgg gccctgggct gcccgatcgc cagcccgagg acttaccatc cacaatgcac 120
cacggaagag gccgttctat gaaaaactga cacagactgt attcctgcat tcaaatgtca 180
gccgtttgta aaatgctgta tcctaggaat aagctgccct ggtaaccagt ctctagctag 240
tgcctcttgc cctctcctca cctccttttc tctcagtgac tctggaacct gaatgcagct 300
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<210> 562
<211> 1386
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (480)
<223> n equals a,t,g, or c

<400> 562
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caccatccgc cctcggcttc cgcggggcgc tgggccgcca gcctcggcac cgtcctttcc 120
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tacatgtacc cctccatgga tcagctggct gaaatgcttc ctggagtcct tcaacagttt 540
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ggcccc 1386

<210> 563
<211> 2638

<212> DNA
<213> Homo sapiens

<400> 563
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caaaatgatt tactttgaga tttgaataat ttgcatagca gtaaaatgtg ttttgtgtaa 360
catacaaata gaaaaatgac ccagtatctt aattgatact tactggagag tatcagaatt 420
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<210> 564
<211> 691

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (569)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (575)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (581)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (619)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (650)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (653)
<223> n equals a,t,g, or c

<400> 564
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tcgagtggat tggaacactt caagccccca a 691

<210> 565
<211> 1967
<212> DNA
<213> Homo sapiens

<400> 565
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ctagaagtta gattatttgc tactgtgaga atattgtcac cactggaagt tactttagtt 240
catttaattt taattttata ttttgtgaat attttaagaa ctgtagagct gctttcaata 300
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actttgaaga tagaaaaacc actttttaag tactaagtca tcatttgcct tgaaagtttc 1440
ctctgcattg ggtttgaagt agtttagtta tgtctttttc tctgtatgta agtagtataa 1500
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aaaaaaaatg ctcagttttg cttgcattcc ttgagaatgt atttatctga agatcaaaac 1680
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catgaaagga ataattcaaa tacagataaa cagagttggc agtatattat agtgataatt 1800
ttgtattttc acaaaaaaaa agttaaactc ttcttttctt tttattataa tgaccagctt 1860
ttggtatttc attgttacca agttctattt ttagaataaa attgttctcc ttctaaaaaa 1920
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaggg gggggag 1967

<210> 566
<211> 1334
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1253)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1307)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1309)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1312)
<223> n equals a,t,g, or c

<400> 566
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cagtcacgtg accgctgact cggggcgttc tccactatcg cttacctacc tccctctgca 120
ggaacccggc gatatggctg ccgctgtgcc ccgcgccgca tttctctccc cgctgcttcc 180
ccttctcctg ggcttcctgc tcctctccgc tccgcatggc ggcagcggcc tgcacaccaa 240
gggcgccctt cccctggata cggtcacttt ctacaaggtc attcccaaaa gcaagttcgt 300
cttggtgaag ttcgacaccc agtaccccta cggtgagaag caggatgagt tcaagcgtct 360
tgctgaaaac tcggcttcca gcgatgatct cttggtggca gaggtgggga tctcagatta 420
tggtgacaag ctgaacatgg agctgagtga gaaatacaag ctggacaaag agagctaccc 480
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ccgccaggcc ctcttgaagc aggggcaaga taacctctca agtgtgaagg agactcagaa 720
gaagtgggcc gagcaatacc tgaagatcat ggggaagatc ttagaccaag ggaggacttt 780
cccagcatca gagatgacac ggatcgccag gctgattgag aagaacaaga tgagtgacgg 840
gaagaaggag gagctccaga agagcttaaa catcctgact gccttccaga agaagggggc 900
cgagaaagag gagctgtaaa aggctgtctt gtgattttcc agggtttggt gggggtaggg 960
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gtctttgaca gatgtaattc tcattcaatt aaagtttcag tgttttggtt aantaaaaaa 1260
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaggg cggccgntnt anaggatccc 1320
tcgaggggcc caag 1334

<210> 567
<211> 1610
<212> DNA
<213> Homo sapiens

<400> 567
gccggccagt gcgggaaccg tttccgaagg accaccggga acagacggat cggcagggcg 60
rggcggaacg gcgtttgcaa tggctgctac tgtgaacttg gaacttgatc ccattttttt 120
gaaagcacta ggtttcttgc attcaaagag taaagattct gctgaaaagc taaaagcact 180
gcttgatgaa tctttggctc ggggcattga ttccagttac cgtccatctc aaaaggatgt 240
ggagccaccc aaaatttcaa gcacaaaaaa catttccatt aagcaagagc ccaaaatatc 300
atccagtctt ccttctggta ataataatgg caaggtcctc acaactgaaa aggtaaagaa 360
ggaagctgaa aagagacctg ctgataaaat gaaatcagac atcactgaag gagttgatat 420
tccaaagaaa cctagattgg agaaaccaga aacacagtca tctcccatta ctgtccaaag 480
tagcaaggat ttacctatgg ctgacctttc cagttttgag gagaccagtg ctgatgattt 540
tgccatggag atgggattgg cctgcgttgt ttgtaggcaa atgatggtgg catctggcaa 600

tcaattagta gaatgtcagg agtgccataa tctctaccac cgagattgtc ataaacccca 660
ggtgacagac aaggaagcga atgaccctcg cctggtgtgg tattgtgccc gatgtaccag 720
acaaatgaaa agaatggctc aaaaaactca gaaaccaccg cagaaaccag cccctgcagt 780
tgtttctgta actccagctg tcaaagatcc attggttaag aaaccagaaa ctaaactgaa 840
acaagagaca acttttctag cgtttaagag aacagaagtc aagacatcca cagttatttc 900
aggaaattct tctagtgcca gcgtttcctc gtcagtaact agtggcttaa ctggatgggc 960
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tggtctggca acatcatcca aaggtggaat aggttccaaa ataggttcca ataacagcac 1140
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tcgctcagtt agttgtgaca atgtcagcaa agtaggtctt cctagtccaa gtagtttagt 1260
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cccaacttca caagaatcac agctcaatgc tatgaagcga ttacagatgg tcaagaagaa 1440
agctgcccaa aagaaactca agaagtaatg tggccaagta ggtttttgta tcatattagc 1500
ctaaagatga aaggcttatt attatgatat aatctgtaat acactgtaat ttaataaaag 1560
tcttcataat caaaaaaaaa aaaaaaaaaa agaaaaaaaa aaaaaaaaaa 1610

<210> 568
<211> 1412
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1018)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1037)
<223> n equals a,t,g, or c

<400> 568
aattcggcac gagagaaaac attgcaaaag ctaaacgact aaaaaaggat tgaaggactg 60
aacaggcttt gcaaccagag gaaaatcatt tggaaaatta cacagctttg gaagaatcca 120
ctaaagtttc ttctttggat ttcttgacag tatgatttag taaatgaaat ttgaccaaat 180
ggaagaatca tgttagttct gacctcaata ctatagtaac ttttaggcgt gggtgtagaa 240
gtttataggt ttctattgac agttattgta aattagcatt tactgtggta caaattcttt 300
ataactgact tagtcatttg ccgcttagca gtttatatac tgaaatgaaa acatcttgtg 360
gggaaaagtg actttagatt atgaactcaa ttcaaatgaa ctctatttaa aatggggtcc 420
tattttggac aaaggaaatt aagaatgtaa aagtcagaac agtcttgagg taaaaagtgt 480
gctttggctt aaaagggata cagtatatta attacatctt ttattattat tgtttatttc 540
ttagaatcat ttctggcttt ctcaaaacaa aataatatta atgagtactt ctatttgctg 600
catttttctt attacagcct ttgagacagc tggtaattat aagtcatttt ccatttttta 660
aaacataatt ttataaagaa ttctcttatc tcgactatgt agaataccac ctactggaca 720
gaacaatttt tgtactcaca aacactgcca ttttcttaga gatggcttga gaggagtaac 780
actatggttt aaagcttgca gtaaaaatgc caaacactgt agtaccttgg aacccagttt 840
attcttgtgc taagcagaac tgtaaaatag ttaaaatgtc ttatcaagta attcgccgat 900
tacaaagaca ccatttgttt tttatttcat tctttgkttt aactcatgtg gtagtgatat 960
ttaatacttt ctgatcaaac aggttcaaag taaaacgtta aatttcacat ttcttttnaa 1020

agaactctta aagtgtnaca gttacgccat acttcataag tggtaaagaa aggtataaaa 1080
tttggaaaca ttttgttggg catagtagtg attgggtgaa aaggataaat tatatcaaaa 1140
tgagaatgtg ctgtaattgg aagtagggag ctaaaggatg tttctttcag tttagtagaa 1200
ctggaacgtt ttactattaa acatggcttt tataaatgca tggtccaata attttattca 1260
ctgttagtat ttaattcact gtcagcttat taatgttttc tgtacccatt aatgaatttt 1320
aaattacaaa aaattgtcta gcagctacag tttaaaaatg aaactagaca ttaaaataaa 1380
tttgataatt ttttataaaa aaaaaaaaaa ag 1412

<210> 569
<211> 1125
<212> DNA
<213> Homo sapiens

<400> 569
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ctgacccaag gggccttcga ggtgccttag gccgcttgcc ttgctctcag aatcgctgcc 120
gccatggcta gtcagtctca ggggattcag cagctgctgc aggccgagaa gcgggcagcc 180
gagaaggtgt ccgaggcccg caaaagaaag aaccggaggc tgaagcaggc caaagaagaa 240
gctcaggctg aaattgaaca gtaccgcctg cagagggaga aagaattcaa ggccaaggaa 300
gctgcggcat tgggatcccg tggcagttgc agcactgaag tggagaagga gacccaggag 360
aagatgacca tcctccagac atacttccgg cagaacaggg atgaagtctt ggacaacctc 420
ttggcttttg tctgtgacat tcggccagaa atccatgaaa actaccgcat aaatggatag 480
aagagagaag cacctgtgct gtggagtggc atttagatg ccctcacgaa tatgaagctt 540
agcacagctc tagttacatt cttatgatat ggcattaaat tatttccata tattatataa 600
taggtccttc cactttttgg agagtagcaa atctagcttt tttgtacaga cttagaaatt 660
atctaaagat ttcatctttt tacctcatat ttcttaggaa tttaatggtt atatgttgtc 720
ttttttcct atgtcttttg gctcaagcaa catgtatatc agtgttgact ttttctttct 780
tagatctagt ttaaaaaaaa aaaaaaccac ataacaattc tttgaagaaa ggaagggatt 840
aaataatttt tttccctaac actttcttga aggtcagggg ctttatctat gaaaaagtag 900
taaatagttc tttgtaacct gtgtgaagca gcagccagcc ttaaagtagt ccattcttgc 960
taatggttag aacagtgaat actagtggaa ttgtttgggc tgcttttagt ttctcttaat 1020
caaaattact agatgataga attcaagaac ttgttacatg tattacttgg tgtatcgata 1080
atcatttaaa agtaaagact ctgtcatgca tttttcccca aaaaa 1125

<210> 570
<211> 1916
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1899)
<223> n equals a,t,g, or c

<400> 570
ggggagggtc agttggaggc aggcgctcgc tgaggcaaaa ggaggcgctc ggcccgcggc 60
ctgacaggga cttagcccgc agagatcgac cccgcgcgcg tgaccccaca cccacccact 120
catccatcta tccactccct gcgccgcctc ctcccaccct gagcagagcc gccgaggatg 180
ataaacaccc aggacagtag tattttgcct ttgagtaact gtccccagct ccagtgctgc 240
aggcacattg ttccagggcc tctgtggtgc tcctgatgcc cctcacccac tgtcgaagat 300
ccccggtggg cgagggggcg gcagggatcc ttctctctca gctctaatat ataaggacga 360

gaagctcact gtgacccagg acctccctgt gaatgatgga aaacctcaca tcgtccactt 420
ccagtatgag gtcaccgagg tgaaggtctc ttcttgggat gcagtcctgt ccagccagag 480
cctgtttgta gaaatcccag atggattatt agctgatggg agcaaagaag gattgttagc 540
actgctagag tttgctgaag agaagatgaa agtgaactat gtcttcatct gcttcaggaa 600
gggccgagaa gacagagctc cactcctgaa gaccttcagc ttcttgggct ttgagattgt 660
acgtccaggc catccctgtg tcccctctcg gccagatgtg atgttcatgg tttatcccct 720
ggaccagaac ttgtccgatg aggactaata gtcatagagg atgctttacc caagagccac 780
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gttgaaattg ttttccataa agaacagtat aaacatatta ttcacatgta atcaccaata 960
gtaaatgaag atgtttatga actggcatta gaagctttct aaactgcgct gtgtgatgtg 1020
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catggcctgg agggctggtg ggcagcactg tcaggctcag gtttccctgc tgttggcttt 1140
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cagtacattt taaatagggg cattgaaatt tactcccacc accagggctt ttttggggga 1440
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tcttgctcct ggctgcaggc ccaggcccca aggtctcctt cttggggtca caaacagcag 1560
taaggaagag gaatatatag caactcaggg cctgggaatt gtggggcaat ccgttcttag 1620
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tagtgtctga gactctgctc tgcagggcct agggtagcgc tgggagtgta gaagtggcct 1740
gcccttaact gttttcacta aacagctttt tctaagggga gagcaagggg gagagatcta 1800
gattgggtga gggggacggg gatgtcaggg aggcaagtgt gttgtgttac tgtgtcaata 1860
aactgattta aagttraaaa aaaaaaaaaa aaaaactcng rgggggcgct atagtg 1916

<210> 571
<211> 1253
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1205)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1207)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1212)
<223> n equals a,t,g, or c

<400> 571
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aggacccgga atgaagacga aggcgctcac cattaaatcg tacggctcgc actgccccct 120
gcccgcagtc cagcgtcttc aaccgtttct gcggcagctc tggaggccgc ggctttggct 180

cagggaaagc catgctccca ggactccttc cttgcagcct taaatcggtc tgtacggaaa 240
attccgcgcc ttagaaaccc acgcttgggt gtaaccttat tattgttctt cctgacctac 300
ttcctgttta tcacttccgg gttcatcatt ttggcatttc ggtgatcggg ttggaactat 360
tgaagcccgc tttcaggttc ttttccccat tttccctttg aaaggaagac ttctggcttc 420
tcctaaatct ccgttctctg ggtaagggga gtccaagcct ctgtcatgag gaacggaaat 480
gcgagggcct cgggtgttac tctaaaatcc gccctcagct tgcacgccgg aagctgcgat 540
tcctgcagcg gaagaggcgt gatctggcct tcgactcgct atgtccacta acaatatgtc 600
ggacccacgg aggccgaaca aagtgctgag gtacaagccc ccgccgagcg aatgtaaccc 660
ggccttggac gacccgacgc cggactacat gaacctgctg ggcatgatct tcagcatgtg 720
cggcctcatg cttaagctga agtggtgtgc ttgggtcgct gtctactgct ccttcatcag 780
ctttgccaac tctcggagct cggaggacac gaagcaaatg atgagtagct tcatgctgtc 840
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atttgctttc tcgttgaaac ctgttgttaa taaagttttt cactctgaaa aaaaaaaaaa 1200
aaaanrnaaa anctygrggg ggggcccgga acccaattcs ccggatagtg agt 1253

<210> 572
<211> 2013
<212> DNA
<213> Homo sapiens

<400> 572
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ccagtgatcc ccaagcatcc agtacagaac caggcatcga gctagctccc tgcacggccg 120
caccctccca gagaactcct tgaggagaac aagtgccctt ggggacagcc ggcakgcgcc 180
cctgtacgtc tgctcatgca ccaggcagca cagccgcagt tcctcagttg ttgttttgac 240
atatttcagt ttccacctca ygtttttaga gcagaaccac actgtctccc tggaggggct 300
cgagggcatg accggggact gaccattctg tgaaagkagc agaatgtgag gagcacgcgt 360
gagcttatgt accgtgaaga tgatcagagg atatcttatt ttaagagtaa aaacccacat 420
aattttattt ctgcttgata gtcatggtag tctgtcatac ccacctctgg gactctgcgt 480
ggctgtttgg ctgtcacttg tagcaataac gacattagtt ctagtcagtg ctgttttaca 540
tttttctttt gatgggttta gtcttgccct ggagtgccga tgatgattct ccctccagag 600
ccacgcttgg gaacatgaag caagtctggc gtgtgggctg cgtgccggcc ttagtgggac 660
ccgtggggtt ggagcatgcc tttaggggca gtgtctgggc cgaagcacgt cccaccacac 720
agtgccagag ccagagaagg ggccccacca ccaaggccaa gcttgaccag gtcagcattg 780
ccatggccca gtgtgccccg tggcctctga agatccctct gtgcagggtc tgcagggatc 840
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cttctgggtc aggactccaa ggtgcagcgg gcttcacagc cctacaattg ggttctcagc 960
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gttcacggga aacaagcctg agtccgctcg cacccgcggc tgctctcccg gctcggcccg 1620
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taacgagagg agtgacgtat tttcatcacc gtttttaatt tgttttctta cgggtttacg 1860
attttgaatt tttcttattt ggttgaaaga attttgattc tatcagcctg agtgagttca 1920
gcctgtaaaa aggatgttaa gctgtgggta aaatatgcaa acgaaaagaa atatattgta 1980
caaattctat ataataagaa aaaaaaaaaa aaa 2013

<210> 573
<211> 669
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (445)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (631)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (638)
<223> n equals a,t,g, or c

<400> 573
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cttcctctcc ctttttttcct tcttccttcc cctcctcgcc gccaccgccc aggaccgccg 180
gccgggggac gagctcggag cagcagccag agtttattaa ccacttaacc tctcagaact 240
gaacaaagac aacattgttc ctggaacgcc ctctttttaa aaaagaaagc ataaccccta 300
ctgtagaact aaatgcactg tgcatgaaac ttggaaaaaa accaatgtat aagcctgttg 360
acccttactc tcggatgcak tcmacctata actacaacat gagaggaggt gcttatcccc 420
cgaggtactt ttacccattt ccagntccac ctttacttta tcaagtggaa ctttctgtgg 480
gaggacagca atttaatggc aaaggaaaga caagacaggc tgcgaaacac gatgctgctg 540
ccaaagcggt tgaggatcct gcagaatgag cccctggcag aagagggctg aggtgaaagg 600
aagagaatcc gaagaagaaa actcaataaa nctgaaanaa agcaaggggt tgagatgcct 660
taaacggga 669

<210> 574
<211> 2432
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (7)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2326)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2367)
<223> n equals a,t,g, or c

<400> 574
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ggtctgtagt ctgagcgcta cccggttgct gctgcccaag gaccgcggag tcggacgcag 180
gcagaccatg tggaccctgg tgagctgggt ggccttaaca gcagggctgg tggctggaac 240
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ctacagctgc tgccgtcccc ttctggacaa atggcccaca acactgagca ggcatctggg 360
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<222> (241)
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gttgctg 3067

<210> 581
<211> 1574
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (457)
<223> n equals a,t,g, or c

<400> 581
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caggtggtgg cgcgcgccgt gtgcttggtc ttcgccttga tcgtgttctc ctgcatctat 180
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gaggatgcct gccgctatgg cagtgccatc ggggtgctgg ccttcctggc ctcggccttc 300
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gtgagggcag ccatcacctt cagcttcttt tccatcttct cctggggtgt gctggcctcc 540
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actccggacc ccaacactgc ctacgcctcc tacccaggtg catctgtgga caactaccaa 660
cagccaccct tcacccagaa cgcggagacc accgagggct accagccgcc ccctgtgtac 720
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aaaaaagggc ggcc 1574

<210> 582
<211> 960
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (924)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (937)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (939)
<223> n equals a,t,g, or c

<400> 582
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aaggcagata gcagccccgt caaggcggga gtggagacca ccacaccctc caaacaaagc 600
aacaacaagt acgcggccag cagctacctg agcctgacgc ctgagcagtg gaagtcccac 660
araagctaca gctgccaggt cacgcatgaa gggagcaccg tggagaagac agtggcccct 720
acagaatgtt cataggttct caaccctcac ccccсaccac gggagactag agctgcagga 780
tcccagggga ggggtctctc ctcccacccc aaggcatcaa gcccttctcc ctgcactcaa 840
taaaccctca ataaatattc tcattgtcaa tcagaaaaaa aaaaaaaaaa aaaaaagggg 900
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<210> 583
<211> 541
<212> DNA
<213> Homo sapiens

<400> 583
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ccgccgccat gcagccctcc agccttctgc cgctcgccct ctgcctgctg gctgcacccg 180
cctccgcgct cgtcaggatc ccgctgcaca agttcacgtc catccgccgg accatgtcgg 240
aggttggggg ctctgtggag gacctgattg ccaaaggccc cgtctcaaag tactcccagg 300
cggtgccagc cgtgaccgag ggcccattc ccgaggtgct caagaactac atggacgccc 360
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cgggctycty caacctgtgg gtcccctcca tccactgcaa actgctggac atcgcttgct 480
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t 541

<210> 584
<211> 2968
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (454)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1437)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2961)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2964)
<223> n equals a,t,g, or c

<400> 584
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ctacccctg tctcccccac aaaggacacc ggctgggatt cggtatcgaa tcgcagttat 180
cgcagacctg gacacagagt caagggccca agaggaaaac acctggttca gttacctgaa 240
aaagggctac ctgaccctgt cagacagtgg ggacaaggtg gccgtggaat gggacaaaga 300
ccatggggtc ctggagtccc acctggcgga gaaggggaga ggcatggagc tatccgacct 360
gattgttttc aatgggaaac tctactccgt ggatgaccgg acgggggtcg tctaccagat 420
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aggcttcaag gccgaatggc tggcagtgaa ggacgagcgt ctgtacgtgg gcggcctggg 540
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gagggagtgt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 2940
aaaaacaaaa aaaaaaaaaa nagnagag 2968

<210> 585
<211> 2608
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (84)
<223> n equals a,t,g, or c

<400> 585
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gtggcgcggc tccgcgtacg cggncttcct ggcgctggcc gtgggctgcg tcttcctgct 120
ggagccagag ctgccaggct cggcgctgcg ctctctctgg agctcgctgt gtctggggcc 180
cgcgcctgcg cccccgggac ccgtctcccc cgagggccgg ttggcggcag ctgggacgcg 240
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gatgtggtgc tctcaggggt gaagctcttg caggcacttg gccttagtcc tgggaatggg 360
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<210> 586
<211> 1893
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1184)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1865)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1883)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1887)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1893)
<223> n equals a,t,g, or c

<400> 586
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agtagccgcc tctgccgccg cggagcttcc cgaacctctt cagccgcccg gagccgctcc 120
cggagcccgg ccgtagaggc tgcaatcgca gccgggagcc cgcagcccgc gccccgagcc 180
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ccttgccctc aataaataaa gttctttttt agttccaaaa aaaaaaaaag ggcggccgtt 1860
taarngatcc aasttacgta ccntgcntgc gan 1893

<210> 587
<211> 2463
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2413)
<223> n equals a,t,g, or c

<400> 587
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tcaaattctg cttggacaat ggagccaagt cggtagtcct tatgagccac ctaggccggc 180
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gcactgctca cagagcccac agctccatgg taggagtcaa tctgccacag aaggctggtg 540
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<211> 1945
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<222> (1240)
<223> n equals a,t,g, or c

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<222> (1939)
<223> n equals a,t,g, or c

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<222> (1945)
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<211> 2307
<212> DNA
<213> Homo sapiens

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<211> 1438
<212> DNA
<213> Homo sapiens

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<210> 592
<211> 1078
<212> DNA
<213> Homo sapiens

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<210> 593
<211> 2492
<212> DNA
<213> Homo sapiens

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<222> (2113)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2452)
<223> n equals a,t,g, or c

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<211> 1904
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

<220>
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<221> misc feature
<222> (1903)
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cagccttcct tcctgggcat ggagtcctgt ggcatccacg aaactacctt caactccatc 960
atgaagtgtg acgtggacat ccgcaaagac ctgtacgcca acacagtgct gtctggcggc 1020
accaccatgt accctggcat tgccgacagg atgcagaagg agatcactgc cctggcaccc 1080
agcacaatga agatcaagat cattgctcct cctgagcgca agtactccgt gtggatcggc 1140
ggctccatcc tggcctcgct gtccaccttc cagcagatgt ggatcagcaa gcaggagtat 1200
gacgagtccg gcccctccat cgtccaccgc aaatgcttct aggcggacta tgacttagtt 1260
gcgttacacc ctttcttgac aaaacctaac ttgcgcagaa aacaagatga gattggcatg 1320
gctttatttg ttttttttgt tttgttttgg tttttttttt ttttttggct tgactcagga 1380
tttaaaaact ggaacggtga aggtgacagc agtcggttgg agcgagcatc ccccaaagtt 1440
cacaatgtgg ccgaggactt tgattgcaca ttgttgtttt tttaatagtc attccaaata 1500
tgagatgcrt tgttacagga agtcccttgc catcctaaaa gccaccccac ttctctctaa 1560
ggagaatggc ccagtcctct cccaagtcca cacaggggag gtgatagcat tgctttcgtg 1620
taaattatgt aatgcaaaat ttttttaatc ttcgccttaa tacttttta ttttgtttta 1680
ttttgaatga tgagccttcg tgccccccct tccccctttt ttgtccccca acttgagatg 1740
tatgaaggct tttggtctcc ctgggagtgg gtggaggcag ccagggctta cctgtacact 1800
gacttgagac cagttgaata aaagtgcaca ccttaaaaaa aaaaaaaaaa aaaaaaaaaa 1860
aaaaaaaaaa aaaaaaanag ggggggccc ccnangggc ccna 1904

<210> 595
<211> 337
<212> DNA
<213> Homo sapiens

<400> 595
ctagttctag atcgcgagcg gcgccctttt tttttytt tgttaagtcg ttccctctac 60
aaaggacttc ctagtgggtg tgaaaggcag cggtggccac agaggcggcg gagagatggc 120
cttcagcrgt tcccaggctc cctacctgag tccagctgtc cccttttctg ggactattca 180
aggaggtctc caggacggac ttcagatcac tgtcaatggg accgttctca gctccagtgg 240
aaccagtgga aatgacattg ccttccactt caaccctcgg tttgaagatg gagggtacgt 300
ggtgtgcaca gcaggcagaa cggaagctgg ggggccc 337

<210> 596
<211> 1288
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1283)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1285)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (1287)
<223> n equals a,t,g, or c

<400> 596
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gggaaagccg cgggaagggt actccaggcg agaggcggac gcgagtcgtc gtggcaggaa 120
aagtgactag ctccccttcg ttgtcagcca gggacgagaa cacagccacg ctcccacccg 180
gctgccaacg atccctcggc ggcgatgtcg gccgccggtg cccgaggcct gcgggccacc 240
taccaccggc tcctcgataa agtggagctg atgctgcccg agaaattgag gccgttgtac 300
aaccatccag caggtcccag aacagtttty ttctgggctc caattatgaa atgggggttg 360
gtgtgtgctg gattggctga tatggccaga cctgcagaaa aacttagcac agctcaatct 420
gctgttttga tggctacagg gtttatttgg tcaagatact cacttgtaat tattccaaaa 480
aattggagtc tgtttgctgt taatttcttt gtgggggcag caggagcctc tcagcttttt 540
cgtatttgga gatataacca agaactaaaa gctaaagcac acaaataaaa gagttcctga 600
tcacctgaac aatctagatg tggacaaaac cattgggacc tagtttatta tttggttatt 660
gataaagcaa agctaactgt gtgtttagaa ggcactgtaa ctggtagcta gttcttgatt 720
caatagaaaa atgcagcaaa cttttaataa cagtctctct acatgactta aggaacttat 780
ctatggatat tagtaacatt tttctaccat ttgtccgtaa taaaccatac ttgctcgtat 840
atacccccctg cctccttctg ttccagtcag ccaacatatg tacataaaag aacacacaaa 900
ttcaagaagt tggaagatta aattatctgc ttatttagtg taggatggtc aggtagctag 960
ctataagtga aaggaaattt tgctgaagag actgagaaat gggtagtgga atgactatca 1020
agatgacctc aaactattta aaaacatttt aacttgccat gaagaatctt gatgattttt 1080
gtataaatgt tgtataaaat tcttttacag ctacagattt ttaaatagga tcattgtaar 1140
gattaatgag ataatgtttt aacatagtgc ctgggtccat gataagtgtt aaatttttca 1200
attaccctca gtaactgata atgtagcaag aaaatactct atattcagac agacctgaat 1260
ttgatcccag ctctatacta ccntngna 1288

<210> 597
<211> 1052
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (937)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (943)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (995)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1004)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1009)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1040)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1051)
<223> n equals a,t,g, or c

<400> 597
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gagaagaaca acctaccttg tccttgatga agcagataga atgcttgata tgggctttga 120
accccaaata aggaagattg tggatcaaat aagacctgat aggcaaactc taatgtggag 180
tgcgacttgg ccaaaagaag taagacagct tgctgaagat ttcctgaaag actatattca 240
tataaacatt ggtgcacttg aactgagtgc aaaccacaac attcttcaga ttgtggatgt 300
gtgtcatgac gtagaaaagg atgaaaaact tattcgtcta atggaagaga tcatgagtga 360
gaaggagaat aaaaccattg tttttgtgga aaccaaaaga agatgtgatg agcttaccag 420
aaaaatgagg agagatgggt ggcctgccat gggtatccat ggtgacaaga gtcaacaaga 480
gcgtgactgg gttctaaatg aattcaaaca tggaaaagct cctattctga ttgctacaga 540
tgtggcctcc agagggctag atgtggaaga tgtgaaattt gtcatcaatt atgactaccc 600
taactcctca gaggattata ttcatcgaat tggaagaact gctcgcagta ccaaaacagg 660
cacagcatac actttcttta cacctaataa cataaagcaa gtgagcgacc ttatctctgt 720
gcttcgtgaa gctaatcaag caattaatcc cmagttgctt cagttggtcg aagacagagg 780
ttcaggtcgt tccaggggta gaggaggcat gaaggatgac cgtcgggaca gatactctgc 840
gggcaaaagg ggtggattta ataccttag agacagggaa aattatgaca gaggttactc 900
tagcctgctt aaaagagatt ttggggcaaa aactcanaat ggnggttaca gtgcttgcaa 960
attcaccaat gggagctttg gaagtaattt tgggncttgc tggnattcng gaccagtttt 1020
aggactggga attccaacan gggccttacc nc 1052

<210> 598
<211> 2093
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (969)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1422)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1425)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (1481)
<223> n equals a,t,g, or c

<400> 598
ccgccgccat gggaccacgt ggggtaagct gggttgagag cagcgggcgc cgttaaggag 60
ctgcagagtc acgtctgtgc aaagactgca ccagagccct tctgtgtcac ggcgggctgt 120
gcacccatgc acacacctac gcacacacaa cactccgcac tgcagtatat tcttgccaaa 180
gatttccttt aaaagcaagc acttttacta attattattt tgtaaatgtt tatcttcttc 240
tgtcttctcc ctccctgaat ctattttact gttgtttatt gttgaatctg tgtgtcagcc 300
aggagagcgc tgtctggcct tgaacatggg ctgggatggg aaagggtctg ggagaagatg 360
ggcaacaaag agccagggag tcatggacat cgcagcgacg cagaccccag caggttcagt 420
cccgtgctgc caccagctgt ccagctgggt gtctggaggg aagagggcag aggagggtca 480
tgtcccttca gctgggggag gggcccagtg agctccacgt ggctttttcc caaagggagc 540
aagagggaag gattgggcga gaaaacaatg gagaggggac ctgcgaagga aaacagggag 600
gaagtgagcg gtttgatcag cctgctatca cggtgttctg gctctcttat ttagccaggc 660
gcttaaggga cagatacatc acatcctaag tttgggaaag gcctttgacc catgtcatct 720
gagcgtctcc tccagtagct ctgaaagctg tggacaccaa tggccaggat tccttctccc 780
ctggtttttg aggatccctg ggtcttctga gactggccag gagagggatg gtggggccag 840
tggttgtgtg aaagcaggag gggcagccct cctggacaag tgtgatcccc ctataaacgg 900
ctctcaggag gttagtgagt aggagattct gccttgttct gatgagcctg tgcaggggct 960
ccaggggganc atgctgtcca gggggcacag aagggtggtg agtgtgatca aatctagtct 1020
cactcccact ttttagtctc actcctactt ttgtccacca cccctgcctc ctggatcttc 1080
tcccactttt tttttcagct ttaggacctg gggagatcct gtgagtcaag gcagacaccc 1140
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ctttacccca ggtccaggcc ctggaatcct gagactcgcg tttccttggc cagtggtaac 1260
acaggacgtg tgtgcgcatg tgcaagtgtg gatgtatgtg tgtgcgtgtg ttttgctcat 1320
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agatctgtcc ctcttggccc ctctgtcctc aaatgtccaa aatgttggag gacctctgtt 1560
catatcccac gcctgggctc ttgccagcag tggagttact gtagagggat gtcccaagct 1620
tgttttccaa tcagtgttaa gctgtttgaa actctcctgt gtctgtgttt tgtttgtgcg 1680
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gacccatcat tgagaacaaa tgtaagaaat cccttcccac caccctccct gcctcccagg 1800
ccctctgcgg gggaaacaag atcacccagc atccttcccc accccagctg tgtatttata 1860
tagatggaaa tatactttat attttgtatc atcgtgccta tagccgctgc caccgtgtat 1920
aaatcctggt gtmtgctcct tatcctggac atgaatgtat tgtacactga cgcgtcccca 1980
ctcctgtaca gctgctttgt ttctttgcaa tgcattgtat ggctttataa atgataaagt 2040
taaagaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2093

<210> 599
<211> 562
<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (349)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (383)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (437)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (445)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (473)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (524)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (549)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (561)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (562)
<223> n equals a,t,g, or c

<400> 599
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ctgaggccac aggcacacac cgccacacct ggctaatttt tattattttt tttgtagaga 120
cgaggtctca ctatgcccag gttggtctca aactcctgtg ctcaagcaat cctcccatct 180

tggctcccta agtgctggga ttataggcat gagccaccgt gcccggcctc atgtctgcat 240
gttaaaagtt ctgagaattc ctatggaaaa taaatttgac tttgcttaat gcagttcctc 300
taaacttact taattccttt ttcttttttt ctttactatt tattaattnt tctcttttct 360
cagaccttgc agggatgaaa ggnccccttt tctcaaaacc ctcttatgat ctctacactc 420
tgcaagggct tctgaangac agcangctga gaaaggccga tcctaacact tanctctttg 480
aagacacttt taaaactggt aacagtattt atagctttaa aagnacccat ggttcttaag 540
gcccgttant aaaaaaaaaa nn 562

<210> 600
<211> 528
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (8)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (11)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (104)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (417)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (444)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (458)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (493)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (507)
<223> n equals a,t,g, or c

<400> 600
nngcaagnng ncaccaaccc tcactaaagg gaacaaaagc tggagctcca ccgcggtgcg 60
gccgctctag aactagtgga tcccccgggc tgcaggaatt cggnacgagg gaggctgagg 120
ctggagtgca gtggtgtgat ctcggctcac tgcaacctct gcctcccagg ttccagcaat 180
tctcctgcct cagcctccct agtggctggg atgacaggcg cctgccatca tgcctgacta 240
gtttttgtat ttttagtaga gacggcgttt caccatgttg gccaggctgg tctcaaactc 300
ctgacctcag gtgatccgcc tacctcagcc tcccaaagtg ctgggattac aggcgtgatc 360
caccacacct ggcccttgca atcttctact ttaaggtttg cagagataaa ccaatanatc 420
cacaccgtac atctgcaata tganttcaag aaaggaanta gtaccttcaa tacttaaaaa 480
tagtcttcca canaaaatac tttattnctg atctatacaa attttcag 528

<210> 601
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (145)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (160)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (172)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (174)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (185)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (191)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (199)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (212)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (218)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (250)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (297)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (302)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (306)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (341)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (389)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (413)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (444)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (450)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (468)
<223> n equals a,t,g, or c

<400> 601
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atattttgcg agtactcaac accaacatcg atgggcggcg gaaaatagcc tttgccatca 120
ctgccattaa gggtgtgggc cgaanatatg ctcatgtggn gttgaggaaa gnanacattg 180
acctnaccaa nagggcggna gaactcactg angatgangt ggaacgtgtg atcaccatta 240
tgcagaatcn acgccagtac aagatcccag actggttctt gaacagacag aatgatngta 300
angatnaatc tacttcaagc taacatgcta tcatttctac nttgagtact gctaaggttt 360
ctttccacaa cttgtacaca atgttattna ctgcccagtt tataatttcc ctnttggttc 420
ccattttaag acttatttaa ttantatgcn ttttaaattt ttgagacntg ataga 475

<210> 602
<211> 288
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (84)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (100)
<223> n equals a,t,g, or c

<400> 602
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cctgtccctg gactctggaa tgtntggctg aagttgaggn tctcttactc tctaggccac 120
ggaattaacc cgagcaggca tggaggcctc tgctctcacc tcatcagcag tgaccagtgt 180
ggccaaagtg gtcagggtgg cctctggctc tgccgtagtt ttgcccctgg ccaggattgc 240
tacagttgtg attggaggag ttgtggccat ggcggctgtg cccatggt 288

<210> 603
<211> 432
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (365)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (408)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (416)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (421)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (425)
<223> n equals a,t,g, or c

<400> 603
ggcgccccgg agagctcttg cgcgtcttgt tcttgcctgg tgtcggtggt tagtttctgc 60
gacttgtgtt gggactgctg ataggaagat gtcttcagga aatgctaaaa ttgggcaccc 120
tgcccccaac ttcaaagcca cagctgttat gccagatggt cagtttaaag atatcagcct 180
gtctgactac aaaaggaaaa tatgttgtgt tcttctttta ccctcttgac ttcacctttg 240
tgtgccccac ggagatcatt gctttcagtg atagggcaga agaatttaag aaactcaact 300
gccaagtgat tggtgcttct gtggattctc acttctgtca tctagcatgg gtcaatacac 360
ctaanaaaca aggaggactg ggacccatga acattccttt ggtatcanac ccaacncaca 420
nttgntcagg at 432

<210> 604
<211> 371
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (282)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (291)
<223> n equals a,t,g, or c

<400> 604
atttagtgtg ataaggagaa gaacctgctg catgtcacag acaccggtgt aggaatgacc 60
agagaagagt tggttaaaaa ccttggtacc atagccaaat ctgggacaag cgagttttta 120
aacaaaatga ctgaagcaca ggaagatggc cagtcaactt ctgatttgat tggccagttt 180
ggtgtcggtt tctattccgc cttccttgta gcagataagg ttattgtcac ttcaaaacac 240
aacaacgata cccagcacat ctgggagtct gactccaatg antttctgt naattgctga 300
cccaagaggg aaacactcta ggacggggga acgacaattt acgtggagta tggaccaatt 360
tccttattaa g 371

<210> 605
<211> 392
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (292)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (322)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (330)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (331)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (342)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (363)
<223> n equals a,t,g, or c

<400> 605
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ctttcaggat taagcgattc ctggccaaga aacaaaagca aaatcgtccc attccccagt 120
ggattcggat gaaaactggg aaataaaatc aggtacaact ccaaaaggag acattggaga 180
agaaccaagc tgggtctatg aaggaattgc acatgagatg gcacacatat ttatgctgtc 240
tggaaggtgc acgatccatg ttaccatatg caagctggaa aatgtgcacc antatctggg 300
agatttcga cgtgtttttc cnctctggan nctgtttatg gnacaaggtt ggtttggttt 360
ggntccatta aattaaatta ggtaaaggcc cc 392

<210> 606
<211> 442
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (255)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (312)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (368)
<223> n equals a,t,g, or c

<400> 606
gcgtcttcag ggtggaagcc tggcgcacgt ccggagagac acccgccatt tcacccagta 60
agcgggcccg gcctgcggag gtgggcggca tgcagctccg ctttgcccgg ctctccgagc 120
acgccacggc ccccacccgg ggctccgcgc gcgccgcggg ctacgacctg tacagtgcct 180
atgattacac aataccacct atggagaaag ctgttgtgaa aacggacatt cagatagcgc 240
tcccttctgg gtgtnatgga agagtggctc cacggtcagg cttggctgca aaacacttta 300
ttgatgtagg antggtgtca tagatgaaga ttataagagg aatgttggtg ttgtactgtt 360
taattttngg caagaaagtt tgaagtcaaa aaaggtgatc gaattgcaca gtcatttgca 420
acggattttt tatccagaaa ta 442

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<211> 182
<212> DNA
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<222> (53)

<223> n equals a,t,g, or c

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<222> (124)
<223> n equals a,t,g, or c

<220>
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<222> (132)
<223> n equals a,t,g, or c

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agaaagtggt tgatccattt tttaagaaag attggtatga tgtgaaagca cctgctatgt 120
tcantataag anatattgga aagacgctcg tcaccaggac ccaaggaacc aaaattgcat 180
ct 182

<210> 608
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<212> DNA
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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>
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<222> (652)
<223> n equals a,t,g, or c

<400> 608
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tccaacatct ccgcatgatg aaacttcggc tcactccttg gcgcctgcct gatcctccaa 120
atcaccacag gactattcct agccatgcac tactcaccag acgcctcaac cgccttttca 180
tcaatcgccc acatcactcg agacgtaaat tatggctgaa tcatccgctg ccttcacgcc 240
aatggcgcct caatattctt tatctgcctc ttcctacaca tcgggcgagg cctatattac 300
ggatcatttc tctactcaga aacctgaaac atcggcatta tcctcctgct tgcaactata 360
gcaacagcct tcataggcta tgtcctcccg tgaggccaaa tatcattctg aggggccaca 420
gtaattacaa acttactatc cgccatccca tacattggga cagacctagt tcaatgaatc 480
tgaggaggct actcagtaga cagtcccacc ctcacacgat tctttacctt tcacttcatc 540
ttgcccttca ttattggcag ncctacagna ctcacctcta ttttttgccg aaacggggat 600
canncaaccc ccttagggaa tcacctnccn tttccgataa aaatcaacct tncacccttt 660
actacacaat cat 673

<210> 609
<211> 553
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (497)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (536)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (545)
<223> n equals a,t,g, or c

<400> 609
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aaacttttgg acgacaatgg gaacattgct gaagaactga gcattctcaa atggaacaca 120
gacagtgtag aagaattcct gagtgaaaag ttggaacgca tataaatctt gcttaaattt 180
tgtcctatcc ttttgttacc ttatcaaatg aaatattaca gcacctagaa aataatttag 240
ttttgcttgc ttccattgat cagtctttta cttgaggcat taaatatcta attaaatcgt 300
gaaatggcag tatagtccat gatatctaag gagttggcaa gcttaacaaa acccattttt 360
tataaatgtc catcctnctg catttgttga taccactaac aaaatgcttt gtaacagact 420
tgcggttaat tatgcaaatg atagtttgng ataattgggg ccaagtttta cgaacaacag 480
atttctaaat tagaganggt taccaggaca gatgatacta tgcctaaggg ctgggngccc 540
ttttnaagga aga 553

<210> 610
<211> 458
<212> DNA
<213> Homo sapiens

<220>
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<223> n equals a,t,g, or c

<220>
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<222> (18)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (215)
<223> n equals a,t,g, or c

<220>
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<222> (225)
<223> n equals a,t,g, or c

<220>
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<222> (281)
<223> n equals a,t,g, or c

<220>
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<222> (312)
<223> n equals a,t,g, or c

<220>
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<222> (314)
<223> n equals a,t,g, or c

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<222> (316)
<223> n equals a,t,g, or c

<220>
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<222> (344)
<223> n equals a,t,g, or c

<220>
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<222> (369)
<223> n equals a,t,g, or c

<220>
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<222> (412)
<223> n equals a,t,g, or c

<220>
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<222> (430)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (442)
<223> n equals a,t,g, or c

<220>
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<222> (456)
<223> n equals a,t,g, or c

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tgactacttt gcgcaatggg acattagttg cattccgagg tcattatttc tggatgctaa 120
gtccattcag tccaccatct ccagctcgca gaattactga agttttgggg aatcctttcc 180
cccattgata ctgttttact aaggggaatt tttcnagaaa aggtngcagc attcagcagt 240

atatttataa acaggaacct gtacagaagt gcccttggaa naaggcctgc tctaaaatta 300
tccagtggta tngngaacg acacaggtta agagacgtcg cttnaacgtg ctaaaaggac 360
ctttccaana cacaccatca gaatccataa tcacctgcca aatggggtat cnagaccaag 420
gggcctccan aaggagttaa gnggttaccg tggggngg 458

<210> 611
<211> 565
<212> DNA
<213> Homo sapiens

<220>
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<222> (5)
<223> n equals a,t,g, or c

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<222> (8)
<223> n equals a,t,g, or c

<220>
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<222> (469)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (471)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (534)
<223> n equals a,t,g, or c

<400> 611
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ctctagaact agtggatccc ccgggctgca ggaattcggc acgaggttgc agtgagccga 120
gatcgcacca ttgcactcca gtctgggcaa cagagtgaga ttccgtctca aaaaaaaaaa 180
gaaaaggaaa aaaaaatagc attatacctc ttccttgtct caaccgccat gaaaattctg 240
aacactccaa attcagttga ataatccaaa acaaaattta taagtataaa ataattttac 300
ttcttatagt aatagtatac tttaaaaagc ctcagggtat attatcttct aaacagctac 360
aattcagtgc agctacatta accaactatg ttctctagtt gaggaacaac taggcctatt 420
tcactgctgt gtagcctcag tgcctaacat gggtgccaaa taaatattng nggattacac 480
tgaattgtaa aaaccattcg tttttgttta caattgccaa aaatctcaaa aggncctgta 540
tttatgtaat tctttgaaat tatta 565

<210> 612
<211> 442
<212> DNA
<213> Homo sapiens

<220>
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<222> (229)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (253)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (294)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (297)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (319)
<223> n equals a,t,g, or c

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<222> (328)
<223> n equals a,t,g, or c

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<222> (333)
<223> n equals a,t,g, or c

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<222> (365)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (413)
<223> n equals a,t,g, or c

<220>
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<222> (415)
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<220>
<221> misc feature
<222> (440)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (441)
<223> n equals a,t,g, or c

<400> 612
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gtcggccacg tcgtccttcg gaggcctggg cggcggctcc gtgcgtattg ggccgggggt 120
cgcttttcgc gcgcccagca ttcacggggg ctccggcggc cgcggcgtat ccgtgtcctc 180
cgcccgcttt gtgtcctcgt cctcctcggg gggctacggc ggcggctang gcggcgtcct 240
gaccgcgtcc gangggctgc tggcgggcaa cgagaagcta accatgcaga actnaangac 300
cgcttggctt ctactggana agttcgcncc tgnaggggca aagggaacta aaagttaaat 360
ccgcnattgt acaaaacagg gcttggcctt cccggataaa gcattataaa gancntcagg 420
aattggggaa aaatttttgn nc 442

<210> 613
<211> 306
<212> DNA
<213> Homo sapiens

<220>
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<223> n equals a,t,g, or c

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<221> misc feature
<222> (102)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (129)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (172)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (185)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (190)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (192)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (199)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (213)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (237)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (272)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (299)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (302)
<223> n equals a,t,g, or c

<400> 613
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cttccgaacc aagtttgaga cggaacaggc tctgcgcatg ancgtggagg ccgacatcaa 120
cggcctgcnc aggtgctgga tgagctgacc ctggcccaga accgaccttg gngatgcagt 180
tcgangcctn angaagagnt ggcctaccta agnaggaccc tgagggggaa tcaattncgt 240
taaggggcca atgggaggcc attaattttg anttggttcc ttccggacct tttggccant 300
cntgtt 306

<210> 614
<211> 555
<212> DNA
<213> Homo sapiens

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<221> misc feature
<222> (392)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (409)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (433)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (497)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (543)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (545)
<223> n equals a,t,g, or c

<400> 614
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accattgaga actccaggat tgtcctgcag atcgacaatg cccgtctggc tgcagatgac 120
ttccgaacca agtttgagac ggaacaggct ctgcgcatga gcgtggaggc cgacatcaac 180
ggcctgcgca gggtgctgga tgagctgacc ctggccagga ccgacctgga gatgcagatc 240
gaaggcctga aggaagagct ggcctacctg aagaagaacc atgaggagga aatcagtacg 300
cttaggggcc aagtgggagg ccaggtcagt gtggaggtgg attccgctcc gggcaccgat 360
ctcgccaaga tcctgagtga catgcgaagc cnatatgagg tcatggccna gcagaaccgg 420
aaggatgctt aancctggtc accagcccgg actgaagaat tgaacccgga ggtcgcttgc 480
cacacggagc aacttcngat gagcaggtcc aaggttactg acctgcggcg caacccttaa 540
ggncntgaga atgaa 555

<210> 615
<211> 575
<212> DNA
<213> Homo sapiens

<220>
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<222> (4)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (28)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (57)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (173)
<223> n equals a,t,g, or c

<400> 615
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ctctagaact agtggatccc ccgggctgca ggaattcggc acgaggctaa ggctgcgttg 120
gggtgaggcc ctcacttcat ccggcgacta gcaccgcgtc cggcagcgcc agncctacac 180
tcgcccgcgc catggcctct gtctccgagc tcgcctgcat ctactcggcc ctcattctgc 240
acgacgatga ggtgacagtc acggaggata agatcaatgc cctcattaaa gcagccggtg 300
taaatgttga gcctttttgg cctggcttgt ttgcaaaggc cctggccaac gtcaacattg 360
ggagcctcat ctgcaatgta ggggccggtg gacctgctcc agcagctggt gctgcaacca 420
gcaggaggtc ctgccccctc cactgctgct gctccagctg aggagaagaa agtggaagca 480
aagaaagaag aatccgagga gtctgatgat gacatgggct ttggtctttt tgactaaacc 540
tcttttataa catgttcaat aaaaagctga acttt 575

<210> 616
<211> 346
<212> DNA
<213> Homo sapiens

<220>
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<222> (117)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (139)
<223> n equals a,t,g, or c

<400> 616
ctcgtgccga attcggcacg agccgccgcc tccgccgcag acgccgccgc gatgcgctac 60
gtcgcctcct acctgctggc tgccctaggg ggcaactcct cccccagcgc caagggnatc 120
aagaagatct tggacaacnt gggtatcgag gcggacgacg accggctcaa caaggttatc 180
agtgagctga atggaaaaaa cattgaagac gtcattgccc agggtattgg caagcttgcc 240
agtgtacctg ctggtggggc tgtagccgtc tctgctgccc caggctctgc agcccctgct 300
gctggttctg cccctgctgc agcagaggag aagaaagatg agaaga 346

<210> 617
<211> 409
<212> DNA
<213> Homo sapiens

<220>
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<222> (356)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (380)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (388)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (397)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (408)
<223> n equals a,t,g, or c

<400> 617
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tcccgttccg ctgcccgccc tgccaccatg acggaacagg ccatctcctt cgccaaagac 120
ttcttggccg gaggcatcgc cgccgccatc tccaagacgg ccgtggctcc gatcgagcgg 180
gtcaagctgc tgctgcaggt ccagcacgcc agcaagcaga tcgccgccga caagcagtac 240
aagggcatcg tggactgcat tgtccgcatc cccaaggagc agggcgtgct gtccttctgg 300
aggggcaacc ttgccaacgt cattcgctac ttccccactc aagccctcaa cttcgncttc 360
aaggataagt acaagcagan cttcctgngg ggcgtgnaca agcacacnc 409

<210> 618
<211> 473
<212> DNA
<213> Homo sapiens

<220>
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<222> (5)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

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<222> (241)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (256)
<223> n equals a,t,g, or c

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<222> (322)
<223> n equals a,t,g, or c

<220>
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<222> (337)
<223> n equals a,t,g, or c

<220>
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<222> (352)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (359)
<223> n equals a,t,g, or c

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<222> (360)
<223> n equals a,t,g, or c

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<222> (365)
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<220>
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<222> (368)
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<222> (416)
<223> n equals a,t,g, or c

<220>
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<222> (436)
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<220>
<221> misc feature
<222> (442)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (446)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (470)
<223> n equals a,t,g, or c

<400> 618
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gagagggggc gactattata caagttggca agttgatcaa agaagctgcc gggaaaagca 120
atctgaagag ggtgaccctg gagcttggag gaaagagccc ttgcattgtg ttagctgatg 180
ccgacttgga caatgctgtt gaatttgcac accatggggt attctaccac cagggccagt 240
nttgtatagc cgcatncagg atttttgtgg aagaatcaat ttatgatgag tttgttcgaa 300
ggagtgttga gcgggttaag antatatcct tgggaantcc tttgacccca gnagttcann 360
caagnccntc agattgacaa ggaccatttg gtaaatactt gaccccattg agagtnggaa 420
gaaagaaggg gccaantgga tntggnggag gccctggggg ataaaggtan ttg 473

<210> 619
<211> 604
<212> DNA
<213> Homo sapiens

<220>
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<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (371)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (440)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (492)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (500)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (537)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (554)
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<221> misc feature
<222> (587)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (593)
<223> n equals a,t,g, or c

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gaactagtgg atcccccggg ctgcaggaat tcggcacgag gtggtccccc tggcagggac 120
aaatggcgag actaccaccc aagggttgga tgggctgtct gagcgctgtg cccagtacaa 180
gaaggacgga gctgacttcg ccaagtggcg ttgtgtgctg aagattgggg aacacacccc 240
ctcagccctc gccatcatgg aaaatgccaa tgttctggcc cgttatgcca gtatctgcca 300
gcagaatggc attgtgccca tcgtggagcc tgagatcctc cctgatgggg accatgactt 360
gaagcgcttg ncagtatgtg accgaaaagg tgcttggctt gctgctacaa ggctcttgag 420
tgaccaccac atctacctgn aaggcacctt gctgaagccc aacatggtcc cccaggccat 480

gcttgcactc anaagttttn ttatgaagga gattgcccat ggcgaacccg tctcaancgc 540
tgtgcccgca caantgcccc cccgcttgtc acttgggatc aacnttncct gtnttggaag 600
gcca 604

<210> 620
<211> 312
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (41)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (307)
<223> n equals a,t,g, or c

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<220>
<221> misc feature
<222> (310)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (311)
<223> n equals a,t,g, or c

<220>
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<222> (312)
<223> n equals a,t,g, or c

<400> 620
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ccagcgagtc cctcttcgtc tctaaccacg cctattaagc ggaggtgttc ccaggctgcc 120
cccaacactc caggccctgc cccctcccac tcttgaagag gaggccgcct cctcggggct 180
ccaggctggc ttgcccgcgc tctttcttcc ctcgtgacag tggtgtgtgg tgtcgtctgt 240
gaatgctaag tccatcaccc tttccggcac actgccaaat aaacagctat ttaaggggga 300
aaaaaanann nn 312

<210> 621
<211> 248
<212> DNA
<213> Homo sapiens

<220>
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<222> (141)
<223> n equals a,t,g, or c

<220>
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<222> (193)
<223> n equals a,t,g, or c

<220>
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<222> (195)
<223> n equals a,t,g, or c

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<222> (198)
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<220>
<221> misc feature
<222> (207)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (246)
<223> n equals a,t,g, or c

<400> 621
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ggttgcacga aacacactgg ggaatggagc aaaacagtct ttgaatatcg aacacgcaag 120
gctgtgagac tacctattgt ngatattgca ccctatgaca ttggtggtcc tgatcaagaa 180
tttggtgtgg acntnggncc tgtttgnttt ttataaacca aactctatct gaaatcccaa 240
caaaanaa 248

<210> 622
<211> 344
<212> DNA
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<223> n equals a,t,g, or c

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<222> (19)
<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

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<222> (273)
<223> n equals a,t,g, or c

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<222> (279)
<223> n equals a,t,g, or c

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<222> (283)
<223> n equals a,t,g, or c

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<222> (297)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (301)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (303)
<223> n equals a,t,g, or c

<220>
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<222> (310)
<223> n equals a,t,g, or c

<220>
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<222> (312)
<223> n equals a,t,g, or c

<220>
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<222> (342)
<223> n equals a,t,g, or c

<400> 622
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gtatgggaaa tgccatgttt gtcaaagagc aactcagtct gctggacagg ttcacggagg 120
atgccaagag gctgtatggc tccgaggcct ttgccactga ctttcaggac tcagctgcag 180
ctaagaagct catcaacgac tacgtgaaga atggaactcg agggactata acctgaacga 240
catacttctc cagctgaagt acacaggcaa tgncagcgna ctnttcatcc tgcctgntca 300
ngncaagatn gnggaagtgg aagccatgtt ggttttcaga gncc 344

<210> 623
<211> 316
<212> DNA
<213> Homo sapiens

<220>
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<222> (248)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (286)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (294)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (308)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (313)
<223> n equals a,t,g, or c

<400> 623
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cggtctgaag ggtctggctg gtgagccagg ttttaaaggc agccgagggg accctgggcc 120
cccaggacca cctcctgtca tcctgccagg aatgaaagac attaaaggag agaaaggaga 180
tgaagggcct atggggctga aaggatacct gggcgcaaaa ggtatccaag gaatgccagg 240
catcccangg ctgtcaggaa tccctgggct gcctgggagg cccggncaca tcanaggaat 300
caagggaac atngga 316

<210> 624
<211> 445
<212> DNA
<213> Homo sapiens

<220>
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<222> (112)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (172)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (185)
<223> n equals a,t,g, or c

<220>
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<222> (187)
<223> n equals a,t,g, or c

<220>
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<222> (222)
<223> n equals a,t,g, or c

<220>
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<222> (241)
<223> n equals a,t,g, or c

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<222> (253)
<223> n equals a,t,g, or c

<220>
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<222> (266)
<223> n equals a,t,g, or c

<220>
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<222> (311)
<223> n equals a,t,g, or c

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<222> (327)
<223> n equals a,t,g, or c

<220>
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<222> (331)
<223> n equals a,t,g, or c

<220>
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<222> (381)
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<220>
<221> misc feature
<222> (383)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (426)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (429)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (438)
<223> n equals a,t,g, or c

<400> 624
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ccagggctat gcgccaagac cgtctttaag gcgctccagg cccctgcctt gnacgaagaa 120
catggtgaag gttggcggct acatccttgg ggagtttggg aaacctgaat tntggggacc 180
cccgntncca gccccccagt ggcagttctc cctgctccac tncaagttcc atctgtgaca 240
ngtggccagg ggncgctgct gctgtnccac ctgacatcaa gttcatcaac ctctttcccc 300
gagaccaagg ncaccatcca gggggtnctg ngggggtcggt tttccagttg cgcaatgttg 360
acgtggagtt gcagcaggag ncntggagta acttcacctt cagttcatgg gtcagcaaca 420
agttcnggnc aggtgttnga ggagt 445

<210> 625
<211> 401
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (30)
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<220>
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<222> (33)
<223> n equals a,t,g, or c

<220>
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<222> (380)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (389)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (390)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (393)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (397)
<223> n equals a,t,g, or c

<400> 625
tcgacccacg cgtccgggcg ggtccgccgn gantaagacc cgctgcccgg cacctctagg 60
gtgtgatctg accggtcgcg ggggaccagc ccagccctat ttcggctcga gcgaggaact 120
tctgctcccg tgactgaact ctgatcttga tagagagtcc cggccatggc agccaaagga 180
ggcaccgtca aagctgcttc agcattcaat gccactgaag atgcccagac cctgaggaag 240
gccatgaagg ggcttggcac cgacgaagat gccatcatca gcgtcctcgc ctaccgcaac 300
acagcccagc gccaggaaat caggacggcc ttacaagagc accattcggc aggggacctt 360
gtgttaagga acggaccccn ttttgtttnn gantggngtg a 401

<210> 626
<211> 315
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (55)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (103)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (129)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (163)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (240)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (257)
<223> n equals a,t,g, or c

<220>
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<222> (296)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (303)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (308)
<223> n equals a,t,g, or c

<400> 626
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gctggcacct gggccccccc gggagctggt gctggtggtc cangtgcata accggcccga 120
atacctcana ctgctgctgg actcacttcg aaaagcccag ggnaattgac aacgtcctcg 180
tcatctttag ccatgacttc tggtcgaccg agatcaatca gctgatcgcc ggggtgaatn 240
tctgtccggt tctgcangtg ttctttcctt tcagcattca gttgttccct aacgantttc 300
cangttantg accta 315

<210> 627

<211> 412
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (211)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (282)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (319)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (320)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (327)
<223> n equals a,t,g, or c

<400> 627
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aagtgggatc gagacatgta agcagcatca tggaggtttg aagatgccgc atttggattg 120
gatgaattcc aaattctgct tgcttgcttt ttaatattga tatgcttata cacttacact 180
ttatgcacaa aatgtagggt tataataatg ntaacatgga catgatcttc tttataattc 240
tactttgagt gctgtctcca tgtttgatgt atctgagcag gntgctccac aggtagctct 300
agcagggctg gcaacttann aggtggngag cagagaattc tcttatccaa catcaacatc 360
ttggtcagat ttgaactctt caatctcttg cactcaaagc ttgataagga aa 412

<210> 628
<211> 577
<212> DNA
<213> Homo sapiens

<220>
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<220>
<221> misc feature
<222> (408)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (418)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (424)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (430)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (438)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (445)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (458)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (460)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (474)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (506)
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<220>
<221> misc feature
<222> (518)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (545)
<223> n equals a,t,g, or c

<220>
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<222> (546)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (560)
<223> n equals a,t,g, or c

<400> 628
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agcttacgta cgcgtgcatg cgacgtcata gctcttctat agtgtcacct aaattcaatt 120
cactggccgt cgttttacaa cgtcgtgact gggaaaaccc tggcgttacc caacttaatc 180
gccttgcagc acatccccct ttcgccagct ggcgtaatag cgaagaggcc cgcaccgatc 240
gcccttccca acagttgcgc agcctgaatg gcaaatggga cgcgccctgt agcggcgcat 300
taagcgcggc gggtgtggtg gttacgcgca gcgtgaccgc tacacttgcc agcgccctac 360
gcccggtcct ttcgtttctt cccttccttt ctcgccacgt tcgccggntt tccccgtnaa 420
gctntaaatn gggggctncc tttanggttc cgattaangn tttacgggac cttngaccca 480
aaaacttgat tagggtgatg gttacntaat gggccatngc ctgataaacg gttttgccct 540
ttgannttgg agtcccgttn ttaaaaggga ctttggt 577

<210> 629
<211> 703
<212> DNA
<213> Homo sapiens

<220>
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<222> (146)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (344)
<223> n equals a,t,g, or c

<220>
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<222> (391)
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<220>
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<222> (414)

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<220>
<221> misc feature
<222> (428)
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<220>
<221> misc feature
<222> (438)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (457)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (494)
<223> n equals a,t,g, or c

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<222> (499)
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<220>
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<220>
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<222> (603)
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<220>
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<220>
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<222> (643)
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<222> (651)
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<220>
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<222> (668)
<223> n equals a,t,g, or c

<400> 629
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cgacgtcata gctcttctat agtgtcacct aaattcaatt cactggccgt cgttttacaa 120
cgtcgtgact gggaaaaccc tggcgntacc caacttaatc gccttgcagc acatccccct 180
ttcgccagct ggcagtaata gcgaagaggc ccgcaccgat cgcccttccc aacagttgcg 240
cagcctgaat ggcgaatggg acgcgccctg tagcggcgca ttaagcgcgg cgggtgtggt 300
ggttacgcgc agcgtgaccg ctacacttgc cagcgcccta gcgnccgctc ctttcgcttt 360
cttcccttcc tttctcgcca cgttcgccgg ntttccccgt caagctctaa atcnggggct 420
ccctttangg ttccgatnta gtgctgtacg gcacctngac cccaaaaaac ttgattaggg 480
tgatggttca cgtngtggnc atcgccctga tagacggntt ttcgcccttt gacgttggag 540
nccacgttct taatagtgga ctctttggtc caaacnggan caacantgaa cccctatctc 600
ggnctattct tttgatttat nagggatttt gncgatttca ggnctattgg ntaaaaaatg 660
gatcttgntt ttaaccaaaa atttaaacgg cggaatttta agc 703

<210> 630
<211> 638
<212> DNA
<213> Homo sapiens

<220>

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<223> n equals a,t,g, or c

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<222> (70)
<223> n equals a,t,g, or c

<220>
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<222> (72)
<223> n equals a,t,g, or c

<220>
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<222> (75)
<223> n equals a,t,g, or c

<220>
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<220>
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<222> (120)
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<222> (153)
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<220>
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<222> (213)
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<220>
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<222> (222)
<223> n equals a,t,g, or c

<220>
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<222> (245)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (256)
<223> n equals a,t,g, or c

<220>
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<222> (305)
<223> n equals a,t,g, or c

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<220>
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<222> (319)
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<220>
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<222> (327)
<223> n equals a,t,g, or c

<220>
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<222> (329)
<223> n equals a,t,g, or c

<220>
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<222> (342)
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<221> misc feature
<222> (351)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (354)
<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>
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<222> (416)
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<220>
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (502)
<223> n equals a,t,g, or c

<220>
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<222> (526)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (537)
<223> n equals a,t,g, or c

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<220>
<221> misc feature
<222> (574)
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<220>
<221> misc feature
<222> (593)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (613)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (629)
<223> n equals a,t,g, or c

<400> 630
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gggcggccgn tntanaggat ccaagcttac gtacgcgtgc atgcnacgtc atagctcttn 120
tatagggtca cctaaattca attcactggc cgncgtttta caacgtcgtg actgggaaaa 180
ccctggcgtt acccaactta atcgccttgc agnacatccc cntttcgcca gctggcgtaa 240
tagcnaaaag gcccgnaccg atcgcccttc ccaacagttg cgcagcctga atggcaaatg 300
ggacncnccc tgtancggng cattaancnc ggcgggtgtg gnggttaccc ncancgngac 360
cgctacactt gccagngccc tagcgcccgc tcctttcgct ttcttccctt cctttntcgc 420
cacgttcgcc ggctttcccc gtcaagctnt aaatcggggg ctccctttag ggttccgatt 480
aagngcttta cgggaccttn gnccccaaaa aaacttgatt aggggngatg gntcacngta 540
aaggggccat tgcccttgat aaaacggttn tttngccctt ttgaccttgg aantccccgt 600
ttctttaaaa aangggacct tttggttcna actgggaa 638

<210> 631
<211> 187
<212> DNA
<213> Homo sapiens

<400> 631
ctaagttcta gatcgcgagc ggccgctcta gaggatccaa gcttacgtac gcgtgcatgc 60
gacgtcatag ctcttctata gtgtcaccta aattcaattc actggccgtc gttttacaac 120
gtcgtgactg ggaaaaccct ggcgttaccc aacttaatcg ccttgcagca catcccccttt 180
tcgccag 187

<210> 632
<211> 305
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (21)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (23)
<223> n equals a,t,g, or c

<400> 632
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cccgggtcga cccacgcgtc cgactagttc tagatcgcga gcggccgctc tagaggatcc 120
aagcttacgt acgcgtgcat gcgacgtcat agctcttcta tagtgtcacc taaattcaat 180
tcactggccg tcgttttaca acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat 240
cgccttgcag cacatccccc tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat 300
cgccc 305

<210> 633
<211> 187
<212> DNA
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<223> n equals a,t,g, or c

<220>
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<222> (181)
<223> n equals a,t,g, or c

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cgcctgcagg taccggtccg gaattcccgg gtcgacccac gcgtccgaaa aaaaaaaaaa 120
aaaaaaaaaa aaaaaaaaaa gggnggacga tctagaggat ccaaagctta cgtacncntn 180
natgcaa 187

<210> 634
<211> 243
<212> DNA
<213> Homo sapiens

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<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

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<221> misc feature
<222> (218)
<223> n equals a,t,g, or c

<220>
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<222> (229)
<223> n equals a,t,g, or c

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caggtaccgg tccggaattc ccgggtngac ccacgcgtcc gtggaaatct gtcctccana 120
atccaggcca naaagttcac agtcaaatgg ggaggggtat tcttnatgca ggagacccca 180
ggccctggag gctgcnacat acctnaatcc tgtcccangc cggatcctnc tgaagccctt 240

ttt 243

<210> 635
<211> 180
<212> DNA
<213> Homo sapiens

<400> 635
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gagggggcgg ccgctctaga ggatccaagc ttacgtacgc gtgcatgcga cgtcatagct 120
cttctatagt gtcacctaaa ttcaattcac tggccgtcgt tttacaacgt cgtgactggg 180

<210> 636
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<212> DNA
<213> Homo sapiens

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<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (497)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (507)
<223> n equals a,t,g, or c

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<222> (639)
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<220>
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<222> (657)
<223> n equals a,t,g, or c

<220>
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<222> (747)
<223> n equals a,t,g, or c

<400> 636
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gggtcgaccc acgcgtccgc tagttctaga tcgcgagcgg ccgctctaga ggatccaagc 120
ttacgtacgc gtgcatgcga cgtcatagct cttctatagt gtcacctaaa ttcaattcac 180
tggccgtcgt tttacaacgt cgtgactggg aaaaccctgg cgttacccaa cttaatcgcc 240
ttgcagcaca tccccctttc gccagctggc gtaatagcga agaggcccgc accgatcgcc 300
cttcccaaca gttgcgcagc ctgaatggcg aatgggacgc gccctgtagc ggcgcattaa 360
gcgcggcggg tgtggtggtt acgcgcagcg tgaccgctac acttgccagc gccctagcgc 420
ccgctccttt cgctttcttc ccttcctttc tcgccacgtt cgccggcttt ccccgtcaag 480
ctctaaatcg ggggctncct ttagggntcc gatttaagtg ctttacggac ctcgacccca 540
aaaaacttga ttagggtgat gggtcacgta gtgggccatc gcctgataga cggtttttcgc 600
ctttgacgtt ggagtcacgt cttaataggg actcttgtnc aaactggaac aacactnaac 660
ctatttggct atcttttgat tataaggatt tgccgattcg gcattggtaa aaatgagtgt 720
tacaaaatta cgcgattaca aaaatan 747

<210> 637
<211> 497
<212> DNA
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<220>
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<222> (415)
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<220>
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<222> (445)
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<220>
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<220>
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<222> (463)
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<220>
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<222> (497)
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acgtcatagc tcttctatag tgtcacctaa attcaattca ctggccgtcg ttttacaacg 120
tcgtgactgg gaaaaccctg gcgttaccca acttaatcgc cttgcagcac atcccccttt 180
cgccagctgg cgtaatagcg aagaggcccg caccgatcgc ccttcccaac agttgcgcag 240
cctgaatggc gaatgggacg cgccctgtag cggcgcatta agcgcggcgg gtgtggtggt 300
tacgcgcagc gtgaccgcta cacttgccaa gcgccctaag cgcccgttcc tttcgctttc 360
ttcctttctt ttttngccac gttcggccgg ctttccccg taaagcttta aatcnggggg 420
gttcccttaa ggggttccga ttaannggtt ttacgggaac ttngacccca aaaaaacttg 480
attaggggg aaggttn 497

<210> 638
<211> 509
<212> DNA
<213> Homo sapiens

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<221> misc feature
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<222> (492)
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<220>
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<222> (496)
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gcgacgtcat agctcttcta tagtgtcacc taaattcaat tcactggccg tcgttttaca 120
acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat cgccttgcag cacatccccc 180
tttcgccagc tggcgtaata gcgaagaggc ccgcaccgat cgcccttccc aacagttgcg 240
cagcctgaat ggcgaatggg acgcgccctg tagcggcgca ttaagcgcgg cgggtgtggt 300
ggttacgcgc agcgtgaccg ntacacttgc cagcgcccta gcgcccgntc ctttcgcttt 360
cttccttctt tctcggcacg gtcgnccggc tttnccccgnc aagctntaaa tcgggggct 420
tccntttagg ggttccgaat taagggcttt accgggaacc ntngaacccc caaaaaactt 480
tgaattaggg tngaangggt tcacggtaa 509

<210> 639
<211> 507
<212> DNA
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<221> misc feature
<222> (214)
<223> n equals a,t,g, or c

<220>
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<222> (263)
<223> n equals a,t,g, or c

<220>
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<222> (298)
<223> n equals a,t,g, or c

<220>
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<222> (334)
<223> n equals a,t,g, or c

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<222> (355)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (356)
<223> n equals a,t,g, or c

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<222> (360)
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<220>
<221> misc feature
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<222> (453)
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<220>
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<222> (485)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (489)
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gcgacgtcat agctcttcta tagtgtcacc taaattcaat tcactggccg tcgttttaca 120
acgtcgtgac tgggaaaacc ctggcgttac ccaacttaat cgccttgcag cacatccccc 180
tttcgccagc tggcataata gcgaagaggc ccgnaccgat cgcccttccc aacagttgcg 240
cagcctgaat ggcgaatggg acncgccctg tagcggcgca ttaagcgcgg cgggtgtngt 300
ggttacgcgc agcgtgaccg ctacacttgc agcnccctag cgcccgctcc tttcnntttn 360
ttnccttcct ttntngcacg tttnacggct ttcccgtcaa gctctanatc gggggctcct 420
ttagggttcn atttaatgtt tacggacctt tanccaaaaa acttgatatg gttatggtta 480
ntgtnttgng ccattgcctt atttccc 507

<210> 640
<211> 496
<212> DNA
<213> Homo sapiens

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<220>
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<222> (33)
<223> n equals a,t,g, or c

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<222> (392)
<223> n equals a,t,g, or c

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<220>
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<222> (396)
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<222> (427)

<223> n equals a,t,g, or c

<220>
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<222> (460)
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<220>
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<222> (463)
<223> n equals a,t,g, or c

<220>
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<222> (478)
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cctcaaggtt aaaccctcgg aatacgatag gaaaatgtaa aggccaagat ccaggataag 120
gaaggnattc ctcctgaatn cagcagagaa ctgaatcttt gcctggncaa gcagctggga 180

aggatgggac gttactttgt gctgaactta caatatttca aaaggggttc ttacttcttn 240
atcttgtgtt gagaatttcg tgggtggtgc ttaggaaagg ggaaggagga agtttttaca 300
accattccca ggaaggntta ggcccagggn aaaggangg t ttaagntggt tgtncncgaa 360
attttttagg gngggttgng attgggcaan tnngtnggct ttggttgggg ggttcccctt 420
tttaanngan ttnggggntt nggggngttt tttttgggnn ggnaaatttt tttaaggnct 480
tttttttggg ggaaaa 496

<210> 641
<211> 186
<212> DNA
<213> Homo sapiens

<220>
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<222> (112)
<223> n equals a,t,g, or c

<220>
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<222> (133)
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<220>
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<222> (148)
<223> n equals a,t,g, or c

<220>
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<222> (167)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (177)
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gcccagtgac accattgaga atgtcaaagc caaaattcaa gacaaggagg gnatcccacc 120
tgaccagcag cgnctgatat ttgccggnaa acagctggaa ggatggncgc aactctntca 180
gactac 186

<210> 642
<211> 519
<212> DNA
<213> Homo sapiens

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<222> (168)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (188)
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<220>
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<222> (209)
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<220>
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<222> (216)
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<220>
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<220>
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<222> (218)
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<220>
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<220>
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<222> (428)
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<220>
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<222> (437)
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<221> misc feature
<222> (494)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (500)
<223> n equals a,t,g, or c

<400> 642
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gctccgatgt atttgatggt gacctgggaa tggggcagcc aagggctgca aagcctcccc 120
acacatgacc ccagccctct acagcggtaa ggtgagggac ccacattncc cctgccctct 180
gagacttngg gggacgttgc ccccctgana tgcagnnngg gcctgaatat gtgaaccagc 240
cagatgttcg gccccagccc ccttcgcccc gaagatgngc tngnctgctg cccgacctnc 300
ttggtgccac tctggnaagn ggccaagaat ctnttcccca gggaagaatt gggtcgtcaa 360
aagnggtttt tgcnttttgg gggttccgtt gagaancccg agtangttta caaccccaag 420
ggaagaanct tcccctnaag ccccaacctt cttccttgct taagccagcc tttgacaacc 480
tctaataatt ggancaagan ccaacaaaac cggggggtc 519

<210> 643
<211> 138
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (11)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (72)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (74)
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<222> (92)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (102)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (103)
<223> n equals a,t,g, or c

<400> 643
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gtgacatcta tnanaggaaa agtgatggca tntatatcat anntctcaag aggacctggg 120
agaagcttct gctgggca 138

<210> 644
<211> 602
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (530)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (554)
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<223> n equals a,t,g, or c

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<221> misc feature
<222> (591)
<223> n equals a,t,g, or c

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<400> 644
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gcagcatggc tgaccaactg actgaagagc agattgcaga attcaaagaa gctttttcac 120
tatttgacaa agatggtgat ggaactataa caacaaagga attgggaact gtaatgagat 180
ctcttgggca gaatcccaca gaagcagagt tacaggacat gattaatgaa gtagatgctg 240
atggtaatgg cacaattgac ttccctgaat ttctgacaat gatggcaaga aaaatgaaag 300
acacagacag tgaagaagaa attagagaag cattccgtgt gtttgataag gatggcaatg 360
gctatattag tgctgcagaa cttcgccatg tgatgacaaa ccttggaaga gaagttaaca 420
gatgaagaag tttgatgaaa tgatcaggga agcagatatt gatggtgatg gtcaagtaaa 480
ctatgaagag tttgtaccaa atgatgacag caaaagtgaa agacctttttn ccagaatggg 540
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gn 602

<210> 645
<211> 112
<212> DNA

<213> Homo sapiens

<220>
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<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

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<222> (41)
<223> n equals a,t,g, or c

<220>
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<222> (48)
<223> n equals a,t,g, or c

<220>
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<222> (59)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (106)
<223> n equals a,t,g, or c

<400> 645
atntgttggg ccggaactgg gctngtttca ccggaaagaa ngtggganct gcctctgana 60
atgtgtatgt ccacatacca caccttagga attctcacga aaagtnttcc aa 112

<210> 646
<211> 514
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (178)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (348)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (389)
<223> n equals a,t,g, or c

<220>
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<222> (391)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (444)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (463)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (466)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (473)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (485)
<223> n equals a,t,g, or c

<400> 646
cagcgggcca ctctggatcc tgggcgacgt cttcatcggc cgctactaca ctgtgtttga 60
ccgtgacaac aacagggtgg gcttcgccga ggctgcccgc ctctagttcc caaggcgtcc 120
gcgcgccagc acagaaacag aggagagtcc cagagcagga ggcccctggc ccagcggncc 180
ctcccacaca cacccacaca ctcgcccgcc cactgtcctg ggcgccctgg aagccggcgg 240
gccaagccga cttgctgttt tgttctgtgg tttcccctcc ctgggttcaa aaatgctgcc 300
tgctgtctgt ctctccatct tgtttggtgg gttaaactga tccaaaanaa aatttgttcc 360
gtgattggaa aaaccaccca acttggaanc nactcttttt cctgggtcct tctctccagg 420
atcccccccg gcctacaagc cgtnggttaa cctacccaac agngcncccg gcnccttgaa 480
ctgcngctaa gcccttccaa ttggccattg gttc 514

<210> 647
<211> 525
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (11)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (14)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (23)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (73)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (480)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (517)
<223> n equals a,t,g, or c

<400> 647
ccctactaat ntgngcaaaa gcncngagct ccaccgcggt ggcggccgct ctagaactag 60
tggatccccc ggnttgcagg aattcggcac gagcacgcag cggcccgtgg acatcgtctt 120
cctgctggac ggctccgagc ggctgggtga gcagaacttc cacaaggccc ggcgcttcgt 180
ggagcaggtg gcgcggcggc tgacgctggc ccggagggac gacgaccctc tcaacgcacg 240
cgtggcgctg ctgcagtttg gtggccccgg cgagcagcag gtggccttcc cgctgagcca 300
caacctcacg gccatccacg aggcgctgga gaccacgcaa tacctgaact ccttctcgca 360
cgtgggcgca ggcgtggtgc acgccatcaa tgccatcgtg cgcagcccgc gtggcggggc 420
ccggaggcac gcagagctgc cttcgtggtc ctcacggacg gcgtcacggg caacgacagn 480
ctgacgagtc ggcgcactcc atgcgcaagc agaacgngga cccac 525

<210> 648
<211> 317
<212> DNA
<213> Homo sapiens

<220>
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<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (118)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (126)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (146)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (159)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (171)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (173)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (176)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (185)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (194)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (207)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (245)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (258)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (297)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (301)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (316)
<223> n equals a,t,g, or c

<400> 648
gcncagatgg gcatgctgaa ggggcctctt cttaacaaat ttctgaccac agccaaagat 60
aagaaccgct gggaggacnc tggtaagcag ctctacaacg tggaggccac atcctatncc 120
ctcttngccc tactgcagct aaaagncttt gactttgtnc ctcccgtcgt ncnttngctc 180
aatgnacaga gatnctacgg tggtggntat ggctctaccc aggccacctt catggtgttc 240
caagncttag ctcaatanca gaaggacggc cctgaccacc aggcactgaa ccttgangtg 300
nacctccaaa tgctcng 317

<210> 649
<211> 575
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (501)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (509)
<223> n equals a,t,g, or c

<400> 649
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ctttcaaagt tcaccaatac tttaatgtag agcttatcca gcctggagca gtcaaggtct 120
acgcctatta caacctggag gaaagctgta cccggttcta ccatccggaa aaggaggatg 180
gaaagctgaa caagctctgc cgtgatgaac tgtgccgctg tgctgaggag aattgcttca 240
tacaaaagtc ggatgacaag gtcaccctgg aagaacggct ggacaaggcc tgtgagccag 300
gagtggacta tgtgtacaag acccgactgg caaggttcaa gctgtccaat gactttgacc 360
gagtacatca tggccattga gcagaccatc aagtcaggct cggatgaggt gcaggttgga 420
cagcagcgca cgttcatcag ccccatcaag tgcagagaag ccctgaagct tgaggagaag 480
aaacactact tcatgtgggg nctcttctnc caattctggg gagagaagcc caaccttagc 540
tacatcatcg ggaaggacac ttgggtggag cactg 575

<210> 650
<211> 277
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (186)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (243)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (256)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (265)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (267)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (269)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (276)
<223> n equals a,t,g, or c

<400> 650
tcgacccacg cgtccggcat tgtctatcat tgcactggag atccaagcac agaagtgtgt 60
agagttaaca gaaggaatag aatgtcttca gacacattcc aagataaatg gcagagattt 120
gaccttctgg caagaacttg tatccaagtg tttaactgaa tattcatcta agcaaagtgg 180
ttccanacca aatgttccag aagtttgaaa atggatttgt tcctggacgt actgcacggc 240
aanctgaagc acaggntact aacgngntna acccanc 277

<210> 651
<211> 357
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (13)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (86)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (89)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (97)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (100)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (106)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (175)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (185)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (221)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (289)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (299)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (321)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (324)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (355)
<223> n equals a,t,g, or c

<400> 651
ggcacaggnt ccngggtgga gctggctgag tcgcgcgctc tgctccaccc gggggggctg 60
ttttttctgg gcctggctcg cggcgnacng agatggnagn gcagtnggac gaggccgtga 120
agtaatacac cctaggagga gattcagaag cacaaccaca gcaagagcac ctggnctgat 180
cctgncacca caaggtgtac gaatttgacc aaatttctgg nagaggcatc cctggtgggg 240
gaggaagttt taaggggaac aagcttggag gtgacgctac ttgaggaant tttgagggnt 300
gttcggggca cttttaccag ntgncccaag ggaaaattgt tcccaaaaac atttnca 357

<210> 652
<211> 190
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (138)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (146)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (148)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (172)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (180)
<223> n equals a,t,g, or c

<400> 652
ggacgctact tcccctatca tagaagagct tatcaccttt catgatcacg ccctcataat 60
cattttcctt atctgcttcc tagtcctgta tgcccttttc ctaacactca caacaaaact 120
aactaatact aacatctnag acgctnanga aatagaaacc gtctgaacta tnctgcccgn 180
catcatccta 190

<210> 653
<211> 603
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (415)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (600)
<223> n equals a,t,g, or c

<400> 653
gcttcgaccc cgccggagga ggagaccccca ttctatacca acacctattc tgatttttcg 60
gtcaccctga agtttatatt cttatcctac caggcttcgg aataatctcc catattgtaa 120
cttactactc cggaaaaaaa gaaccatttg gatacatagg tatggtctga gctatgatat 180
caattggctt cctagggttt atcgtgtgag cacaccatat atttacagta ggaatagacg 240
tagacacacg agcatatttc acctccgcta ccataatcat cgctatcccc accggcgtca 300
aagtatttag ctgactcgcc acactccacg gaagcaatat gaaatgatct gctgcagtgc 360
tctgagccct aggattcatc tttcttttca ccgtaggtgg cctgactggc attgnattag 420
caaactcatc actagacatc gtactacacg acacgtacta ccgttgtagc ccacttccac 480
tatgtcctat caataggagc tggatttgcc atcataggaa ggcttcattc actgatttcc 540
ctattctcag gctacaccct agaccaaacc tacgccaaaa atcatttcac tatcataatn 600
cac 603

<210> 654
<211> 356
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (198)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (270)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (302)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (328)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (340)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (347)
<223> n equals a,t,g, or c

<400> 654
ggttttttc ttcgcaggat ttttctgagc cttttaccac tccagcctag cccctacccc 60
ccaattagga gggcactggc cccaacagg catcaccccg ctaaatcccc tagaagtccc 120

actcctaaac acatccgtat tactcgcatc aggagtatca atcacctgag ctcaccatag 180
tctaatagaa aacaaccnaa accaaataat tcaagcactg cttattacaa ttttactggg 240
tctctatttt accctcctac aaagcctcan agtacttcga gtctcccttc accatttccg 300
anggcatcta cggctcaaca ttttttgnag cccaggcttn cacgganttt cacgtc 356

<210> 655
<211> 682
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (660)
<223> n equals a,t,g, or c

<400> 655
gcgcaagtag gtctacaaga cgctacttcc cctatcatag aagagcttat cacctttcat 60
gatcacgccc tcataatcat tttccttatc tgcttcctag tcctgtatgc ccttttccta 120
acactcacaa caaaactaac taatactaac atctcagacg ctcaggaaat agaaaccgtc 180
tgaactatcc tgcccgccat catcctagtc ctcatcgccc tcccatccct acgcatcctt 240
tacataacag acgaggtcaa cgatccctcc cttaccatca aatcaattgg ccaccaatgg 300
tactgaacct acgagtacac cgactacggc ggactaatct tcaactccta catacttccc 360
ccattattcc tagaaccagg cgacctgcga ctccttgacg ttgacaatcg agtagtactc 420
ccgattgaag cccccattcg tataataatt acatcacaag acgtcttgca ctcatgagct 480
gtccccacat taggcttaaa aacagatgca attcccggac gtctaaacca aaccactttc 540
accgctacac gaccgggggt atactacggt caatgctctg aaatctgtgg agcaaaccac 600
agtttcatgc ccatcggcct agaattaatt cccctaaaaa tctttgaaat aagggcccgn 660
atttacccta tagcacccct ct 682

<210> 656
<211> 520
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (429)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (442)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (449)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (483)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (485)
<223> n equals a,t,g, or c

<400> 656
gagaagagct tatcaccttt catgatcacg ccctcataat cattttcctt atctgcttcc 60
tagtcctgta tgcccttttc ctaacactca caacaaaact aactaatact aacatctcag 120
acgctcagga aatagaaacc gtctgaacta tcctgcccgc catcatccta gtcctcatcg 180
ccctcccatc cctacgcatc ctttacataa cagacgaggt caacgatccc tcccttacca 240
tcaaatcaat tggcaccaat ggtactgaac ctacgagtac accgactacg gcggactaat 300
cttcaactcc tacatacttc ccccattatt cctagaacca ggcgacctgc gactccttga 360
cggtgacaat cgagtagtac tcccgattga agccccattc gtataataat tacatcacaa 420
gacgcttgna ctcaagagct gncccacant aggcttaaaa acaggatgca atttccgggc 480
ggntnaaaca aaacaatttt accggtacac gaacgggggg 520

<210> 657
<211> 353
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (227)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (340)
<223> n equals a,t,g, or c

<400> 657
gcactttctg ccaaagaaat ctctcctttt gcttctagca ccgactagat ttccttcagc 60
tgatgattga ctcccagaat tcgaaagaaa ctgagtccca caaagctctg tctgatctgg 120
agctcgcagc ccagtcaata atcttcattt ttgctggcta tgaaaccacc agcagtgttc 180
tttccttcac tttatatgaa ctggccactc accctgatgt ccagcanaaa ctgcaaaagg 240
gagattgatg cagttttgcc caataaggca ccacctacct atgatgccgt ggtacagatg 300
gattaccttg acatggtggt gaatgaaacc tcaaattatn cccgttggta tta 353

<210> 658
<211> 362
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (203)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (215)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (240)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (262)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (310)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (321)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (333)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (338)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (362)
<223> n equals a,t,g, or c

<400> 658
ggcanaggcc accaccatcc tgcattgccc actttacttg gccttctcct ggctctaact 60
caggcagcca agacccctcc cacttccttc tttggcctcc ctctcctcag gtatgaaaat 120
gaagctggcc ctgcgcccag gcgtttgaag gctgacatca acggcttgcg ccgagtcctg 180
ggatgagctg accctggcca ggnctgacct ggagntgcag atcgagggcc tgaatgaggn 240

agctagcctt acctgaagtg gnaccacgaa ggagggagat ggaaggagtt tcagcagcca 300
gttggccggn caagttcaat nttggagatg ggncgganca ccgggtgtgg gacctgaccc 360
gn 362

<210> 659
<211> 447
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (100)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (147)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (168)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (175)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (202)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (204)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (228)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (240)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (247)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (286)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (294)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (353)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (445)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (446)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (447)
<223> n equals a,t,g, or c

<400> 659
gcttctncgc tccttctagg atctccgcct ggntcggccc gcctgcntcc actcctgcct 60
ctaccatgtc catcaaggtg acccagaagt cctacaaggn gtccacctct agccccc ggg 120

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ccttcagcag ccgctcctac acgaatnggc ccggttcccg catcaacncc tcganttctt 180
cccgaatagg cagcagcaac tntngcagtg gcctgggcgg cggctatngt ggggccagcn 240
gcatggnagg catcaccgca gttacggtca accagagcct gctganccccc cttntcctgg 300
aggtggaccc caacatccag gccgtgcgca cccaggagaa ggagcagatc aanaccctca 360
acaacaagtt tgcctcttca tagacaaggt aggttcctgg agcagcagaa caagatgttg 420
gaaaccaagt agagctcctt gagcnnn                                     447

<210> 660
<211> 295
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (70)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (73)
<223> n equals a,t,g, or c

<220>
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<222> (82)
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agtagaacgn gancctccag gntgcnatgc aagtntgtcg caatgttctc ctgggaccct 120
nagctggtgc nagggggtgg ggcntccaaa atggctgtgg cccatgcntt ganagaaaaa 180
tccanggcca tggactggtg tgggaacaat ggccatacag ggctgttgnc cagggcccta 240
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<210> 661
<211> 212
<212> DNA
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ctcatcacca acgatgaggc atacgctgag gagtttggca acgagacgtg gggcgtaaca 120
aaggcagcag agaaacaaat gaaggacaaa caggacgagg agcagaggct taaggaggag 180
gaagaagaca agaaacgcaa agaggangan ga 212

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cctgggctgg accntttcat cagacaggct tattagactc tatgctagaa catgaagctt 120
atnggatcng 130

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tatctccaag aatgggcaga cccgagagca tgcccttctg gcttacacac tgggtgtgaa 120
acaactaatt gtcggtgnna acaaaatgga ttccactgag ccaccctaca gccagaagag 180
atatgaggaa attgntaagg aagtnagcac ttaccnttaa gaaaaaactg gg 232

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caccacgtcc cgaattctca gacgacacct ggagactgtc ccgacactcc cctgagaggt 180
ttctggggcc cgctgcggtc acgagggggg gcccggttac ccaattcgtc ctatagtgat 240
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<211> 376
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<222> (334)
<223> n equals a,t,g, or c

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<222> (335)
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<222> (336)

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aagccaaaat gggaaaggaa aagactcata tcaacattgt cgtcattgga cacgtagatt 120
cgggcaagtc caccactact ggccatctga tctataaatg cggtggcatc gacaaaagaa 180
ccattgaaaa atttgagaag gaggctgctg agatgggaaa gggctccttc aagtatgcct 240
gggtcttgga taaactgaaa gctgagcgtg aacgtggtat cnccattgga tatctccttg 300
tggaaatttg agaccagcaa gtactatgtg actnnncatt gnatgccccc aggacacaga 360
gactttatcc agaaac 376

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<222> (323)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (325)
<223> n equals a,t,g, or c

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<222> (332)
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cgaccgctcg cagcgctctc ttgaccacta tgagcctcct gtccagccgc gcggcccgtg 120
tccccggtcc ttcgagctcc ttgtgcgcgc tgttggtgct gctgctgctg ctgacgcagc 180
cagggcccat cgccagcgct ggtcctgccg ntgctgtgtt ganagagctg cgttgccgtt 240
tgtttacaga ccacgcaagg agtccatccc aaaaatgatc agtaatntgc aagtgtncgc 300
cataggccca acagtgctcc aangngggaa gn 332

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gganctgntc atgtccttgn atccanacaa attgtgccga cgacgccatg gaccctggta 180
ctaaaganag agcttgttgc gcatttggaa ttgcaccatg cacgggcctg accttctggg 240
naccccagct gtgtaggcag aggacagggt gacaattttg tctttgcgca tggcntaatg 300
ccatctgtgg tcatgacagg ttgttcatca agtnnggant caggcaatga aggcngtggg 360
t 361

<210> 668
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<212> DNA
<213> Homo sapiens

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ttgcacacgc ctgaaaagtg ggtgaggttc aagtacccaa agctcatctc ctattcctac 180
atggttcgtg gggccactt tgcggccttt gaggagccgg agctgctcgc ccaggacatc 240
cgcaagttcc tgtcggtgct ggagcggcat gnanccaccc ctctcccccc gcttgccact 300
tcccccaca atgccctcca ggntttcttg ggggaagata accntttctg aggatgantt 360
tgcctccgtc ccntgnccag ttgggancc agttcaaccc ctnaaccttc nagttaattc 420
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aaaaaaaatc nggggggggc ccgtaacaat tgnccnaa 518

<210> 669
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<212> DNA
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gccgctctag aactagtgga tcccccgggc tgcaggaatt cggcacgaga gatagaggag 120
gcttccctcc aagaggaccc cggggttccc gagggaaccc ctctggagga ggaaacgtcc 180
agcaccgagc tggagactgg cagtgtccca atccttcaat tggtgatttc tgctgtgatg 240
taattgtatg caggggttgt ggaaaccaga acttcgcctg gagaacagag tgcaaccagt 300
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atcgtggtgg tcccggtgga atgttcagag gtggccgtgg tggagacaga ggtggcttcc 420
gtggtggccg gggcatggac cgaggtggct ttngtggagg aagacgaggt ggccctgggg 480
ggcccctgga cctttgatgg aacagatggg aggaagaaga ggaggacgtg gaggacctgg 540
gaaaa 545

<210> 670
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<212> DNA
<213> Homo sapiens

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gctacagtca acatcttgat ntcactgtgc caactgcggt gcctgccctt canagccctg 180
cactttgttt tntcccctgg cttcatcnac tacatcagtg gcacccctca tgctctgatt 240
gtgcgtcgct acctctccct gctggacacg gccgtggagc tgganctccc aagataccgg 300
ggtccccgcc ttccccgaan gcagtaagtg cccatctttc cccaacctct cntcaccgac 360
cgtgcccgct gcaagtacng tcacaa 386

<210> 671
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gtgtggccct gatggtgctc tgtgagaccc accgcgcccg catggtcaaa caccactgct 240
gcccgggctg cggctacttc tgcacggcgg gcaccttcct ggagtgccac cctgacttcc 300
gtgtggccca ccgcttccac aaggcctgtg tgtctcagct gaatgggatg gtcttctgtc 360
cccactgtgg ggaggatact tctgaagctc aagangtgac catccccggg gtgacggggt 420
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tttngacctg agaacagctt cctatgntaa tgccattgng aangtcttca aagtgtacan 180
tgaagctggt gtgaccttca catngatgga ncatggctga cttncncact atcctcttca 240
catgtaactt ntgcagacct atcanaagtt tacatgtaac cacagnnntc cctttctctn 300
ctgactnatt aataatggct accattctta acangttaat ccaagtncag cncgtttaag 360
ggngnaaagg antcaaggtt nggcgggttc atntncaagn tgcgtgtggn agtagtaatt 420
ctnctgncan cagtgggncc atttttgggt attttnnctn tnaantanan agggctantt 480
tnatcttgtt gttgcagnct ttnc 504

<210> 673
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<212> DNA
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<400> 673
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aactagtgga acccccaggg ctgcaggaat tcgggcacga ggnagagcgg acnngtgagc 120
agtactgcgg cctcctctcc tctcctaacc tcgctctcgc ggcctagctt tacccgcccg 180
cctgctcggc gaccagaaca ccttccacca tgaccacctc agcaagttcc cacttaaata 240
aaggcatcaa gcaggtgtac atgtccctgc ctcagggtga gaaagtccag gccatgtata 300
tctggatcga tggtactgga gaaggactgc gctgcaagac ccggaccctg gacagtgagc 360
ccaagtgtgt ggaagagttg cctgagtgga atttcgatgg ctctagtact tnacagtctg 420
angcttccag t 431

<210> 674
<211> 370
<212> DNA
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<400> 674
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ggaaggtgct tttgcacttg ngtttaaaag tgttcatttt cccgggcaag cagntggcac 120
aaggcgaggt agccctctgt tgattggtgt acggagtgaa cataaacttt ctactgatca 180
cattcctata ctctacagaa caggcaaaga caagaaagga agctgcaatc tctctcgngt 240
ggacagcaca acctgccttn tcccggngga agaaaaagca gnggagtatt actttgcttc 300
tgatgcaann gctgcataga acacaccaat cgcgtcatct ttctggaaga tgatgatgtn 360
gcagcaagna 370

<210> 675
<211> 363
<212> DNA
<213> Homo sapiens

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<222> (65)
<223> n equals a,t,g, or c

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<221> misc feature
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<222> (318)
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<223> n equals a,t,g, or c

<220>
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<222> (329)
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<400> 675
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cagtnccttc aagcctacaa gccccgagag aatgatgant tggcactgga gaaagccgac 120
gtggtgatgg tgactcacca gagcagtgca cggctggctg gagggcgtga ggctctcaga 180
cggggagcga ggctggtttc ctgtgacagc nntgngagtt catttccaac ccagaggtcc 240
gtgacacaga acctgaaggg aagcttcatc gagtgcaaga cttgccaaac tacagctngt 300
gggaacagca agcctnantt ttctnctgna gaaggagttt tcgtgagctg gaagaacaag 360
ttg 363

<210> 676
<211> 441
<212> DNA

<213> Homo sapiens

<220>
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<222> (214)
<223> n equals a,t,g, or c

<220>
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<222> (353)
<223> n equals a,t,g, or c

<220>
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<222> (397)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (404)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (413)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (440)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (441)
<223> n equals a,t,g, or c

<400> 676
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gctgcagaag gacaagcagg tctaccgggc cacgcaccgc ctgctgctgc tgggtgctgg 120
agaatctggt aaaagcacca ttgtgaagca gatgaggatc ctgcatgtta atgggtttaa 180
tggagacagt gagaaggcaa ccaaagtgca gganatcaaa aacaacctga aagaggcgat 240
tgaaaccatt gtggccgcca tgagcaacct ggtgcccccc gtggagctgg ccaaccccga 300
aaaccagttc agagtggact acatcctgag tgtgatgaac gtgcctgact ttnacttccc 360
tcccgaattc tatgagcatg ccaaggctct gtgggangat gaangagtgc gtncctgcta 420
cgaacgctcc aacgaatacn n 441

<210> 677
<211> 550
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (217)
<223> n equals a,t,g, or c

<220>
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<222> (429)
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<222> (482)
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<220>
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<222> (484)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (487)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (523)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (542)
<223> n equals a,t,g, or c

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ggatcatcaa cgagcccacg gccgccgcca tcgcctacgg cctggacaga acgggcaagg 120
gggagcgcaa cgtgctcatc tttgacctgg gcgggggcac cttcgacgtg tccatcctga 180
cgatcgacga cggcatcttc gaggtgaagg ccacggncgg ggacacccac ctgggtgggg 240
aggactttga caacaggctg gtgaaccact tcgtggagga gttcaagaga aaacacaaga 300
aggacatcag ccagaacaag cgagccgtga ggcggctgcg caccgctgcg agagggccaa 360
gaggaccctg tcgtccagca cccaggccag cctggagatc gacttccttg ttttgagggc 420
atcgacttnt acacgttcat caccagggcg aaggttcgaa ggagctgtgc ttccgacctt 480
gntnccnaaa cacccctggg aaccccgtgg gaaaaaaggc ttnttgcgcc gaaaggccca 540
ancttgggac 550

<210> 678
<211> 435
<212> DNA

<213> Homo sapiens

<220>
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<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (134)
<223> n equals a,t,g, or c

<220>
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<222> (295)
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<220>
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<223> n equals a,t,g, or c

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<222> (376)
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<220>
<221> misc feature
<222> (385)
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<220>
<221> misc feature
<222> (401)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (423)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (434)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (435)
<223> n equals a,t,g, or c

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gtaactattg gaatcaaggc tatggcaact atggatataa cagccaaggt tacggtggtt 120
atggaggata tggnctacac tggttacaac aactactatg gatatggtga ttatagcaac 180
cagcagagtg gttatgggaa ggtatccagg cgaggtggtc atcaaaatag ctacaaacca 240
tacttaaatt attccatttg caacttatcc ccaacaggtg gtgaagcata ttttnccatt 300
tgaaggttcc tttgaggggg gctccgcccn ggncttaatt ggcnttccaa ctaaattttt 360
gggtatccag tccccnatgg gagtntgcgg tggggccccc nggagtttaa ttcggggtcc 420
ccntaaagga tttnn 435

<210> 679
<211> 390
<212> DNA
<213> Homo sapiens

<220>
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<220>
<221> misc feature
<222> (217)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (287)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (330)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (333)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (371)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (390)
<223> n equals a,t,g, or c

<400> 679
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tccctggaag ctcctgcatg gcagctctga cagtgacact gatggtgctg aactccccac 120
tggctttggc tggggacacc cgaccacgtt tcttggagca ggtnaaacat gaatgtcatt 180
tcttcaacgg gacggaacgg gtgcggttcc tggacanata cttctatcac caagaagaat 240
acgtgcgctt cgacagcgac gtgggggaat accgggcggt gacgganctg gggcggccta 300
actccgaata ctggaacagc cagaaagacn ccngggacag aagcgggccg cggtggacac 360
ctactgcaga nacactacgg ggttgggtgn 390

<210> 680
<211> 343
<212> DNA
<213> Homo sapiens

<220>
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<222> (2)
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<222> (3)
<223> n equals a,t,g, or c

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<222> (8)
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<220>
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<222> (18)
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<223> n equals a,t,g, or c

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<222> (223)
<223> n equals a,t,g, or c

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<222> (240)

<223> n equals a,t,g, or c

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<220>
<221> misc feature
<222> (292)
<223> n equals a,t,g, or c

<220>
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<222> (331)
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cagattatgc cattgccagg cgcatagtag atttgcattc aagaattgag gaatcaattg 120
nnaatatcta tnccctcgat gatatcagaa gatatctncn ctatgcaaga aagtntaaac 180
ccaagaattc caaagantca gnggacttca ttgtggagca atntaaacat ctccgccccgn 240
aagatgggtt ctggagtagc ccagtcttca tngagggntn cagttgcggc cncattgagg 300
gccttggatc cgtctctctt ggaagccaat ngctccgggt gcc 343

<210> 681
<211> 523
<212> DNA
<213> Homo sapiens

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<222> (17)
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<220>

<221> misc feature
<222> (22)
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<220>
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<220>
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<222> (487)
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<222> (500)
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<221> misc feature
<222> (503)
<223> n equals a,t,g, or c

<220>
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<222> (514)
<223> n equals a,t,g, or c

<400> 681
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gacccacgcg tncgcccaat tttaccaatc tatcacccta tagaagagct aatgttagta 120
taagtaacat gaaaacattc ncctccgcat aagcctgcgt cagattaaaa cactgaactg 180
acaattaaca gcccaatatc tacaatcaac caacaagtca ttattaccct cactgtcaac 240
ccaacacagg catgctcata aggaaaggtt aaaaaaagta aaaggaactc ggcaaatctt 300
accccgcctg tttaccaaaa acatcacctc tagcatcacc agtattagag gcaccgcctg 360
cccagtgaca catgtttaac ggncgcggta ccctaaccgt gcaaaggtag cataatcact 420
tggtccttaa ttagggacct gnatgaatgg ctccacgagg gtcagctggc tcttactttt 480
aaccagngaa attgacctgn cgngaagagg cggnatgaca cag 523

<210> 682
<211> 713
<212> DNA
<213> Homo sapiens

<220>
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<222> (423)
<223> n equals a,t,g, or c

<220>
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<222> (583)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (595)
<223> n equals a,t,g, or c

<220>
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<222> (605)
<223> n equals a,t,g, or c

<220>
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<222> (626)
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<220>
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<222> (633)
<223> n equals a,t,g, or c

<220>
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<222> (640)
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<220>
<221> misc feature

<222> (646)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (660)
<223> n equals a,t,g, or c

<400> 682
ggtcaaccca acacaggcat gctcataagg aaaggttaaa aaaagtaaaa ggaactcggc 60
aaatcttacc ccgcctgttt accaaaaaca tcacctctag catcaccagt attagaggca 120
ccgcctgccc agtgacacat gtttaacggc cgcggtaccc taaccgtgca aaggtagcat 180
aatcacttgt tccttaaata gggacctgta tgaatggctc cacgagggtt cagctgtctc 240
ttacttttaa ccagtgaaat tgacctgccc gtgaagaggc gggcatgaca cagcaagacg 300
agaagaccct atggagcttt aatttattaa tgcaaacagt acctaacaaa cccacaggtc 360
ctaaactacc aaacctgcat taaaaatttc ggttggggcg acctcggagc agaacccaac 420
ctncgagcag tacatgctaa gacttcacca gtcaaagcga actactatac tcaattgatc 480
caataacttg accaacggaa caagttaccc tagggataac agcgcaatcc tattctagag 540
tccatatcaa caatagggtt tacgaacctc gatgtttgat cangacattc ccatngtgca 600
gcccnctatt taaaaggttc gttggntcac gantaaaggn cctacntgaa ctgagttcan 660
aaccggagta aattccaagg cgggttttta tctaccttaa aattcccccc tgg 713

<210> 683
<211> 289
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>
<221> misc feature
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<220>
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<220>
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<221> misc feature
<222> (252)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (287)
<223> n equals a,t,g, or c

<400> 683
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agtggatccc ccnggctgcn tgaattcggc acgagcggca cgaggccctg cggggtgtac 120
acccccgtt gcggctcggg cctgctctgc tacccgcccc gaggggtgga gaagcccctg 180
cacacactga tgcacgggca aggcgtgtgc atggagctgg cgganatcga ggccatncan 240
gaaagcctgc ancccctctga caaggacgag ggtgaccacc ccaacanca 289

<210> 684
<211> 464
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (353)
<223> n equals a,t,g, or c

<400> 684
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agaactcacc atggaatttg ggctgagctg gctttttctt gtggctattt taaaaggtgt 120

ccagtgtgag gtgcaattgg tggagtctgg gggaggcttg gtacagcctg gggggtccct 180
gagactctcc tgtacagtct ctggattcac ctttcgcaac tatgccatga gttgggtccg 240
ccagggtcca gggaaggggc tggaatgggt ctcagcaatt gacggtagtg gttataacac 300
atactacgag aggtccctgc agggccgctt tagtgtctcc agagacaatt ccnagaacac 360
actatatctg caaatgaaca gcctgggagc cgaggacacg gccatctatt attgtgcgaa 420
gacagaacgt atgggtactg gctggtacgg acgaaatgac tact 464

<210> 685
<211> 545
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
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<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (14)
<223> n equals a,t,g, or c

<220>
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<222> (16)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (20)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (326)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (428)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (438)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (442)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (456)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (457)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (505)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (509)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (536)
<223> n equals a,t,g, or c

<400> 685
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aggtaccggt ccggaattcc cgggtcgacc cacgcgtccg gaccgtcacc cctggagaga 120
cggcctccat ctcctgcagg tctagtcaga ccctcctgca tgtcaatgga cacaactatt 180
tggattggta catgcagaag ccagggcagc ctccacagct cgtggtctat aggggttcca 240
atcgggcctc cggggtccct gacaggttca gtggcggtgg atcaggcaca gattttacac 300
ttagaatcac cacggtggag gctgangatg ttggcgttta ttactgcatg caagctctac 360
aaagtccgta cacttttggc caggggacca agctggagat caaacgaact gtgggctgca 420
ccatctgnct tcatcttncc gncatctgat gaacanntga aatctggaac tgcctctggt 480
gggggcctgc tgaataactt ctatnccana gaggcccaaa gtaccagtgg aaaggnggga 540
taacg 545

<210> 686
<211> 496
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (358)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (417)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (460)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (472)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (481)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (488)
<223> n equals a,t,g, or c

<400> 686
ctactaaagg gaacaaaagc tggagctcca ccgcggtggc ggccgctcta gaactagtgg 60
atcccccggg ctgcaggaat tcggcacgag cggctgggcg ctgaggatca gccgcttcct 120
gcctggattc cacagcttcg cgccgtgtac tgtcgcccca tccctgcgcg cccagcctgc 180
caagcagcgt gccccggttg caggcgtcat gcagcgggcg cgacccacgc tctgggccgc 240
tgcgctgact ctgctggtgc tgctccgcgg gccgccggtg gcgcgggctg gcgcgagctc 300
ggggggcttg ggtcccgtgg tgcgctgcga accgtgcgac gcgcgtgcac tggcccantg 360
cgcgccttcc gcccgccgtg tgcgccggaa cttggtgcgc caagccgggc ttgcggntgc 420
tgcctgacgt gcgcactgag cgaagggcca gccgtgcggn atctacaccg ancgctgtgg 480
nttccggnct tcgttg 496

<210> 687
<211> 476
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (7)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (56)
<223> n equals a,t,g, or c

<400> 687
gcncganacn aaccctcact aaagggaaca aaagctggag ctccaccgcg gtgcgnccgc 60
tctagaacta gtggatcccc cgggctgcag gaattcggca cgagattgat gacaccaata 120
tcacacgact gcagctggag acagagatcg aggctctcaa ggaggagctg ctcttcatga 180
agaagaacca cgaagaggaa gtaaaaggcc tacaagccca gattgccagc tctgggttga 240
ccgtggaggt agatgccccc aaatctcagg acctcgccaa gatcatggca gacatccggg 300
cccaatatga cgagctggct cggaagaacc gagaggagct agacaagtac tggtctcagc 360
agattgagga gagcaccaca gtggtcacca cacagtctgc tgaggttgga gctgctgaga 420
cgacgctcac agagctgaga cgtacagtcc agtccttgga gatcgacctg ggactt 476

<210> 688
<211> 483
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<400> 688
anantaaccc tcactaaagg gaacaaaagc tggagctcca ccgcggtgcg gccgctctag 60
aactagtgga tcccccgggc tgcaggaatt cggcacgagc aggttcccgc ccggaagaag 120
cgaccaaagc gcctgaggac cggcaacatg gtgcggtcgg ggaataaggc agctgttgtg 180
ctgtgtatgg acgtgggctt taccatgagt aactccattc ctggtataga atcccccattt 240
gaacaagcaa agaaggtgat aaccatgttt gtacagcgac aggtgtttgc tgagaacaag 300
gatgagattg ctttagtcct gtttggtaca gatggcactg acaatcccct ttctggtggg 360
gatcagtatc agaacatcac agtgcacaga catctgatgc taccagattt tgatttgctg 420
gaggacattg aaaagcaaaa tccaaccagg ttctcaacag gctgacttcc tgggatgcac 480
taa 483

<210> 689
<211> 339
<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (109)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (135)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (155)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (236)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (260)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (280)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (289)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (337)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (338)
<223> n equals a,t,g, or c

<400> 689
aggcaggagg aagccgatcg aaaactcaga gaggaggaag agaagaggag gctaaaggaa 60
gagattgaaa ggcgaggagc agaagctgct gagaaacgcc agaagatgnc agaagatggc 120
ttgtcagatg acagnaaacc attcaagtgt ttcantccta aaaggttcat ctcttcaaga 180

tagaagagcg agcagatttt tgattaagtc tgtgcagaaa agcagtggtg ttcaantcga 240
cccttcaagc agcattagtn ttccaagttt gacagcagan tggagcatnt taccatggca 300
tttgagggga ccaaaagcag ccaaaacctt aaaaaanna 339

<210> 690
<211> 594
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (473)
<223> n equals a,t,g, or c

<400> 690
gntgctttct ccaccagaag ggcacacttt catctaattt ggggtatcac tgagctgaag 60
acaaagagaa gggggagaaa acctagcaga ccaccatgtg ctatgggaag tgtgcacgat 120
gcatcggaca ttctctggtg gggctcgccc tcctgtgcat cgcggctaat attttgcttt 180
actttcccaa tggggaaaca aagtatgcct ccgaaaacca cctcagccgc ttcgtgtggt 240
tcttttctgg catcgtagga ggtggcctgc tgatgctcct gccagcattt gtcttcattg 300
ggctggaaca ggatgactgc tgtggctgct gtggccatga aaactgtggc aaacgatgtg 360
cgatgctttc ttctgtattg gctgctctca ttggaattgc aggatctggc tactgtgtca 420
ttgtggcagc ccttggctta gcagaaggac cactatgtct tgattccctc ggncagtgga 480
actacacctt tgccagcacc gagggccaag taccttctgg ataccttcac atggtccgag 540
tgcactgaac ccaacacatt ggggaatgga atggatctct ggtttctatc ctct 594

<210> 691
<211> 538
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<400> 691
ganganacna accctcacta aagggaacaa aagctggagc tccaccgcgg tgcgnccgct 60
ctagaactag tggatccccc gggctgcagg aattcggcac gagcgcatga ctttgtcttc 120
tccgcacgac tgttacagag gtctccagag ccttctctct cctgtgcaaa atggcaactc 180
ttaaggaaaa actcattgca ccagttgcgg aagaagaggc aacagttcca aacaataaga 240
tcactgtagt gggtgttgga caagttggta tggcgtgtgc tatcagcatt ctgggaaagt 300
ctctggctga tgaacttgct cttgtggatg ttttggaaga taagcttaaa ggagaaatga 360
tggatctgca gcatgggagc ttatttcttc agacacctaa aattttggca gataaagatt 420
attctgtgac cgccaattct aagattgtag tggtaactgc aggagtccgt cagcaagaag 480
gggagagtcg gctcaatctg gtgcagagaa atgttaatgt cttcaaattc attattcc 538

<210> 692
<211> 201
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (125)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (143)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (161)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (165)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (183)
<223> n equals a,t,g, or c

<400> 692
gctcattgcc acgcgccccc gacgaccgcc cgacgtgcat tcccgattcc ttttggttcc 60
aagtccaata tggcaactct aaaggatcag ctgatttata atcttctaaa ggaagaacag 120
acccnccaga ataagattac agntgttggg gttggtgctg ntggnatggc ctgtgccatc 180
aanatcttaa tgaaggactt g 201

<210> 693
<211> 589
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (2)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (23)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (271)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (312)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (342)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (354)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (377)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (401)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (424)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (437)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (466)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (491)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (551)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (571)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (572)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (576)
<223> n equals a,t,g, or c

<400> 693
nncaaaaagt acctaggtga cantatagaa ggtacgcctg caggtaccgg tccggaattc 60
ccggggttgt taacttgttt attgcagctt ataatggtta caaataaagc aatagcatca 120
caaatttcac aaataaagca tttttttcac tgcattctag ttgtggtttg tccaaactca 180
tcaatgtatc ttatcatgtc tggatcgatc ctgcattaat gaacggccaa cgcgcgggga 240
gaggcggttt gcgtattggc tggcgtaata ncgaaaagcc cgcaccgatc gcccttccca 300
acagttgcgc ancctgaatg gcgaatggga cgcgccctgt ancggcgcat taancgcggc 360
gggtgtggtg gttaccncaa cgtgaccgct acacttgcca ncgccctaac gcccgctcct 420
ttcnctttct tcccctncct ttctccccca cgttccgccg ggtttncccc gtcaaactct 480
aaatccgggg ntccccttta agggttccca atttaattgc ttaacggcac ctccaacccc 540
aaaaaaactt naataagggg tgaatggttc nnctanttgg gccaccccc 589

<210> 694
<211> 386
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (59)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (135)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (149)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (173)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (202)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (204)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (244)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (326)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (340)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (369)
<223> n equals a,t,g, or c

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<221> misc feature
<222> (370)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (383)
<223> n equals a,t,g, or c

<400> 694
ggcaaagcat ggggcagcga gtgtgagaaa tgccctctgc ctggcacaga ggccttcana 60
gagatctgcc ctgccggcca cggctacacc tacgcgagct ccgacatccg cctgtccatg 120
aggaaagccg aggangaaga actggcaang cccccaaggg agcaagggca gangagcagc 180
tgggcactgc ccgggccaac ananaagcag cccctccggg ttcgtcacgg acacctggct 240
tgangccggg accatccctg acaaggttga ctctcaagct ggccaggtca cgaccagtgt 300
cactcatgca cctgcctggg tcacanggaa atgccaçaan cccacccaat gcctgaacag 360
ggaattgcnn aaaattccgg aanaaa 386

<210> 695
<211> 475
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (231)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (278)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (423)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (459)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (463)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (465)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (466)
<223> n equals a,t,g, or c

<400> 695
ggttcacagc atatattggt ggattcttgt ccatagtgca tctgctttaa gaattaacga 60
aagcagtgtc aagacagtaa ggattcaaac catttgccaa aaatgagtct aagtgcattt 120
actctcttcc tggcattgat tggtggtacc agtggccagt actatgatta tgattttccc 180
ctatcaattt atgggcaatc atcaccaaac tgtgcaccag aatgtaactg ncctgaaagc 240
tacccaagtg ccatgtactg tgatgagctg aaattganaa gtgtaccaat ggtgcctcct 300
ggaatcaagt atctttacct taggaataac cagattgacc atattgatga aaaggccttt 360
gagaatgtaa ctgatctgca gtggctcatt ctagatcaca accttctaga aaactccaag 420
atnaaaggga gagttttctc taaattgaaa caactgaana agntnntata accac 475

<210> 696
<211> 444
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (402)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (410)
<223> n equals a,t,g, or c

<400> 696
tatcaagtgt actccaaaat ccaggcaaca aacacatggc tgtttctaag tagctgtaac 60
ggaaatgaaa cttctctttg ggactgcaag aactggcaat ggggtggact tacctgtgat 120
cactatgaag aagccaaaat tacctgctca gcccacaggg aacccagact ggttggaggg 180
gacattccct gttctggacg tgttgaagtg aagcatggtg acacgtgggg ctccatctgt 240
gattcagact tctctctgga agctgccagc gttctatgca gggaattaca gtgtggcaca 300
gttgtctcta tcctgggggg agctcacttt ggagagggaa tggacagatc tgggctgaag 360
aattccagtg ttgagggaca tgaatcccca tctttcatct tnccagtagn aaccccgccc 420
aaaaggaact tgtagccaca gcaa 444

<210> 697
<211> 411
<212> DNA

<213> Homo sapiens

<220>
<221> misc feature
<222> (104)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (305)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (338)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (370)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (375)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (391)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (410)
<223> n equals a,t,g, or c

<400> 697
aacatggcgg gtgtggagga ggtagcggcc tccgggagcc acctgaatgg cgacctggat 60
ccagacgaca gggaagaagg agctgcctct acggctgagg aaanagccaa gaaaaaaaga 120
cgaaagaaga agaagagcaa agggccttct gcaggtaaag agagttttat gttttcccag 180
tcccctccgg gaacggctga actgtttggc tcaggcccgt tgagggggcc gggaccgggg 240
ccccagagcc ccgactagac tgattcttgg gcctgacagg gtggcaaagc cgggctatag 300
atcanggtgc acctgagctt tctctgatgt atgcccangc agatctccag gtattcagag 360
cacctgcttn cccancctgt tagtcttagt nacccaaccc tcctgtgcan a 411

<210> 698
<211> 135
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (21)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (27)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (54)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (65)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<400> 698
ggcgtgggtt tccgggaggg nacctgnggg gcccagaccc agcgcatccg gtgnagggtg 60
ccctncaact ggaagatgna tttcgagccg atttcaagta caaagtttta gaacttgggg 120
tgcgtgtgat taggg 135

<210> 699
<211> 434
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (15)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (18)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (56)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (61)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (321)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (368)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (369)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (391)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (394)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (427)
<223> n equals a,t,g, or c

<400> 699
cgtacangag ctganggnga gcgcgcctgc aggtcgacac tagtggatcc aaagantgtc 60
ngcacagttt tctctcttgg agcatgcatg gaaggcctga atattttgct taacagactg 120
ttggggattt cattatatgc agagcagcct gcaaaaggag aggtgtggag cgaagatgtc 180
cgaaaactgg ctgttgttca tgaatctgaa ggattgttgg ggtacattta ctgtgatttt 240
tttcagcgag cagacaaacc acatcaggat tgccatttca ctatccgtgg aggcagacta 300
aaaggaagat gggagactat ncaactccca gttgtaagtt cttatgctgg aatcttcccc 360
gttcccgnna gggagttctc caactttggc naangcctgg gcatgatggg aaaacctttc 420
ccaggangg ggac 434

<210> 700
<211> 435

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (118)
<223> n equals a,t,g, or c

<400> 700
gccgagcgca cgccttgccg ccgccccgca gaaatgcttc ggttacccac agtctttcgc 60
cagatgagac cggtgtccag ggtactggct cctcatctca ctcgggctta tgccaaanat 120
gtaaaatttg gtgcagatgc ccgagcctta atgcttcaag gtgtagacct tttagccgat 180
gctgtggccg ttacaatggg gccaaaggga agaacagtga ttattgagca gagttgggga 240
agtcccaaag taacaaaaga tggtgtgact gttgcaaagt caattgactt aaaagataaa 300
tacaagaaca ttggagctaa acttgttcaa gatgttgcca ataacacaaa tgaagaagct 360
ggggatggca ctaccactgc tactgtactg gcacgctcta tagccaagga aggcttcgag 420
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<212> DNA
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<400> 701
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tcccaaagta acaaaagatg gtgtgactgt tgcaaagtca attgacttaa aagataaata 180
caagaacatt ggagctaaac ttgttcaaga tgttgccaat aacacaaatg aagaagctgg 240
ggatggcact accactgcta ctgtactggc acgctctata gccaaggaag gcttcgagaa 300
gattagcaaa ggtgctaatc cagtggaaat caggagaggt gtgatgttag ctgttgatgc 360
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cattgccgga aagtcaacga gttatctgga acaacccccc gatgcctggg gcactggggg 180
ccagcggaac agcggccacg aantctctgc gctangcggt tgaggtggcn tgcagagcnt 240
gctggggaaa cntgagccac agccag 266

<210> 703
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accacgctac tcctacctat ctccccttttt atactaataa tcttataaaa aaaaaaaaaa 180
aaaaaaaaaa aaangggggg gccgggnncc natttngccc aaaggggggg ggttttaaaa 240
ttca 244

<210> 704
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ccaaccttcc cgccagacta cggcttcccc gaacgcaagg ancgcganat ggtggccaca 180

cancangana tgatggacgc gcactnaagc tccanctgcg ggantactgc gcccaccaac 240
tcatccgggt gctcaattnc aaccttaaan cttcccccac ttccttggct tgcnaaccag 300
gaacgggaca aatnggaata ntnccaaaca ccccanaant tttnttnccc ttaaanantt 360
tttaaacgga aacgaagggt ntcccccccg gaaaaaaaac nggggnaaaa aaaggggaaa 420
ttttttnccc ccccccgcc cgnggaaatt ttcccccccg tt 462

<210> 705
<211> 436
<212> DNA
<213> Homo sapiens

<400> 705
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ggtgttgcgg ctttataagc gggcgctacg ccacctcgag tcgtggtgcg tccagagaga 120
caaataccga tactttgctt gtttgatgag agcccggttt gaagaacata agaatgaaaa 180
ggatatggcg aaggccaccc agctgctgaa ggaggccgag gaagaattct ggtaccgtca 240
gcatccacag ccatacatct tccctgactc tcctgggggc acctcctatg agagatacga 300
ttgctacaag gtcccagaat ggtgcttaga tgactggcat ccttctgaga aggcaatgta 360
tcctgattac tttgccaaga gagaacagtg gaagaaactg cgggagggaa agctgggaac 420
gagaggttaa gcagct 436

<210> 706
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<212> DNA
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agngcctgcg tncgtgagaa ttcagcatgg aatgactcta ctatttnctg ggatttctgn 120
tnctggntgn aagattgcca cttgatgccg ccaaacgatt ncatgatgag ctgggnaatg 180
aaagaccttn tgcttacatg anggagcaca atcaattaaa tggctggtnt tctgatgaaa 240
atgactggaa tgaaaaactc tacccagtgt ggaagcggng agacatgang tgngaaaaac 300
tgctggaagg gaggcccgtg tgcaaggcgg tcctgaccag ngactnacca acccttggng 360
ggctcaaata naacattngc cggngaacct gatattccct aaangccaaa aggaagaagc 420
caatggcaac ataggctatg anaagaactg ganaaatgaa gctgggntaa acagctgaac 480
canaagg 487

<210> 707
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<212> DNA
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tatcttttcg gttgtgaact aaaggccgac aaagattatc actttaaggt ggataatnat 180
gaaaatgagc accagttatc tttaagaacg gtcngtttng gggctggtgc aaaggatgag 240
ttgcacattg ttgaagcaga ggcaatgaat tacgaaggca gtccaattaa agtaacactg 300
gcaactttga aaatgtctgt acagccaacg gttttcccct tgggggcttt gaataacacc 360
accanggncc ttaaggttga antgtggttc agggccatgc cnattagngg acag 414

<210> 708
<211> 360
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gcgcgcctcc tccgccgccg cggactccgg cagctttatc gccagagtcc ctgaactctc 120
gctttctttt taatcccctg catcggatca ccggcgtgcc ccaccatgtc agacgcagcc 180
gtagacacca gctccgaaat caccaccaag gacttaaagg agaagaagga agttgtggaa 240
gaggcagaaa tggaagagac gccctgctaa cgggatgcta atgaggnaat ggggagcagg 300
aggtgacatg aggtagccga gaagaggaag aagtngggag aanagagaga anaanaagtt 360

<210> 709
<211> 253
<212> DNA
<213> Homo sapiens

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gtcgacccac gngtccgctn cggtggtgaa caagtctcca gcaccatatn tggtttgtct 120
ggcccaccat cccggcgngg acctttttccg ttagcgtggg tgatattgtt cctgctcgag 180
gcncaaatng gtccttggna tctccttcca tctgcccatt aactctcgca agtgcctccg 240
ngaggaaatt cnc 253

<210> 710
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<212> DNA
<213> Homo sapiens

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tgctcttcaa aacatcattc tttatcacct acaccaggag ttttcattgg aaaaggattt 180
gaacctggtg ttactaacat ttttaaagac cacacaaggn agcaaaatct ttctggaagg 240
aagtgaaatg gttacacttc tggtgaatgg atttggaaat ccaaaagant ctgacatcca 300
tggnccacca anggtggtaa tttcatgttg taggttaaac tncnctttc cagcagncac 360
acctttggg natggntcaa ctggtnggga tacttgatta tttnatncaa tnncctcccn 420
atttaaggtt ttttccgggg tgggcccctt caagggaatn ccngggctnt tttttnacac 480
ctnaattttt tccccc 496

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<211> 461
<212> DNA
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tgcccagtgt atcttggatg ctgctttcct gcctcatgct gctgtctcag gttcaaggtg 180
aagaacccca gagggaactg ccctctgcac ggatccgctg ncccaaaggc tccaaggcct 240
atggctccca ctgctatgcc ttgtttttgt caccaaaatc ctggacagat gcagatctgg 300
cctgccagaa gcggccctct ggaaacctgg tgtctgngct cagtggggct gagggatcct 360
tcgngcctcc ctggtgaaga gcattggtaa cagctactca tacgtctgga ttgggctcca 420
tgaccccaca cagggcaccg agcccaatgg ataaaggttg g 461

<210> 712
<211> 392
<212> DNA
<213> Homo sapiens

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caacctggca gccgccgccg tggaagagca gtatagctgt gactatggat ctggcagatt 240
ctttatcctt tgtggacttg gaggaattat tagctgtggc acaacacata cagcattggt 300
tcctctagat ctggttaaat gcagangcag gtttgttttt gcatgctgga cttagagcna 360
ttgaagcntg actgangtta agtattagna ta 392

<210> 713
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<212> DNA
<213> Homo sapiens

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<222> (703)
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<400> 713
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aggatcacca gataccaggg tgttaatctt tatgtgaaaa atcttgatga tggtattgat 120
gatgaacgtc tccggaaaga gttttctcca tttggtacaa tcactagtgc aaaggttatg 180
atggagggtg gtcgcagcaa agggtttggt tttgtatgtt tctcctcccc agaanaagcc 240
actaaagcag ttacanaaat gaacggtaga attgtggcca caaagccatt gtatgtagct 300
ttagctcagc gcaaagaaga gcgccaggct cacctcacta accagtatat gcagagaatg 360
gcaagtgtac ganctgttcc caaccctgta atcaacccct accagccagc acctccttca 420
ggttacttca tggcagctat cccacagact cagaacgtgc tgcatactat cctcctagcc 480
aaattgctca actaanacca agtcctcgct ggactgctca gggtgccata actcatccat 540
tccaaaatat gcccggtgct atccgcccag ctgctcctan aacaccattt agtactatga 600
naacagcttc ttctcagcaa catcttaatg cacagccaca anttacaatg cacancctgc 660
tgttcatgtt caaggtcagg aacctttgan tgcttccatg ttngcatctg cccccccca 720
aaacaaaacc aatt                                                    734
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<210> 714
<211> 500
<212> DNA
<213> Homo sapiens

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<220>
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<222> (26)
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<220>
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<220>
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tctagcaact agtggatccc ccgggcctgt caggaattcg gcacgagctg ggacaagcga 120
gtttttaaac aaagtgactg aggcacagga agatggccag tcaacttctg aattgattgg 180
ccagtttggt gtcggtttct attccgcctt ccttgtagca gataaggtta ttgtcacttc 240
aaaacacaac aacgataccc agcacatctg ggagtctgac tccaatgaat tttctgtaat 300
tgctgaccca agaggaaaca ctctaggacg gggaacgaca attacccttg tcttaaaaga 360
agaagcatct gattaccttg aattggatac aattaaaaat ctcgtcaaaa aatattcaca 420

gttcataaac tttcctattt atgtatggng cagcaagact gaaactgttn aggagcccat 480
ggaggaagaa ggagcagcca 500

<210> 715
<211> 491
<212> DNA
<213> Homo sapiens

<220>
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<223> n equals a,t,g, or c

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<222> (58)
<223> n equals a,t,g, or c

<220>
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<222> (62)
<223> n equals a,t,g, or c

<220>
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<222> (65)
<223> n equals a,t,g, or c

<220>
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<223> n equals a,t,g, or c

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<222> (278)
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<222> (398)
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<220>
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<220>
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<222> (473)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (474)
<223> n equals a,t,g, or c

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anaantacaa caagtgggaa acgatagagg cttggactca acaagtcgcc actganaatc 120
cagccctcat ctctcgcagt gttatcggaa ccacatttga gggacgcgct atttacctcc 180
tgaaggttgg caaagctgga caaaataagc ctgccatttt catggactgt gggtttccca 240
tgccaganan ttggatttct ccctgcattc ngccagtngg ttttntaaaa aangcggttc 300
ccttcctatn gacntttana ncccanttga caaacttcnc caacaattta aanttttatn 360
ttcccgccct gtggccccaa tattgaaggg caacttcnac cccgggaacn aaaacccaat 420
tntggaaaaa aaaacccccc cccccccctgg tgggattctt gctttggttg ggnnccaccc 480
caaaaaaatt t 491

<210> 716
<211> 331
<212> DNA
<213> Homo sapiens

<220>
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<222> (242)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (303)
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<220>
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<222> (321)
<223> n equals a,t,g, or c

<220>
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<222> (322)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (326)
<223> n equals a,t,g, or c

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gctacccggt gtgcggcagc gacggcacca cctacccgag cggctgccag ctgcgcgccg 120
ccagccagag ggccgagagc cgcggggaga aggccatcac ccaggtcagc aagggcacct 180
gcgagcaagg tccttccata gtgacgcccc ccaaggacat ctggaatgtc actggtgccc 240
angtgtactt gagctgtgag gtcatcggaa tcccgacacc tgtcctcatc tggaacaagg 300
tanaaagggg tcactatgga nntcanagga c 331

<210> 717
<211> 486
<212> DNA
<213> Homo sapiens

<220>
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<222> (5)
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ctagtggntc cccgggnct gcaggaattc ggcacgagna tattagncag cggttattcg 120
gtgagcggtg gtggtttatt cttccgtgga gttaagggct ccgtggacat ctcaggtctt 180
cagggtcttc catctggaac tatataaagt tcagaaaaca tgtctcgaga tatgactcca 240
ggaccactat attttctcca gaaggtcgct tataccaagt tgaatatgcc atggaagcta 300
ttggacatgc aggcacctgt ttgggaattt tagcaaatga tggtgttttg cttgcagcag 360
agagacgcaa catccacaag cttcttgatg aagtcttttt ttctgaaaaa atttataaac 420
tcaatgagga catggcttgc agtgtggcag gcataacttt ctgatgctaa tgttctgact 480
aatgac 486

<210> 718
<211> 479
<212> DNA
<213> Homo sapiens

<220>
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<222> (436)
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accctcaact cagatggata cacccctgag ccagacaaac cgcggccgat gcccatggac 120
acgagcgtgt atgagagccc ctacagcgac ccagaggagc tcaaggacaa gaagctcttc 180
ctgaagcgcg ataacctcct catagctgac attgaacttg gctgcggcaa ctttggctca 240
gtgcgccagg gcgtgtaccg catgcgcaag aagcagatcg acgtggccat caaggtgctg 300
aagcagggca cggagaaggc agacacggaa gagatgatgc gcgaggcgca gatcatgcac 360
cagctggaca acccctacat cgtgcggctc attggcgtct gccaggccga agccctcatg 420
ctggtcatgg agatgntggg ggcgggcgct gcacaagttc ctggtcggca agaaggaag 479

<210> 719
<211> 572
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (418)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (421)
<223> n equals a,t,g, or c

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<222> (501)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (503)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (526)
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<220>
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<222> (546)
<223> n equals a,t,g, or c

<220>
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<222> (559)
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<400> 719
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gatgattgtc atagaactgg gcaccaatcc gctgaagagc tcaggaattg aaaatggggc 120

tttccaggga atgaagaagc tctcctacat ccgcattgct gataccaata tcaccagcat 180
tcctcaaggt cttcctcctt cccttacgga attacatctt gatggcaaca aaatcagcag 240
agttgatgca gctagcctga aaggactgaa taatttggct aagttgggat tgagtttcaa 300
cagcatctct gctgttgaca atggctctct ggccaacacg cctcatctga gggagcttca 360
cttggacaac aacaagctta ccagagtacc tggtgggctg cagagcataa agtacatnca 420
nggtggctac cttcataaca accatatctc tgtagttgga tcaaagtgac ttctggccac 480
ctggacacaa ccacccaaaa ngnttcttaa ttccgggtgg gaagcntttt aacaaacccg 540
ggccangact ggggagaana cagccatcca cc 572

<210> 720
<211> 487
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (376)
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<220>
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<222> (447)
<223> n equals a,t,g, or c

<220>
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<222> (459)
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<222> (460)
<223> n equals a,t,g, or c

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<222> (467)
<223> n equals a,t,g, or c

<220>
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<222> (468)
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<400> 720
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agggcagtgc cattgatagg aagcggcacc atgtactaca gacggctcat ccctcccctt 120
tgtcagtgta tagagggttc tttggatgta gacacttttc aaagaccaat gagctgctgc 180
agaagtctgg caagaagccc attgactgga aggagctgtg atcatcagct gaggggtggc 240
ctttgagaag ctgctgttaa cgtatttgcc agttacgaag ttccactgaa aattttccta 300
ttaattctta agtactctgc ataaggggga aaagcttcca gaaagcagcc atgaaccagg 360
ctgtccagga atgganсctg tatccaacca caaacaacaa aggctaccct ttgacccaaa 420
tgtctttctc tgcaacatgg cttcggncta aaatatgcnn aagacannat gagggccaat 480
acttaat 487

<210> 721
<211> 464
<212> DNA
<213> Homo sapiens

<220>
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<222> (222)
<223> n equals a,t,g, or c

<220>
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<222> (312)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (347)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (349)
<223> n equals a,t,g, or c

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<220>
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<222> (415)
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<220>
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<222> (436)
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<220>
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<222> (443)
<223> n equals a,t,g, or c

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<222> (448)
<223> n equals a,t,g, or c

<220>
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<222> (455)
<223> n equals a,t,g, or c

<400> 721
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tcctgggttg tgaggagtcg ccgctgccgc cactgcctgt gcttcatgag gaagatgctc 120
gccgccgtct cccgcgtgct gtctggcgct tctcagaagc cggcaagcag agtgctggta 180
gcatcccgta attttgcaaa tgatgctaca tttgaaatta anaaatgtga ccttcaccgg 240
ctggaagaag ccctcctgtc acaacagtgc tcaccaaggg aagatgggct caaatactac 300
aggatgatgc anactgtacc cgaatggaat tgaaacagat cactgtntna acagaaaatt 360
atcntggttt ctgtccttgt gtgatgtcag aacttgctgt gtggcctgga gccgnatcac 420
cccaaacact ctccanctac ggntccgntt atttnccggg cttc 464

<210> 722
<211> 320
<212> DNA
<213> Homo sapiens

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<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (43)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (113)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (142)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (152)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (153)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (182)
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<220>
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<222> (211)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (263)
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<220>
<221> misc feature
<222> (275)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (281)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (299)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (308)
<223> n equals a,t,g, or c

<400> 722
gttgcacagc anctgcacgc gccgtggctc cggatctctt cgnctttgca gcgtagcccg 60
agtcggtcag cgccggatga cctcagcagc catgtcgaag ccccatagtg aanccgggac 120
tgccttcatt cagacccagc anctgcacgc anncatggct gacacattcc tggagcacat 180
gngccgcctg gacattgatt caccacccat nacaggccgg aacactggca tcatctgtac 240
cattggccca gcttcccgat cangtggaga cggtnaagga natgattaaa gcctggaang 300
aatgtggntc gtctgaactt 320

<210> 723

<211> 152
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (87)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (111)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (127)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (148)
<223> n equals a,t,g, or c

<400> 723
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gacctgcctc ctcatcgtnt tcagcangga tcagtttccg gaggtctacg nccctactgt 120
cctttgngaa ctatattgcg cacattgngg cg 152

<210> 724
<211> 573
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (463)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (514)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (553)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (559)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (569)
<223> n equals a,t,g, or c

<400> 724
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aaaattgcat ctgatggtct caagggtcgt gtgtttgaag tgagtcttgc tgatttgcag 120
aatgatgaag ttgcatttag aaaattcaag ctgattactg aagatgttca gggtaaaaac 180
tgcctgacta acttccatgg catggatctt acccgtgaca aaatgtgttc catggtcaaa 240
aaatggcaga caatgattga agctcacgtt gatgtcaaga ctaccgatgg ttacttgctt 300
cgtctgttct gtgttggttt tactaaaaaa cgcaacaatc agatacggaa gacctcttat 360
gctcagcacc aacaggtccg ccaaatccgg aagaagatga tggaaatcat gacccgagag 420
gtgcagacaa atgacttgaa agaagtggtc aataaattga ttncagacgc attggaaaag 480
acatagaaaa ggcttggcaa tctattatcc tctncatgat ggcttcgtta gaaaagtaaa 540
aatgctgaag aanccaagnt tgaatgggna aac 573

<210> 725
<211> 403
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<400> 725
gcttgaaant aaccctcact aaagggaaca aaagctggag ctccaccgcg gtgcggccgc 60
tctagaacta gtggatcccc cgggctgcag gaattcggca cgagtcctgg tccgcgccag 120
agcccagcgc gcctcgtcgc catgcctcgg aaaattgagg aaatcaagga cttcctgctc 180
acagcccgac gaaaggatgc caaatctgtc aagatcaaga aaaataagga caacgtgaag 240
tttaaagttc gatgcagcag atacctttac accctggtca tcactgacaa agagaaggca 300
gagaaactga agcagtccct gccccccggt ttggcagtga aggaactgaa atgaaccaga 360
cacactgatt ggaactgtat tatattaaaa tactaaaaat cct 403

<210> 726
<211> 502
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature

<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (8)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (256)
<223> n equals a,t,g, or c

<220>
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<222> (281)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (380)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (391)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (428)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (456)
<223> n equals a,t,g, or c

<400> 726
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gccgctctag aactagtgga tcccccgggc tgcaggaatt cggcacgaga gccatcaggt 120
aagccaagat gggtgcatac aagtacatcc aggagctatg gagaaagaag cagtctgatg 180
tcatgcgctt tcttctgagg gtccgctgct ggcagtaccg ccagctctct gctctccaca 240
gggctccccg ccccanccgg cctgataaag cgcgccgact nggctacaag gccaagcaag 300
gttacgttat atataggatt cgtgttcgac gtggtggccg aaaacgccca gttcctaagg 360
gtgcaattac ggcaagcctn tccatcatgg ngttaaccag ctaaagtttg ctcgaagcct 420

tcagtccntt gcagaggagc gagctggacg ccactntggg gctctgagag tcctgaattc 480
ttactgggtt ggtgaagatt cc 502

<210> 727
<211> 361
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (17)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (309)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (318)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (360)
<223> n equals a,t,g, or c

<400> 727
ggcacgagcg aacgcgnaga gcacgccatg aaggcctcgg gcacgctacg agagtacaag 60
gtagtgggtc gctgcctgcc cacccccaaa tgccacacgc cgcccctcta ccgcatgcga 120
atctttgcgc ctaatcatgt cgtcgccaag tcccgcttct ggtactttgt atctcagtta 180
aagaagatga agaagtcttc aggggagatt gtctactgtg ggcaggtgtt tgagaagtcc 240
cccctgcggg tgaagaactt cgggatctgg ctgcgctatg actcccggag cggcacccac 300
aacatgtanc gggaatancg ggacctgacc aacgcaggcg ctgtcaacca gtgtaacggn 360
g 361

<210> 728
<211> 401
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (200)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (234)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (251)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (319)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (332)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (334)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (360)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (389)
<223> n equals a,t,g, or c

<400> 728
gaagangctc gcctctagtg tcctccgctg tggcaagaag aagtctggtt agaccccaat 60
gagaccaatg aaatcgccaa tgccaactcc cgtcagcaga tccggaagct catcaaagat 120
gggctgatca tccgcaagcc tgtgacggtc cattcccggg ctcgatgccg gaaaaacacc 180
ttggcccgcc ggaaaggcan gcacatgggc atagttagcg gaaaggtaca gccnatgccc 240
gaatgccaaa naaggtcaca tggattaaga aaatgaagat tttgcgcccg ctgctcaaaa 300
aatacgtgaa tcttaaaana tcgatcgcca cntntttcac agcctgttcc taaagttaan 360
ggaatttttt caaaaacaac cgattctcnt ggaacacttc c 401

<210> 729
<211> 530
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (12)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (14)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (60)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (527)
<223> n equals a,t,g, or c

<400> 729
gcacagngan ancnaaccct cactaaaggg aacaaaagct ggagctccac cgcggtgcgn 60
ccgctctaga actagtggat cccccgggct gcaggaattc ggcacgagcc gccatcttcc 120
agtaattcgc caaaatgacg aacacaaagg gaaagaggag aggcacccga tatatgttct 180
ctaggccttt tagaaaacat ggagttgttc ctttggccac atatatgcga atctataaga 240
aaggtgatat tgtagacatc aagggaatgg gtactgttca aaaaggaatg ccccacaagt 300
gttaccatgg caaaactgga agagtctaca atgttaccca gcatgctgtt ggcattgttg 360
taaacaaaca agttaagggc aagattcttg ccaagagaat taatgtgcgt attgagcaca 420
ttaagcactc taagagccga gatagcttcc tgaaacgtgt gaaggaaaat gatcagaaaa 480
agaaagaagc caaagagaaa ggtacctggg ttcaactaaa gcgccancct 530

<210> 730
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (33)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (87)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (97)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (111)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (121)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (124)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (125)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (142)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (181)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (183)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (190)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (198)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (206)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (229)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (241)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (248)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (262)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (269)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (284)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (322)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (333)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (354)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (367)
<223> n equals a,t,g, or c

<400> 730
gggtggttgc tgccgaaatg ggcaagttca tgnaaccaag aaagtggtgc ttgtnctggc 60
tggacgctac tccggacgca aagctgntca tcgtaanaga acattgaatg ntggcacctc 120
naanngcccc tacagccatg cnctggtggc tgggaattga accgctaccc ccgcaaatga 180
ncngctgccn tggggcanga agaagntcgc caggaggtca aagatatant cttttgtgaa 240
ngtgtgtnac tacaatcacc tnatgcccnc aaggtactct gtgngatatt ccccttgggg 300
caaagctgta cgttcattag gntgtcttcc ganattcctg gctcttaaac gctnggcccg 360
aaggagnccc aggtc 375

<210> 731
<211> 207
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (143)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (177)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (187)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (201)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (207)
<223> n equals a,t,g, or c

<400> 731
gcgccgctgc gaagggagcc gccgccatgt ctgcgcatct gcaatggatg gtcgtgcgga 60
actgctccag tttcctgatc aagaggaata agcagaccta cagcactgag cccaataact 120
tgaaggcccg caattccttc cgntacaacg gactgattca ccgcaagact gtgggcntgg 180
agccggnagc cgacggcaaa ngtgtcn 207

<210> 732
<211> 702
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (620)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (628)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (655)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (686)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (690)
<223> n equals a,t,g, or c

<400> 732
ggcagaatgn ctcccgcaaa gaagggtggc gagaagaaaa agggccgttc tgccatcaac 60
gaagtggtaa cccgagaata caccatcaac attcacaagc gcatccatgg agtgggcttc 120
aagaagcgtg cacctcgggc actcaaagag attcggaaat ttgccatgaa ggagatggga 180
actccagatg tgcgcattga caccaggctc aacaaagctg tctgggccaa aggaataagg 240
aatgtgccat accgaatccg tgtgcggctg tccagaaaac gtaatgagga tgaagattca 300
ccaaataagc tatatacttt ggttacctat gtacctgtta ccactttcaa aaatctacag 360
acagtcaatg tggatgagaa ctaatcgctg atcgtcagat caaataaagt tataaaattg 420
caaaaaaaaa aaaaaagggc ggccgctcta gaggatccaa gcttacgtac gcgtgcatgc 480
gacgtcatag ctcttctata gtgtcaccta aattcaattc actgccgtcg gtttacaacg 540

tcgtgactgg gaaaaccctg cgttacccaa cttaatcgcc ttgcagcaca tccccctttcg 600
ccagctgcgt aataacgaan aggcccgnac cgatcgcctt tccacagttg cgcancctga 660
atggcgaatg gacgcgcctt taccgngcan taagcgccgc gg 702

<210> 733
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (62)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (99)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (101)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (118)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (126)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (152)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (185)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (212)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (260)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (310)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (356)
<223> n equals a,t,g, or c

<400> 733
naattaaccc tcactaaagg gngcaaaagc tggtgctcca ccgcggtgcg accgctctag 60
anctagtggt tcccccgggc tgcaggattt cggcacganc ncgtgcagat tcgagcanag 120
gagcgnaagg gaacgtcatc gtttggaaag cntcgcaata agacgcacac gttgtgccgc 180
cgctntggct ctaaggccta ccaccttcag angtcgacct gtggcaaatt tggctaccct 240
gccaagcgca agagaaagtn taactggagt gccaaggcta aaagacgaaa taccaccgga 300
actggtcgan tgaggcacct aaaatttgta taccgcagat tcaggcatgg tttccntgaa 360
ggaacaacac ctaaacccaa gagggcagct gttgcagcat ccagttcatc ttaagattgt 420
caacgattag tcatgcaata a 441

<210> 734
<211> 379
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (323)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (324)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (342)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (346)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (375)
<223> n equals a,t,g, or c

<400> 734
ggccgcagaa gcgagatgac gaagggaacg tcatcgtttg gnaagcgtcg caataagacg 60
cacacgttgt gccgccgctg tggctctaag gcctaccacc ttcagaagtc gacctgtggc 120
aaatgtggct accctgccaa gcgcaagaga aagtataact ggagtgccaa ggctaaaaga 180
cgaaatacca ccggaactgg tcgaatgagg cacctaaaaa ttgtataccg cagattcagg 240
catggattcc gtgaaggaac aacacctaaa cccaagaggg cagctgttgc agcattccag 300
ttcatcttta agaatgtcaa cgnntttagt catgcaataa antgtnctgg ggttttaaaa 360
aattaaaaga aaagnaaaa 379

<210> 735
<211> 187
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (172)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (176)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (177)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (179)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (185)
<223> n equals a,t,g, or c

<400> 735
gcgggatcgt cggtaaatac gggacccgct atggggcctc cctccggaaa atggtgaaga 60
aaattgaaat cagccagcac gccaagtaca cttgctcttt ctgtggcaaa accaagatga 120
agagacgagc tgtggggatc tggcactgtg gttcctgcat gaagacagtg gntggnngng 180
cctgnac 187

<210> 736
<211> 576
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (94)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (334)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (340)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (361)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (371)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (397)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (409)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (429)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (436)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (440)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (444)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (452)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (466)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (479)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (490)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (519)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (553)
<223> n equals a,t,g, or c

<400> 736

tcgacccacg cgtccgccca cgctccggcc tcagccctac cagcactggt catgtctaaa 60
ggtcatcgta ttgaggaagt tcctgaactt cttntggtag ttgaagataa agttgaaggc 120
tacaagaaga ccaaggaagc tgttttgctc cttaagaaac ttaaagcctg ggaatgatat 180
caaaaaggtc tatgcctctc agcgaatgag agctgggcaa aggcaaaatg gagaaaccgt 240
cgccgtatcc agcgcagggc ccgtgcatca tctataatga ggataatggt atcatcaagg 300
ccttccagaa acatccctgg aattactctg cttnaatgtn aagcaagctg aaacattttg 360
naagcttgct ncctggtggg gcatgtgggg acgtttncgg cattgggang gaaatggctt 420
ttccgggant ttaganggan tgtnacgggc antgggcgta aagcgntttc cctccaagng 480
ttaactacan tcttcccagg caccaagatg gattaatana gatcttggca gaatctggaa 540
aagcccagag gtnccaaggg cccttcgggc accagc 576

<210> 737
<211> 297
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (7)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (243)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (254)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (261)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (266)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (275)
<223> n equals a,t,g, or c

<400> 737
gctccgncat ggcgtgtgct cgcccactga tatcggtgta ctccgaaaag ggggagtcat 60
ctggcaaaaa tgtcactttg cctgctgtat tcaaggctcc tattcgacca gatattgtga 120
actttgttca caccaacttg cgcaaaaaca acagacagcc ctatgctgtc agtgaattag 180
caggtcatca gactagtgct gagtcttggg gtactggcag agctgtggct cgaattccca 240

ganttcgagg tggngggact naccgntctg gccanggtgc ttttggaaac atgtgtc 297

<210> 738
<211> 354
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (26)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (74)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (80)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (84)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (98)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (120)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (148)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (193)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (286)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (303)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (329)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (351)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (353)
<223> n equals a,t,g, or c

<400> 738
gcgagaatga agactattct cagcantcag actgtcgaca ttccagaaaa tgtcgacatt 60
actctgaagg gacncacagn tatngtgaag ggccccanag gaaccctgcg gagggacttn 120
aatcacatca atgtataact cagccttntt ggaaagaaaa aaaagaggct ccgggttgac 180
aaatggtggg gtnacagaaa ggaactggct accgttcgga ctatttgtag tcatgtacag 240
aacatgatca agggtgttac actgggcttc cgttacaaga tgaggnctgt gtatgctcac 300
ttncccatca acgttgttat ccaagagant gggtctattg ttgaaatcca nant 354

<210> 739
<211> 504
<212> DNA
<213> Homo sapiens

<400> 739
ccgccatcat gggtcgcatg catgctcccg ggaagggcct gtcccagtcg gctttaccct 60
atcgacgcag cgtccccact tggttgaagt tgacatctga cgacgtgaag gagcagattt 120
acaaactggc caagaagggc cttactcctt cacagatcgg tgtaatcctg agagattcac 180
atggtgttgc acaagtacgt tttgtgacag gcaataaaat tttaagaatt cttaagtcta 240
agggacttgc tcctgatctt cctgaagatc tctaccattt aattaagaaa gcagttgctg 300
ttcgaaagca tcttgagagg aacagaaagg ataaggatgc taaattccgt ctgattctaa 360
tagagagccg gattcaccgt ttggctcgat attataagac caagcgagtc ctccctccca 420
attggaaata tgaatcatct acagcctctg ccctggtcgc ataaatttgt ctgtgtactc 480
aagcaataaa atgattgttt aact 504

<210> 740
<211> 399
<212> DNA
<213> Homo sapiens

<400> 740

ggacccgcca acatgggccg cgttcgcacc aaaaccgtga agaaggcggc ccgggtcatc 60
atagaaaagt actacacgcg cctgggcaac gacttccaca cgaacaagcg cgtgtgcgag 120
gagatcgcca ttatccccag caaaaagctc cgcaacaaga tagcaggtta cgtcacgcat 180
ctgatgaagc gaattcagag aggcccagta agaggtatct ccatcaagct gcaggaggag 240
gagagagaaa ggagagacaa ttatgttcct gaggtctcag ccttggatca ggagattatt 300
gaagtagatc ctgacactaa ggaaatgctg aagcttttgg acttcggcag tctgtccaac 360
cttcagtcac tcagcctaca gttgggatga tttcaaaac 399

<210> 741
<211> 431
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (335)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (393)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (417)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (425)
<223> n equals a,t,g, or c

<400> 741
aaacaacggt cgtgccaaaa agggccgcgg ccatgtgcag cccattcgct gcacgaactg 60
cgcccggtgc gtgcccaagg ataaggccat caagaagttt gtcattcgga acattgtaga 120
agccgctgct gtcagggaca tatctgaagc aagcgtcttc gacgcctacg tgcttcccaa 180
gctctatgtc aagctgcatt attgcgtgac tgtgccatcc atagcaaggt tgttaggaat 240
cgatcccgct aagcccggaa ggaccgaaca cccccaccac gattcagacc tgctggcgct 300
gcaccttcga cctccaccaa agcccatgta aagangccgt tttgtaagg acggaaggaa 360
aattaccttg gaaaaataaa atggaagttg tantttaaa aaaaaaaaaa aaacccnagg 420
ggggncccgt c 431

<210> 742
<211> 357
<212> DNA
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<220>
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<222> (178)

<223> n equals a,t,g, or c

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<223> n equals a,t,g, or c

<220>
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<222> (273)
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<220>
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<222> (297)
<223> n equals a,t,g, or c

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<222> (324)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (352)
<223> n equals a,t,g, or c

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<222> (353)
<223> n equals a,t,g, or c

<400> 742
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ttcatggatg tcatcagcat tgacaagacg ggagagaatt tccgtctgat ctatgacacc 120
aagggtcgct ttgctgtaca tcgtattaca cctgaggagg ccaagtacaa gttgtgcnaa 180
gtgagaaaga tctttgtggg cacaaaagga atccctcatc tggtgactca tgatgcccgn 240
accatccgct accccgatcc cctcatcaag gtnaatgatc cattcatatt gatttanaga 300
ctggcaagat tactgatttc atcnatttcg acactggtaa cctgtgtatg gnnactg 357

<210> 743
<211> 249
<212> DNA
<213> Homo sapiens

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<222> (42)
<223> n equals a,t,g, or c

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<222> (77)
<223> n equals a,t,g, or c

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<222> (115)
<223> n equals a,t,g, or c

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<222> (122)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (158)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (200)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (215)
<223> n equals a,t,g, or c

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<222> (221)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (248)
<223> n equals a,t,g, or c

<400> 743
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taactccatg atgatgnacg ggcgcaacaa cggcaagaag ctcatgactg tgcgnatcgt 120
cnagcatgcc ttcgagatca tacgcctgct cacaggcnaa gaaccctctg caggtcctgg 180
tgaacgccat catcaacatn ggtccccggg aagantccac ncgcattggg cgcgccggga 240
ctgttgana 249

<210> 744
<211> 383
<212> DNA
<213> Homo sapiens

<400> 744
gaagaattgc atcgtgctca tcgacagcac accgtaccga cagtggtacg agtcccacta 60
tgcgctgccc ctgggccgca agaagggagc caagctgact cctgaggaag aagagatttt 120
aaacaaaaaa cgatctaaaa aaattcagaa gaaatatgat gaaaggaaaa agaatgccaa 180
aatcagcagt ctcctggagg agcagttcca gcagggcaag cttcttgcgt gcatcgcttc 240
aaggccggga cagtgtggcc gagcagatgg ctatgtgcta gagggcaaag agttggagtt 300
ctatcttagg aaaatcaagg cccgcaaagg caaataaatc cttgttttgt cttcacccat 360
gtaataaagg tgtttattgg ttt 383

<210> 745
<211> 452
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (314)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (328)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (334)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (352)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (403)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (416)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (429)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (435)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (451)
<223> n equals a,t,g, or c

<400> 745
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ggcagccttc ctcaaaaagt ccgggaagct gaaagtcccc gaatgggtgg ataccgtcaa 120
gctggccaag cacaaagagc ttgctcccta cgatgagaac tggttctaca cgcgagctgc 180
ttccacagcg cggcacctgt acctccgggg tggcgctggg gttggctcca tgaccaagat 240
ctatgggggа cgtcagagaa acggcgtcat gcccagccac ttcagccgag gctccaagag 300
tgtggcccgc cggntcctcc aagccctngg aggngctgaa aatggtggaa anggaccaag 360
atggcggccc gcaaactgac acctcaggga caaagagatc tgnacagaat cgccgnacag 420
gtggcagcnt gccancaaag aagcattaga nc 452

<210> 746
<211> 114
<212> DNA
<213> Homo sapiens

<220>
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<222> (11)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<220>
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<222> (85)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (98)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (103)

<223> n equals a,t,g, or c

<400> 746
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ctgtctgcaa accaatgtgc cgtgncagcc aaggacangg tgnactgtgg ctac 114

<210> 747
<211> 165
<212> DNA
<213> Homo sapiens

<400> 747
ggcacagcca cccagggcct gagtcctgtc cacaccccag gtgacggccg gctccacaag 60
gcagtgagcg tgggcccccg ggtgcacatc attgaggagc tgcagatctt ctcatcggga 120
cagcccgtgg cagaatctgc tcctgggaca cccacagggg ggctg 165

<210> 748
<211> 583
<212> DNA
<213> Homo sapiens

<220>
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<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (291)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (341)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (387)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (458)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (462)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (480)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (537)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (541)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (543)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (546)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (580)
<223> n equals a,t,g, or c

<400> 748
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aagagcactg gactccggaa ggacacagca ttgttggttt tgccatgtac tattttacct 120
atgacccgtg gattggcaag ttattgtatc ttgaggactt cttcgtgatg agtgattata 180
gaggctttgg cataggatca gaaattctga agaatctaag ccaggttgca atgaggtgtc 240
gctgcagcag catgcacttt tttggtagca gaatggaatg aaccattcat naacttctat 300
aaaagaagag gtgcttctga tctgtccagt gaagaaggtt ngagacttgt taagaatcga 360
caaggagtct tgctaaaaat ggcaacntag gagtgaggaa tgcttgctgt agatgacaac 420
ctccattcta ttttagaata aaattcccca actttctntt gnttttctat gctggttggn 480
agtgaaatta atttaaatga gcacccattt caaaagcttt aattaccaag tgggcgnttg 540
ntnccntgtt ttgaaaattg aaggtcttgt tttaaaaggn ggc 583

<210> 749
<211> 419
<212> DNA
<213> Homo sapiens

<220>
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<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (16)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (24)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (169)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (342)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (351)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (376)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (398)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (419)
<223> n equals a,t,g, or c

<400> 749
acncggaggc ttcttnatta cggncgggnn tgatgaggga aagctggtga cgcctgcagg 60
tgaccggtcc ggaattcccg ggtcgaccca cgcgtccggg cgtgatgtct cacagaaagt 120
tctccgctcc cagacatggg tccctcggct tcctgcctcg gaagcgcana gcaggcatcg 180
tgggaaggtg aagagcttcc ctaaggatga cccgtccaag ccggtccacc tcacagcctt 240
cctgggatac aaggctggca tgactcacat cgtgcgggaa gtcgacaggc cgggatccaa 300
ggtgaacaag aaggagggtg gtggaggctg tgaccattgt anagacacca nccatggtgg 360
tttgtgggca ttgttngcta cgttggaaaa ccctcgangg ctccggaact tcaagaatn 419

<210> 750
<211> 507
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (453)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (475)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (497)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (499)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (503)
<223> n equals a,t,g, or c

<400> 750
ggccgaacat ggagatcaag attatatctg gcactgcatt gatctcttct tagatttcat 60
tactgtcttc agaaaactca tgatgatcct ggccatgaat gaaaaggata agaagaaaga 120
gaagaaatga agtgaccatc cagcctttcc caattagact tcctctcctt ccacccctca 180
tttccttttt gcacacatta caggtggtgt gttctgtgat aatgaaaagc atcagaaaag 240
cttttgtact ttgtggtttc ctctattttg aattttttga tcaaaaaact gattagcaga 300
atatagtttg gagtttggct tcatcttcct ggggttcccc tcactccctt ttttggcaac 360
cccatctgta gcctcttcct ctactcaggc agtcgacccg ccacgatgag aagtgggacc 420
agcagagggc gccaacttca ggagcccgct ttnccaccca gcttcattca cccantggac 480
ctgaactgtt tgggtananc ccnccgg 507

<210> 751

<211> 435
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (11)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (23)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (31)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (34)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (110)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (134)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (151)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (158)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (199)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (215)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (218)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (226)
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<220>
<221> misc feature
<222> (239)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (243)
<223> n equals a,t,g, or c

<220>
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<222> (257)
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<220>
<221> misc feature
<222> (295)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (321)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (324)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (331)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (355)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (363)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (365)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (403)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (420)
<223> n equals a,t,g, or c

<400> 751
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ggatcccccg ggctgcaggt agcctgagct tagctcagcg ccggggcttn accaagacct 120
acactgttgg ctgngaggaa tgcacagtgg ntccctgntt atccatcccc tgcaaactgc 180
agagtggcac tcattgctng tggacggacc agctnctnca aggctntgaa aagggcttnc 240
agncccgtca ccttgcntgc ctgcctcggg agccagggct gggcacctgg cagtncctgc 300
ggtcccagat agcctgaata ntgnccggag nggaagctga agcctgcaca gtgtncaccc 360
tgntnccact cccatctttc tttcggacaa tgaaataaag agntaccacc cagcaaaaan 420
aaaaaaaaaa acctg 435

<210> 752
<211> 591
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (195)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (240)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (319)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (345)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (365)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (407)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (452)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (456)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (480)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (556)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (570)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (572)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (579)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (586)
<223> n equals a,t,g, or c

<400> 752
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gcttctggca tcctgttgtt gctgtggctg atagccccca gcagggcctg cacctgtgtc 120
ccaccccacc cacagacggc cttctgcaat tccgacctcg tcatcagggc caagttcgtg 180
gggacaccag aagtnaacca gaccacctta taccagcgtt atgagatcaa gatgaccaan 240
atgtataaag ggttccaagc cttaggggat gccgctgaca tccggttcgt ctacaccccc 300
gccatggaga gtgtctgcng atactttcac aggtcccaca accgnagcga ggagtttctc 360
attgntggaa aactgcagga tggacttttg cacatcacta cctgcanttt tgtggctccc 420
tggaacagcc tgagcttagc tcagcgccgg gncttnacca agacctacac tgttggctgn 480
gaggaaatgc acaagtgctt ccctgtttat ccatcccctg caaactgcag agtgggcact 540
cattgcttgt aggacngacc agctcctacn angctcttna aaaggncttt c 591

<210> 753
<211> 547
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (429)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (454)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (489)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (503)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (512)
<223> n equals a,t,g, or c

<400> 753
aagcacttgt ccagatgagc agtgtgtgaa ttctcctgga tcttaccagt gcgttccctg 60
cacagaagga ttccgaggct ggaatggaca gtgccttgat gtggacgagt gcctggaacc 120
aaacgtctgc gcaaatggtg attgttccaa ccttgaaggc tcctacatgt gttcatgcca 180
caaaggctat acccggactc cggaccacaa gcactgtaga gatattgatg aatgtcagca 240
agggaatcta tgtgtaaacg ggcagtgcaa aaataccgag ggctccttca ggtgcactgt 300
ggacaggggt taccagctgt cggcagctaa agaccagttt gaagacattg atgaatgcca 360
caccgtcatc tctgttgctc atgggcatgc aagaacactg aagctctttt ccatgtgttt 420
tttgaccang gttacagaac atctgggctt gganacactg tgaaaaattt caatgaatgc 480
ttggaagana aaatttttgc canaaaagaa antgctttat actgcagggt cctatgatgt 540
cttgtcc 547

<210> 754
<211> 384
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (307)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (374)
<223> n equals a,t,g, or c

<400> 754
gctcggctcc agcgccatgg cgccctccag gaagttcttc gttgggggaa actggaagat 60
gaacgggcgg aagcagagtc tgggggagct catcggcact ctgaacgcgg ccaaggtgcc 120
ggccgacacc gaggtggttt gtgctccccc tactgcctat atcgacttcg cccggcagaa 180
gctagatccc aagattgctg tggctgcgca gaactgctac aaagtgacta atggggcttt 240
tactggggag atcagccctg gcatgatcaa agactgcgga ccacgtgggt ggtcctgggg 300
cactcanaga gaagcatgtc tttggggaat cagatgagct gattgggcag aaagtggccc 360
atgctctggc aganggactc ggat 384

<210> 755
<211> 253
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (60)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (217)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (240)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (244)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (252)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (253)
<223> n equals a,t,g, or c

<400> 755
tgtagatctt tgaagactct gattctctga gactgaggag agatgtctta ccagcagcan 60
cagtgcaagc agccctgcca gccacctcct gtgtgcccca cgccaaagtg cccaagagcc 120
atgtccaccc ccgaagtgcc ctgagcctta cctgcctcct ccttgtccac ctgagcattg 180
cccacctcca ccttgccagt ataaatgccc tcctgtngca accataccac cctggcagcn 240
gaanttcccc cnn 253

<210> 756
<211> 183
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (9)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (48)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (57)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (83)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (108)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (141)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (144)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (146)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (148)
<223> n equals a,t,g, or c

<400> 756
ggcanaaana aggtaggaat aaggctagac ctttaacttc cctaaggnat acttttntag 60
ctaccttctg ccctgtgtnt ggnacctaca tccttaatga ttgtcctntt acccattctg 120
gaattttttt ttttttaaaa naantncnga aagcattttg aaaaaaaaaa aacaaaaaaa 180
aag 183

<210> 757
<211> 99
<212> DNA
<213> Homo sapiens

<220>
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<222> (12)

<223> n equals a,t,g, or c

<220>
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<220>
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<223> n equals a,t,g, or c

<220>
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<222> (45)
<223> n equals a,t,g, or c

<220>
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<222> (77)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (82)
<223> n equals a,t,g, or c

<400> 757
agcctttaat anatcatata ggaaantggt agntgcagta cggtnggaat tccgggtgac 60
tcagcgtccg ggattgnanc anctgggatt ggagtttgg 99

<210> 758
<211> 60
<212> DNA
<213> Homo sapiens

<220>
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<222> (36)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<400> 758
ggcacgaggt tttttttttt tttttttttt tttttntntn ttttnntttt ttaaaaaaaa 60

<210> 759
<211> 66
<212> DNA
<213> Homo sapiens

<220>
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<222> (6)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (59)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (63)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (65)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (66)
<223> n equals a,t,g, or c

<400> 759
agaganaacc gagttttttt tttttttttt tttttttttt tttttttttt tttttttttnc 60
ccntnn 66

<210> 760
<211> 487
<212> DNA
<213> Homo sapiens

<220>
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<222> (409)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (433)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (473)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (475)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (477)
<223> n equals a,t,g, or c

<400> 760
tacagatgga gcaaatgtcc taacagagaa atagaggtga tgctgctaaa gggagaaatg 60
ccaggcggac aaagttcagt gtcgggaatt ttccccgtga cattcactgg ggcatgagat 120
tttggaagaa gttttttact ttggtttagt ctttttttcc ttccttttta ttcagctaga 180
atttctggtg ggttgatggt agggtataat gtgtctgtgt tgcttcaaat tggtctgaaa 240
ggctatcctg ctgaaagtcc tgctttccta tctagcattt atttctctgg caaacttttc 300
tttcttttct tttttaaagt aaacttgtgt attgagctta actgtatttc agtatttcca 360
gcttatgtgt acattattcc aatgataccc aacagttatt tatattttnt aacaaattca 420
cagtctgaat gangacttta tttcatggat tataataagg aatgaggtaa ttngngnctc 480
acattca 487

<210> 761
<211> 422
<212> DNA
<213> Homo sapiens

<220>
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<222> (253)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (297)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (350)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (353)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (382)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (403)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (406)
<223> n equals a,t,g, or c

<400> 761
gaaaaggcta aaatcatgaa ttagttacaa gcaacagtac caacttatgt gacccctgag 60
gggtggggct gtgagctctt aatttgtttt tgattctgaa aaactctgct tcctggcatc 120
caggagttag agattgagcc tttcatcttc tttctcaaaa ctagtttttg atgctttctt 180
tcatgggaat agtcactttt ttatttagta aatcgcattg ctggaaccac caaggatgtg 240
gaatgtcctt gantgtatta tttatgcaag tcacagtcac gtttgccatc atggcantat 300
ttgaaacact aataatgtgt ttttactttt ttatccccgt taaaatgatn ttnaaaagga 360
aaaaggtggt tatagcccct anaatttctg ggtccaaatt atnccnaaaa tttcctaaaa 420
aa 422

<210> 762
<211> 375
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (279)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (315)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (373)
<223> n equals a,t,g, or c

<400> 762
tttgaccact tgccaagtcc ctgtctcttt cagacacaga caagcttcat ttaaattatt 60
tcaactgatg aagtaacaat aaagttataa atgataatga tcagatgaaa taatttataa 120
ctttattgtt acttcatcag tgtttccttt tgaaaggtgt atgaattcat tacattttta 180
ttctaatgta ttatctgtag attagaagat aaaatcaagc atgtatctgc ctatactttg 240
tgagttcacc tgtctttata ctcaaaagtg tcccttaana gtgtccttcc ctgaaataaa 300
tacctaaggg agtgnaacag tctctggagg accactttga gcctttggaa gttaagggtt 360
cctcagccac ctngt 375

<210> 763
<211> 372
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (261)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (301)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (320)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (338)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (344)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (354)
<223> n equals a,t,g, or c

<400> 763
caatatgtag cttactcttt ttttcccccc ttcttaaacc accagtggtt catttttaag 60
attttttcat caagagaaga ataactttac taaattttat ttctttattt gcaaaagaat 120
ctttattaaa acaaacaatc ttaactatgc acatgatgtg accagatcat cttgaaaata 180
ttcctcttta gtaggaactc tttgttttta actcttggta tggtcagaat ataatacttc 240
cataattact tataattcct ntccgggtac tgggggctat aaatacaact tttttaaatg 300
naattcatgg ttatcaaccn ggctccaagt accattangg ggtnccctat gggnaattac 360
cttgggaaag tc 372

<210> 764
<211> 195
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (60)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (67)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (71)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (86)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (94)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (128)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (146)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (151)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (153)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (183)
<223> n equals a,t,g, or c

<400> 764
cggacgcgtg ggcggacgcg tggggaaagg taagctctag cttaangtct angatttgtn 60
ctttganatt naggaaggta aggatnggtc agangatgta acttgatgtg agcagtaata 120
aacctgtntt aaatatcata ctgtgnatat ntnattgaaa atttatttca gagcggaaaa 180
acnttagcta aaatc 195

<210> 765
<211> 103
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (76)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (83)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (91)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (94)
<223> n equals a,t,g, or c

<400> 765
attaataatg gataccattc taaacaagtn aatccaagtt aagcccgtta aggagaaaga 60
aattaaggtt agcggntcat gtncaagctg ngtntgaaag tgg 103

<210> 766
<211> 538
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (285)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (316)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (327)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (379)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (436)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (441)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (445)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (450)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (474)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (504)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (516)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (520)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (522)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (526)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (534)
<223> n equals a,t,g, or c

<400> 766
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ggcttcatcc tcaccgagcg cctgggcagc ggcacgtacg ccacggtgta caaggcctac 120
gccaagaagg acactcgtga agtggtagcc ataaagtgtg tagccaagaa aagtctgaac 180
aaggcatcgg tggagaacct cctcacggag attgagatcc tcaaggcatt cgacatcccc 240
acattgtgca gctgaaagac tttcagtgtg agctgggggc ggggncgctg ccaaaaggag 300
tggagaagga catctntttc aggccgnctc tctgcctctt aaaacaacag ttgggaacag 360

ttgaaccaat taatcttanc ttcaatccat tgggaagttt ttttgccggc caaggggggg 420
gccggaaacc ttggtncttc nggcntttcn aatcccaatt aaaccccggc caanggaatt 480
ttcttggccc cttgaaagaa aaanggtttg ggcccncccn tnggtncctt tccnaatg 538

<210> 767
<211> 415
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (350)
<223> n equals a,t,g, or c

<400> 767
ctttcccaag ggaaacactc agctttctat agaaaattgc actttttgtc gagtaatcct 60
ctgcagtgat acttctggta gatgtcaccc agtggttttt gttaggtcaa atgttcctgt 120
atagtttttg caaatagagc tgtatactgt ttaaatgtag caggtgaact gaactggggt 180
ttgctcacct gcacagtaaa ggcaaacttc aacagcaaaa ctgcaaaaag gtggttttg 240
cagtaggaga aaggaggatg tttatttgca gggcgccaag caaggagaat tgggcagctc 300
atgcttgaga cccaatctcc atgatgacct acaagctaga gtatttaaan gcagtggtaa 360
atttccagga aagccagaag ttaaaggcca aaattgtaaa tcagtcgaga tcggg 415

<210> 768
<211> 425
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (351)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (381)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (389)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (422)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (423)

<223> n equals a,t,g, or c

<400> 768
ctttgtacag gggctcagtt cagggaagag ttgagcttct ctctgagggg tccctagggg 60
gacccctcag gccaggccct gatccagttc tccagggtct ttctcagggt caggtccatg 120
gggagaccat ggggtgcttg tctgacactg acctcgccct gctgagtccc cccatcagac 180
tgtccttcct ctgcagcgag tgtctgcagg gtctggatcc aggaaaggaa ttctgatctg 240
tggaagtttg tctcccccgt gtgtgtcctg cactaaatgt ccaaaccctg atacaggatg 300
taatgcagag agggccacag gcacaaccca ggcctgacaa tcccgtatgt nggaagtaga 360
actgaccccc aacacccaga ngtcatgtng aaatactcac ggtatacatg gaaaaaaaaa 420
annaa 425

<210> 769
<211> 256
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (34)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (60)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (83)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (85)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (112)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (120)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (151)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (163)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (200)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (211)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (235)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (250)
<223> n equals a,t,g, or c

<400> 769
attctagatg tagcttgtgc agatgtagca gganaatagg aaaacctacc atctcagtgn 60
gcaccagctg gcctcccaaa ggngnggcag ccgtgcttat atttttatgg tnacaatggn 120
cacaaaatta ttatcaacct aactaaaaca ntccttttct ctnttttcct ggaattatca 180
tggagttttc taattctctn ttttgggaat ngtagattgt ttttgaaatg ctttnacgat 240
gttaaaatan tttatt 256

<210> 770
<211> 316
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (158)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (173)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (200)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (228)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (266)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (267)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (281)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (284)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (291)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (294)
<223> n equals a,t,g, or c

<400> 770
ggnagaggtt caacgatgtg gtgtggcatg taagctggtc catcanagcc aacatcctgg 60
ctgtctctgg tggagacaat aaggaggagt tacagatgca gccacagatt gatcatctgc 120
ctttaacgtg aatcggagat gctttgtaat ctactgtncc agctgaagca ctncatgtta 180

cgaggaagaa actacaagtn atgttcaaat ctattttggg tcattttnat gtacctttgg 240
gttcaggcat tatttggggg gttttnnttc caaaggaact naantaaagt natnttgctt 300
attaaaaaaa ggaaaa 316

<210> 771
<211> 68
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (8)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (14)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (22)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (36)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (55)
<223> n equals a,t,g, or c

<400> 771
caaaagcngg agcnccaccg cnggcgaccg cnctanaact agtggatccc ccggnctgca 60
ggaattca 68

<210> 772
<211> 258
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (17)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (19)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (42)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (45)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (60)
<223> n equals a,t,g, or c

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<222> (139)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (155)
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<220>
<221> misc feature
<222> (225)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (235)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (250)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (257)
<223> n equals a,t,g, or c

<400> 772
cggacggtgg gtttttntnt tttttttttt tttttttttt tnttntnttt tttttttatn 60
nttgggtcat ttccacatgc tttattccag caatcaaaat aattaaaaac atctcaaatt 120
attatacaca tacaaaatng gtacagagtc ttttncttcc tcccacccct agggggaaaa 180
actgctttnt gctttgggaa gttgtctctg aaacccgggg acagnggacg caggncagac 240
taggagggan ccgggang 258

<210> 773
<211> 587
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (535)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (559)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (565)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (570)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (572)

<223> n equals a,t,g, or c

<400> 773
ggatcccaac tgctcctgcg ccgccggtaa gaggctgggg atgcccagtg tagactgtag 60
cgctagagaa gcaatttctg acccctcttt ctttctctgg tcactcaatt tcaggacagg 120
agttgctcct tcccaaagag ttttggggta tctttctctc cattctaggt tattcggagc 180
cccctttttta ccgttaagga gatctgagtt aatggcttgc tcaagttccc aggaatcggt 240
tgtggactga ggaactcggc cccgggctct tagtacgccg tcccttgttc aggtatccag 300
ggacggttct cacctctgtc ttttctcctt gcaggtgact cctgcacctg cgccggctcc 360
tgcaaatgca aagagtgcaa atgcacctcc tgcaagaaaa gtaagtggga tcctctcttt 420
cctctacccc ttcctgtcct ccagcctgtc ccctcttcac catcctcagg ggaattaaag 480
caagtctggg gatgccccat tgcgccggga aattggtggc ctcctcagtg atccntatca 540
aggagaagca aggaatccnt aattnccggn gnccgttgta cttaact 587

<210> 774
<211> 89
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (20)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (74)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (76)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (77)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (83)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (86)
<223> n equals a,t,g, or c

<400> 774
ggcagaggga aacatcaggn atgctaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60
aaaaaaaaaa aaanannana aanaantat 89

<210> 775
<211> 113
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
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<222> (30)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (57)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (59)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (75)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (77)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (106)
<223> n equals a,t,g, or c

<400> 775
ggtccggcgn ggtggaggga aacgcctccn tntctatata aggaatttcc cggtgtntnc 60
gggtcctttt ccctntnttc agagtggggg gcccaaattt gggcgntctg ttt 113

<210> 776
<211> 66
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (13)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (49)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (65)
<223> n equals a,t,g, or c

<400> 776
ggcanaggat ttnaaccctc accttcgtgt ttcccccaat gtttaaaang tttggatggt 60
ttgtng 66

<210> 777
<211> 441
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (401)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (436)
<223> n equals a,t,g, or c

<400> 777
atttgtatga aagaacttaa gcaaccttaa tattggctga gacttttaaa agagaaggag 60

aatttacttt tttgcctaat taggaggaag cttggtcata aggaaaaaga gctgtgttta 120
ggaaatagtg tgtgcccttt gaattaatgg agtgacaccg tgattcatga caggattcca 180
tttactggct gtatgccagc tgctgacagt ctataagtct taatagagat ggagtagagg 240
agctgaaggt tggcatctgc tcattgatga caactatgtt tacaatatgt tgtggactag 300
ttggggcact gaggcaggag aatcacgtgg agcccacggg ttcaagacca gcctgggaaa 360
catagcaaga ccttgtttct aaaaaaaaaa aaaaaaaaac ncgagggggg gcccggtacc 420
caattcgccc taaagngagt c 441

<210> 778
<211> 483
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (335)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (356)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (471)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (472)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (478)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (481)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (482)
<223> n equals a,t,g, or c

<400> 778
gcttactttt aaccagtgaa attgacctgc ccgtgaagag gcgggcataa cacagcaaga 60
cgagaagacc ctatggagct ttaatttatt aatgcaaaca gtacctaaca aacccacagg 120

tcctaaacta ccaaacctgc attaaaaatt tcggttgggg cgacctcgga gcagaaccca 180
acctccgagc agtacatgct aagacttcac cagtcaaagc gaactactat actcaattga 240
tccaataact tgaccaacgg aacaagttac cctagggata acagcgcaat cctattctag 300
agtccatatc aacaataggg tttacgacct cgatnttgga tcaggacatc ccgatngtgc 360
agccgctatt aaaggttcgt ttgttcaacg attaaagtcc tacgtgatct gagttcagac 420
cggagtaatc caggtcggtt tctatctact tcaaattcct ccctggaaaa nnagaagngg 480
nng 483

<210> 779
<211> 389
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (261)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (325)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (337)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (362)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (367)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (389)
<223> n equals a,t,g, or c

<400> 779
ccctcttccc ggctccagct ccgccgccag ctccagcctt tgctccccct cccaaagtcc 60
cctccccgga gcggagcgca cctagggtcc ctcttccgtc cccccagccc agctacccgt 120
tcagaccagc agcctcgggg ggcacccccc cgccagcctg cctccctccc gctcagccct 180
gccaggttcc cccagccatg aatctcttcc gattcctggg aaaactctcc caactcctcg 240
ccatcatctt gctactgctc naaatctgga attcccgctc gtgcgccgaa attcaggaaa 300
aaaacagtcc cgtttggtgt ggggntttca atggccnaat ttgaaatcct ttcacaataa 360
tntttantct aaaaattttt ttaaagggn 389

<210> 780
<211> 66
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (18)
<223> n equals a,t,g, or c

<400> 780
ttgtttttaa aactatgnac caggtttcta atgatgaaat aaagcacctg tttgttttat 60
accaaa 66

<210> 781
<211> 255
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (46)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (83)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (94)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (133)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (150)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (163)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (172)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (179)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (182)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (184)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (209)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (224)
<223> n equals a,t,g, or c

<400> 781
ggcagagcag agcagacgca caggccggaa aaggcgcatc taacgngtat ctaggctttg 60
gtaactgcgg acaagttgct ttnacctgaa tttnatgata catttcatta aggttccagt 120
tataaaatat ttngttaaat atttattaan gtggactata gantgcaaac tnccatttnc 180
cngntaaact tgtttttaaa ttatggccnt aggtaaccca tatngtaggg tattaatttc 240
cttggaacca aacca 255

<210> 782
<211> 348
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (3)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (28)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (75)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (123)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (135)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (178)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (182)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (296)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (298)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (307)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (323)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (324)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (345)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (346)
<223> n equals a,t,g, or c

<400> 782
ttnagtagag acagggtttc accatgtnag tnaggctggt ctcgaactcc tgacctcagg 60
tgaatccacc cgagnttggc ctcccaagtg gctgggcatt ataggcgtga gcactcacgt 120
ccncgcctca aaatngcata ttcaaagaag caatttcagt tcctttctaa gctttgtnag 180
tnaaggggct ccactgactt cctaggccct gtaaatttaa accagtcttt aaggttttgc 240
caggaaagtt cccttctttc caagtgggtt tttccaaatg ggcacaatgg caagcnanac 300
agaggangaa acattaaaaa aannaaaaaa aatttggggg ggggnncc 348

<210> 783
<211> 160
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (47)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (49)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (78)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (82)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (131)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (141)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (142)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (144)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (146)
<223> n equals a,t,g, or c

<400> 783
ggcacgagct acaatggcac tgtggactna tgtttccttc gccgagngnc tggagcgggg 60
atctgatgaa aaggtcanac tnaaacgcct tgcacggctt ctcggcttga tcacagctcc 120
ctaggtaggt naccacagag nngncncttc tagtgagcct 160

<210> 784
<211> 81
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (25)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (77)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (78)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (81)
<223> n equals a,t,g, or c

<400> 784
ggcacgagcc gggatcgtgc cattncattc cagtctgggt gacagagcta gactccatct 60
caaaaaaaaa aaaaaannng n 81

<210> 785
<211> 541
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (175)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (265)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (354)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (355)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (356)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (361)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (364)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (369)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (393)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (399)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (405)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (411)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (463)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (489)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (521)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (530)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (539)

<223> n equals a,t,g, or c

<400> 785
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tccctcttcc ctctccctgc ccagccctcc cttccttcct ctgccggcaa ggcagggacc 120
cacagtggct gcctgcctcc gggagggaag gagagggagg gtgggtgggt gggangggggc 180
cttcctccag ggaatgtgac tctcccaggc cccagaatag ctcctggacc caagcccaag 240
gcccagcctg ggacaaagct ccganggtcg gctggccgga gctattttta cctcccgcct 300
cccctgctgg tgcccccacc tggacgtctt gctgcagagt ctgacactgg attnnnaaaa 360
nctnaaaang aaccctggta cccaattctg ggncccggnc ctaanctcgg ncccaaccca 420
tcatctgtgg acaatggagt ctggaataaa tgctgtttgt canatcaaca aaaaaaaaaa 480
aaaaggggng gccgctttag aggattcaaa gcttaagtaa nggtgcatgn gaagttcana 540
a 541

<210> 786
<211> 433
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (230)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (350)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (400)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (402)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (405)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (422)
<223> n equals a,t,g, or c

<400> 786
cccacgcgtc cggtctaaca cgtgcgcgag tcgggggctc gcacgaaagc cgccgtggcg 60

caatgaaggt gaaggccggc gcgctcgccg gccgaggtgg gatcccgagg cctctccagt 120
ccgccgaggg cgcaccaccg gcccgtctcg cccgccgcgc cggggaggtg gagcacgagc 180
gcacgtgtta ggacccgaaa gatggtgaac tatgcctggg cagggcgaan cagaaggaaa 240
ctctggtgga ggtccgtagc ggtcctgacg tgcaaatcgg tcgtccgacc tgggtatagg 300
ggcgaaagac taaatcgaac catcttagta agctggtttc cctccgaaan tttccctcaa 360
gataagcttg gcgctctcgc aagaccccga aggaaccccn gncanggaat ttttatccgg 420
tnaaagcgaa ttg 433

<210> 787
<211> 527
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (492)
<223> n equals a,t,g, or c

<400> 787
cccaggatgt gtggcgagag cctgggccag cccacagcgt tcctagtcag gcagccacac 60
cttggtcctc atcttggtcc cttccaatct gaaacctcgt gcctggctcg tctgccacct 120
acatttctct ttccagctgc tgttttgtaa aaagaaaaag aaaaaagaag cccaaactag 180
tgagagtaat atctaattat ctcatttttt gtaggtctgt gataaagaac ttagtcatcc 240
cttccacctc ctactgtgaa gaacagaccc tgggtcccac actgaaatcc cctctagtca 300
cccattccca ccccccaggg agctgcctcc caggcagggg gtgcagaaaa tgattgatgg 360
gctggggaac cctggagagc ctcgactccg gaagtctcaa ggtgcctcct cctctcctta 420
gctggcccgt tggttttctg agcagggggc tgaactgtga acaagtcaga caaataaagc 480
aagggtctgc ancatctgca atgtcaaaaa aaaaaaaaaa aaaaaaa 527

<210> 788
<211> 203
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (121)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (160)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (179)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (181)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (192)
<223> n equals a,t,g, or c

<400> 788
gcttcatgtg gtctgacaat ttatttttgc catcattttt ttaattaaag aaaaaatttc 60
cagaagagga aaaaaaaact acaaaaaaca aaacattgaa ggttgatatt ttatgtggaa 120
naacatttga attgaattca gaatttttct gaaggtgtan atactttttt ttttttttna 180
ncaaaaaccc tnatttcaaa agg 203

<210> 789
<211> 124
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (38)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (70)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (87)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (94)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (113)
<223> n equals a,t,g, or c

<400> 789
ggcacgagca gcctacagcc gcctgcatct gtatccancg ccaggtcccg ccagtcccag 60
ctgcgcgcgn cccccagtcc cgcaccngtt cggnccaggc taagttagcc ctnaccatgc 120
cggt 124

<210> 790
<211> 293

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (44)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (52)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (79)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (125)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (134)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (141)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (160)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (179)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (184)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (222)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (266)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (275)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (281)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (287)
<223> n equals a,t,g, or c

<400> 790
ggcanagcgg cagtccagga cctgcaggcc ccagaggacc tgtnggaccc antggacctc 60
ctggcaaaga tggaaccant ggacatccag gtgccattgg accaccaggg cctcgaggta 120
acagnggtga aagnggatct nagggctccc cagggccacn cagggcaacc agggccctnc 180
tggnacctcc tggtgcccct ggtccttgct gtggtggtgt tngagccgct gccattgctg 240
ggattgggag gttgaaaaag cttggncggt tttgnccccg ngtttantgg ggg 293

<210> 791
<211> 129
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (93)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (104)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (113)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (116)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (119)
<223> n equals a,t,g, or c

<400> 791
gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 60
aaaaaaaaaa aaaaaaaggg gcggccgttt tanaggatcc aagnttacgt acncgngcnt 120
gcaacgtca 129

<210> 792
<211> 267
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (247)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (250)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (253)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (265)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (267)
<223> n equals a,t,g, or c

<400> 792
ggcacgagcg gccttgagcg cgacgaagac gtgtaggcct gctttccgag gggcgagcgc 60
ggcgccgcgg ggaggagggc ctgcgcgcag tcccgggcgc gttctagggc gccatgctgc 120

gggaagtctc gcgcgattag tggggaggtc tcgcggcttc tggctacttg gtggcgaggt 180
gaagagcttc tgcaggtgct gggggcggcg aacgcggcgg gaaagaaaaa aaaaaaaaaa 240
aaaaaanctn ggnaagtatt tttanan 267

<210> 793
<211> 453
<212> DNA
<213> Homo sapiens

<220>
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<220>
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<222> (443)
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gccgtagnag ccggggacag gtcagtccga gacgagagaa gcggtcagtg ttgtacagtg 120
ttttgggcat gcacgtgata ctcacacagt ggcttctgct caccaacaga tgaagacaga 180
tgcaccaacg aggctgatgg gaaccatcct gtagaggtcc atctgcgttc agacccagac 240
gatgccagag ctatgactgg gcctgcaggt gtggcgccga ggggagatca gccatggagc 300
agccacagga ggaagcccct gaggtccggg aagaggagga gaaagangaa gtggcagaag 360
cagaaggagc cccagagctc aattggggac cacagcatgc acttccttcc agcagctaca 420
cagactctcc cggagctcct cgncaacctt atg 453

<210> 794
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<212> DNA
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ggngggggcg cgccggtctc ccggagcggg accgggtcgg aggatggncg agaatcacga 120
gcgacggtgg tngtggngtg t 141

<210> 795
<211> 167
<212> DNA
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<220>
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<220>
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<223> n equals a,t,g, or c

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<222> (149)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (164)
<223> n equals a,t,g, or c

<400> 795
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ngcggcacag cagcagcgac gcagcggcga cantcagagc agggaggccg cnccacctgc 120
gggccggccg gagcgggcag ccccangcnc cctccccggg cacncgc 167

<210> 796
<211> 331
<212> DNA
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<220>
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<220>
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<222> (241)
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<220>
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<222> (242)
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<220>
<221> misc feature

<222> (244)
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<220>
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<222> (260)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (280)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (328)
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nctccactca gctaatgtna caacatgngn nctacttctc nctnnctttt acannnacag 120
gannnnggcc nnagttaata tatccngtgt acctcactgt ccaatatgaa aaccgtaaag 180
tgccttatag gnatttgcgt aactaacaca ccctggttca ttganctnta cttgctgaag 240
nngnaaaaga caggataagn tttcaatagt ggcataccan atgggacttt tgatgaaatg 300
aatatcaata ttttctgcaa ttccatgngc t 331

<210> 797
<211> 699
<212> DNA
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<222> (521)
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<222> (564)
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<222> (597)
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<222> (598)
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<220>
<221> misc feature
<222> (635)
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<220>
<221> misc feature
<222> (643)
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<221> misc feature
<222> (678)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (695)
<223> n equals a,t,g, or c

<400> 797
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tagaaattga aacctggcgc aatagatata gtaccgcaag ggaaagatga aaaattataa 120
ccaagcataa tatagcaagg actaacccct ataccttctg cataatgaat taactagaaa 180
taactttgca aggagagcca aagctaagac ccccgaaacc agacgagcta cctaagaaca 240
gctaaaagag cacacccgtc tatgtagcaa aatagtggga agatttatag gtagaggcga 300
caaacctacc gagcctggtg atagctggtt gtccaagata gaatcttagt tcaactttaa 360
atttgcccac agaaccctct aaatcccctt gtaaatttaa ctgntagtcc aaagaggaac 420
agctctttgg acactaggaa aaaaccttgt agagagagta aaaaatttaa cacccatagt 480
aggcctaaaa gcagccacca attaagaaag cgttcaagct naacacccac tacctaaaaa 540
aatcccaaac atataactga actnctacac ccaattgggc caatctatna ccctatnnaa 600
gaactaatgg tagtataagt acatgaaaac cattnttctt cgnataagcc ttgcgtnaga 660
attaaaacac tgaactgnac attaaacagc caatntcta 699

<210> 798
<211> 138

<212> DNA
<213> Homo sapiens

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<220>
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<220>
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<222> (133)
<223> n equals a,t,g, or c

<400> 798
cccggcacag agtcgatgct caataaatgt gtgttgactg catgaatgac ctggaaaaaa 60
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaanccccn 120
gggggGnncc ccnccccc 138

<210> 799
<211> 496
<212> DNA
<213> Homo sapiens

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<220>
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<222> (442)

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<220>
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<222> (443)
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<220>
<221> misc feature
<222> (485)
<223> n equals a,t,g, or c

<220>
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<222> (490)
<223> n equals a,t,g, or c

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agcttgtatc tgatatcagc actggattgt agaacttgtt gctgattttg accttgtatt 120
gaagttaact gttccccttg gtatttgttt aataccctgt acatatcttt gagttcaacc 180
tttagtacgt gtggcttggt cacttcgtgg ctaaggtaag aacgtgcttg tggaagacaa 240
gtctgtggct tggtgagtct gtgtggccag cagcctctga tctgtgcagg gtattaacgt 300
gtcaaggctg agtgttctgg ggaattctct agaggctggc aagaaccagt tggttttgtc 360
cttgcggggt ctgtcaaggg ttggaaatcc caagccgtag gacccagttc cctnccttaa 420
ccgaagtctt tggccaaaca cnngggccgt aactggcctt gagttggaac ggttgcataa 480
gccgnaaagn atcaac 496

<210> 800
<211> 516
<212> DNA
<213> Homo sapiens

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<222> (29)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (30)
<223> n equals a,t,g, or c

<220>
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<222> (44)

<223> n equals a,t,g, or c

<220>
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<222> (80)
<223> n equals a,t,g, or c

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<222> (107)
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<220>
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<222> (122)
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<222> (173)
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<220>
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<222> (193)
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<222> (199)
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<222> (275)
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<222> (370)
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<222> (500)
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<400> 800

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cacaccaccc cttgccaaan tcatctgcct gctccccggg gggagangac cgccggcctc 120
tnctactagc ccaccagccc accagggana aaataancca tganangcng cgnccgccac 180
ccngtgtncn cantccccnc cttcccgntt cccttagaan cctgccgcgt cctatctcat 240
gacgctcatg gaaccncttt ctttgatctn ctntntctta tctccccctc tttntngttc 300
taaagaaaat cattttgatg caaggtcctg cctgnnatca natccgaagt gctcctgcag 360
tnacccttn cctggcattt ctcttccacg cgacaagtct gctagtgaga tcttgcatga 420
ctcactttgt ttccaaaacc cggggctatt ttgcatctca agtttcctgg ggcctgcttc 480
ctgtgtncca cttaagggcn nctgggccaa gactgt 516

<210> 801
<211> 284
<212> DNA
<213> Homo sapiens

<220>
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<223> n equals a,t,g, or c

<220>
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<222> (6)
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<220>
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<222> (12)
<223> n equals a,t,g, or c

<220>
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<222> (28)
<223> n equals a,t,g, or c

<400> 801
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cgaccttcgc gtttttatat atatagatat atatatagat atatatagat atatatatag 120
atatatatag atatatatat agatatatat agatatatat agatatatat agatatatag 180
atatatatag atatatatag atatatagat atatatagat atatatagat atatagatat 240
atatagatat atagatatat atatatctgg ctcatgcatg aaaa 284

<210> 802
<211> 153
<212> DNA
<213> Homo sapiens

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<220>
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<222> (140)
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<220>
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<222> (143)
<223> n equals a,t,g, or c

<400> 802
cggacggctg tgtagcgcgt gggtgtaaga cttgcccaag tcccanagca cctcacctcc 60
cgaagccacc atccccaccc tgtcttccac anccgcctga aagccacaat gagaatgant 120
cacactgagg cctngatgtn ctntaatcac ttg 153

<210> 803
<211> 383
<212> DNA
<213> Homo sapiens

<220>
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<222> (271)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (301)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (370)
<223> n equals a,t,g, or c

<220>
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<222> (374)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (375)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (383)
<223> n equals a,t,g, or c

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attgtgcctt tattttatga gccccagttt tctgggctta gtttaaaaaa aaaatcaagt 120
ctaaacattg catttagaaa gcttttgttc ttggataaaa agtcatacac tttaaaaaaa 180
aaaaaaactt tttccaggaa aatatattga aatcatgctg ctgagcctct attttctttc 240
tttggatgtt ttggattcag tattccttta nccataaatt tttagcattt aaaaattcac 300
nggatggtac attaagccaa taaactggct ttaatggatt acccaaaaaa aaaaaaaaaa 360
aaagggggn cgcnncagag ggn 383

<210> 804
<211> 509
<212> DNA
<213> Homo sapiens

<220>
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<222> (94)
<223> n equals a,t,g, or c

<220>
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<222> (397)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (399)
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<220>
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<220>
<221> misc feature

<222> (434)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (478)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (501)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (504)
<223> n equals a,t,g, or c

<400> 804
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ctctggagct cagcacagcc ctggagcacc aggngtacat tacttttctt gaagacctca 120
agagttttgt caagagccag tagagcagac agatgctgaa agccatagtt tcatggcagg 180
ctttggccag tgaacaaatc ctactctgaa gctagacatg tgctttgaaa tgattatcat 240
cctaatatca tgggggaaaa aataccagat ttaaattata tgttttgtgc tctcatttat 300
ttatcatttt tttctgtaca aatctattat ttctaggttt ttgtattaca tgatagacat 360
aaattgggtt atctcctcca ggcagtttgt cttttcnant nctccccctt caaccgtgtc 420
acaaagacca gacngtgtcg ggaaagtttt ttttctccgt attgttaaag gttccatnca 480
attaggttta ataaaggctt nttntccag 509

<210> 805
<211> 753
<212> DNA
<213> Homo sapiens

<220>
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<222> (648)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (668)
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<220>
<221> misc feature

<222> (718)
<223> n equals a,t,g, or c

<220>
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<222> (736)
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<400> 805
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ataggcgata gaaattgaaa cctggcgcaa tagatatagt accgcaaggg aaagatgaaa 120
aattataacc aagcataata tagcaaggac taacccctat accttctgca taatgaatta 180
actagaaata actttgcaag gagagccaaa gctaagaccc ccgaaaccag acgagctacc 240
taagaacagc taaaagagca cacccgtcta tgtagcaaaa tagtgggaag atttataggt 300
agaggcgaca aacctaccga gcctggtgat agctggttgt ccaagataga atcttagttc 360
aactttaaat ttgcccacag aaccctctaa atccccttgt aaatttaact gttagtccaa 420
agaggaacag ctctttggac actaggaaaa aaccttgtag agagagtaaa aaatttaaca 480
cccatagtag gcctaaaagc agccaccaat taagaaagcg ttcaagctca acacccacta 540
cctaaaaaat cccaaacata taactgaact cctcacaccc aattggacca atctatcacc 600
ctatagaaga actaatggta gtataagtaa catgaaaaca ttctcctncg cataagcctg 660
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aaagaaattt ctcaatcctt cagccggtga tagcacgttc ttaatgtctc tttttattgc 180
ctgtaatgtt attgcagatc cacatctctc gctcaactgt taatgtctca acctccagag 240
gcacccccacc cagcacactg tcagtaaagg ggcagaatga aacagtgaga gttaagggta 300
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ttttttttta atcattatga aanagtggga agcttngnag gtna 404

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ttcctctcag agccgcccaa actgccttga tgtgtggagg ggangcaaga tgggtaaggg 180
ctcaggaagt tgctccanga acagtagctg atganctgcc cagagtgcct ggctccagcc 240
tgtacccttg gtatgccntg aacatntggt ttccccaccc aantgcggct aagtctcttt 300
ttccttggat cagccaggcg aaattggggc tttgacaagg aattttctaa ggaaaccttg 360
ttaaccagac aaaacacaac cagggttaca gggggtatgn aagggttttc tgncccngga 420
ggnttnag                                                          428

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gtaacgcagg tgtcctaagg cgagctcagg gaggacagaa acctcccgtg gagcagaagg 180
gcaaaagctc gcttgatctt cattttcagt acgaatacag accgtgaaag ccgggcctca 240
cgatcctcct gaccttnncg ntttncagcn ggaggtgtca gaaaantnac cacagggata 300
actcgcttgt cgcggccaag cgttcatagc gacgtcgctt tnccangtnc gatgtcggat 360
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ccccatagtg attgagtctt caaaaccacc gattctgaga gcaaggaaga ttttggaaga 180
aaatctgact gtggattatg acaaagatta tcttttttct taagtaatct atttagatcg 240
ggctgactgt acaaatgact cctggaaaaa actcttcacc tagtctagaa taagggaggt 300
gggagaatga tgacttaccc tgaagtcctt cccttgactg cccgcactgg ggcctgttct 360
gtgccctggg agcatnntgc ccagctaagt ggggttcagg cagtgggcag ctttcccaat 420
nantcgattt ccatnccagn gganttaaaa ccagttggcc aaatttccaa gnccttgnaa 480
ntaaggantc catttaccaa cccgcggttt tgtggtcagt gccccaaggg ggtaggttga 540
agggggctta acaaacatgg aagtnggggg nanaagggat nan 583

<210> 810
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<212> DNA
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gtatacagat gagggtgtcc gctgctgctt tccttcggaa tccagtgctt ccacagagat 120
tancctgtan cttatatttg acattcttca ctgtctgttg ttnancnacc gtagcttttt 180
accgttcact tccccttcca actatgtcca gatgtgcagg ctcctccnct ctggactttc 240
tccaaaggca ctgaccctng gnctnnactt tg 272

<210> 811
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<222> (259)
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cagatctttt taaaaagata cttctgtaac ttaagaaacc tgggcattta aatcatattt 120
tgtctttagg taaaagcttt ggtttgtgtt cgtgttttgt ttgtttcact tgtttccctc 180
ccagccccaa accttttgtt ctctccgtga acttaccttt cccttttttct ttctcttttt 240
ttttttgga anattaatng tttncaataa aatttncatn gccattaaaa aaaaaaaaaa 300

<210> 812
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<212> DNA
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gaaattgaaa cctggcgcaa tagatatagt accgcaaggg aaagatgaaa aattatagcc 120
aagcataata tagcaaggac taacccctat accttctgca taatgaatta actagaaata 180
actttgcaag gagagccaaa gctaagaccc ccgaaaccag acgagctacc tnagaacagc 240
tgaaagagca cacccgtcta tgtagcaaaa tagtgggaag atttataggt tgangcgaca 300
aacctaccga gcctggtgat agctngttgt tccaanattg aatccttagt tccactttta 360
atttggcccc aaaaaccccc taattcccct tggttaattt taactgttng tcccaaaaaa 420
ggaaccngct ctttgggacc cttanggaaa aaaaccttgn ttaaaaanaa ttaaaaaa 478

<210> 813
<211> 63
<212> DNA
<213> Homo sapiens

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tga 63

<210> 814
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<212> DNA
<213> Homo sapiens

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gagggtcctg ctg 73

<210> 815
<211> 102
<212> DNA
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tctcctttgc ctggccggga gggccttggc ngnccctcan cn 102

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aggcgggcat aacacagcaa gacgagaaga ccctatggag ctttaattta ttaatgcaaa 120
cagtacctaa caaacccaca ggtcctaaac taccaaacct gcattaaaaa tttcggttgg 180

ggcgacctcg gagcagaacc caacctccga gcagtacatg ctaagacttc accagtcaaa 240
gcgaactact atactcaatt gatccaataa cttgaccaac ggaacaagtt accctaggga 300
taacagcgca atcctattct agagtccata tcaacaatan ggtttacnac ctcgatgnnn 360
ggatcaggac attccaatg 379

<210> 817
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cgcgttcgct gcctccttca gctccaggat gatcggccag aagacgctct actccttttt 120
ctcccccagc cccgccaaga agcgacangg ccccaagncc cgagccggcc gtcaagggga 180
ccggngtggc tngggttgct naagaaagcg gaatncgggg ggcatcccag ccaagaangn 240
cccggctggg naggagaanc tngggaacgc cggcctcctt ggncgctgaa ttnccgaaca 300
ttttggaacc ggattccaga ggaacaaagg gcccgnggnc cttgnttaan aatncggggg 360
ccngnaaang ttnccccttg gggntttttg gaanaanaac ctgggaaaga aagcanctta 420
aggggggggn atttcgggg gaaancgtta tttttaatca aagctaaatt ggggattttn 480
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<210> 818
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<212> DNA
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<223> n equals a,t,g, or c

<220>
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<222> (275)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (279)
<223> n equals a,t,g, or c

<220>
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<222> (320)
<223> n equals a,t,g, or c

<400> 818
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ctcactaatg ggaacanaag ctggagctcc accgngtagg cggncggtct agaactagtg 120
tgatcccccg ggctgcagga attcggcncg agaggaaana gaaaccgtct gaactatgct 180
gnnngccatc atnctnggcc tcatcgcnnt tccatcccta cgcatgcttt acatagcana 240
cgaggtgacg atgccnccct taccatcaag atcanttgnc caccaatggt acttgaacct 300
acgagtacac ccgaccaccn ggtggacta 329

<210> 819
<211> 648
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (369)
<223> n equals a,t,g, or c

<220>
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<222> (518)
<223> n equals a,t,g, or c

<220>
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<220>
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<222> (547)
<223> n equals a,t,g, or c

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<222> (565)
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<221> misc feature
<222> (584)
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<220>
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<222> (626)
<223> n equals a,t,g, or c

<400> 819
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atctgttgtt ctgtggtcac agtgacctta gctacatagc agactttccc aaatgtattg 120
attacaaata aacagttgtt acttagcaag acctgaaaat atgtctgcag gtttctcctt 180
gaagcaaatg tgtgggatca ttgcatttcc agaaatctgc ctccttcacc ctccgttgac 240
agtatatgtc atgcctcact ttcttctagc tgagctttaa atcattagag cttaaattgt 300
cagatcgttc attgcctttc cagggttatt tagtaaagtt tgttgaaaac aaaaacgcct 360
tttcttggnt ctttttcag ttattttgaa ggccagcatc ctgattaaat gctgacacat 420
taatgaatga ccagcaacag ctttcagctc ttaaaaagac acttatattt gaatttacat 480
gctgggtacc tgggtccaat ggtggcaaaa ggccactntt cattaaaagg ggtcctccat 540
ttcntanccc caaggacttc ctcanttttc aaattgggaa gggnacctaa aagggggtac 600
aattaaaacc ctggggtaaa gggggnaaaa aaaaaaaaaa aaaaaaaa 648

<210> 820
<211> 469
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (238)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (284)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (293)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (308)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (319)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (370)
<223> n equals a,t,g, or c

<220>
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<222> (396)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (421)
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<222> (428)
<223> n equals a,t,g, or c

<220>
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<222> (465)
<223> n equals a,t,g, or c

<400> 820
gccactccac cttactacca gacaacctta gccaaaccat ttacccaaat aaagtatagg 60
cgatagaaat tgaaacctgg cgcaatagat atagtaccgc aagggaaaga tgaaaaatta 120
taaccaagca taatatagca aggactaacc cctatacctt ctgcataatg aattaactag 180
aaataacttt gcaaggagag ccaaagctaa aacccccaat aaaccttgaa cagtgaanaa 240
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaacctcgag gtcnacggta tcnataacct 300
tgatatcnaa ttcggcacna gcaaccctca ttccccaacc cacgccggag gctgcgcctg 360
caggacctgn ctgaccgatt ggtggatcct ctgaanatga acacgactca ccactgctca 420
ncgaggcntg cttgagcaaa atccgccaat tataaaaaaa aaacnctcc 469

<210> 821
<211> 432
<212> DNA
<213> Homo sapiens

<220>

<221> misc feature
<222> (344)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (385)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (419)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (422)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (425)
<223> n equals a,t,g, or c

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ttgcacgctc tttaagagtc tgcactggag gaactctgcc attaccagct cccttgttgc 120
agaaggaagg ggaaacatac atttattcat gccagtctgt tgcatgcagg ctttttggct 180
tcctaccttg caacaaaata attgcaccaa ctccttagtg ccgattccgc ccacagagag 240
tcctggagcc acagtctttt ttgctttgca ttgtaaggag agggactaaa gtgctagaga 300
ctatgtcgct ttcctgagct aacgagagcg ctcgtgaact ggantcaact gctttcaggg 360
aaaaagaaaa aaaaaaaaaa aaaanccggg gggggcccg gtaacccatt tccccctana 420
gnggnggggt tt 432

<210> 822
<211> 428
<212> DNA
<213> Homo sapiens

<220>
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<222> (323)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (367)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (382)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (385)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (425)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (427)
<223> n equals a,t,g, or c

<400> 822
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tcattagtga aagtggtctt ttatgtcctc ccagcagaca gacatcaagg atgagttaac 120
caggagacta ctcctgtgga ctgtggagct ctggaaggct tggtgggagt gaatttgccc 180
acaccttaca attgtggcag gatccagaag agcctgtctt tttatatcca ttccttggat 240
gtcattgggc ctctcccacc gatttcatta cggtgccacg catccatggg atctggggta 300
gtccggaaaa acaaaaggag ggnagacagc ctggtaatgg ataagatcct taccacagtt 360
ttcccanggg gaatacctta tnaanccttc aactttttt tttcccttaa gaattaaaac 420
ggggnana 428

<210> 823
<211> 100
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (32)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (54)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (63)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (71)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (78)
<223> n equals a,t,g, or c

<400> 823
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agntgaccca ntctccgncc ctccctgtct gcagctggta 100

<210> 824
<211> 173
<212> DNA
<213> Homo sapiens

<220>
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<222> (79)
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<220>
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<222> (111)
<223> n equals a,t,g, or c

<220>
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<222> (117)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (156)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (165)
<223> n equals a,t,g, or c

<400> 824
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gcccccatcc cgggaggana tgaccaagaa acagtcagct gaactgcctg nttctanagg 120
tttctatccc acgaaatccc cttgaattgg gaaacnattg ggcanccgaa aaa 173

<210> 825
<211> 341
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (283)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (313)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (317)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (335)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (339)
<223> n equals a,t,g, or c

<400> 825
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tataggcgat agaaattgaa acctggcgca atagatatag taccgcaagg ggaaagatga 120
aaaattataa ccaagcataa tatagcaagg actaacccct ataccttctg cataatgaat 180
taactagaaa taactttgca aggagagcca aagctaagac ccccgaaacc agaacgagct 240
accttagaac agcttaaaga gcacacccct ctatttttgc canaatagtg ggaaagattt 300
ataggttgaa ggnaacnaac ctaccgagcc tggtnaatnc t 341

<210> 826
<211> 492
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (337)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (416)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (446)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (471)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (475)
<223> n equals a,t,g, or c

<220>
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<222> (480)
<223> n equals a,t,g, or c

<400> 826
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ataggcgata gaaattgaaa cctggcgcaa tagatatagt accgcaaggg aaagatgaaa 120
aattataacc aagcataata tagcaaggac taacccctat accttctgca taatgaatta 180
actagaaata actttgcaag gagagccaaa gctaagaccc ccgaaaccag acgagctacc 240
taagaacagc taaaagagca caccccgtcta tgtagcaaaa tagtgggaag atttataggt 300
agaggcgaca aacctaccga gcctggtgat agctggntgt ccaagataga atcttagttc 360
aactttaaat ttgcccacag aaccctctaa atccccttgt aaatttaact gttagnccaa 420
agaggaacaa gctctttgga cactangaaa aaaccttgta tagagaggaa naaanatttn 480
acaacccata ct 492

<210> 827
<211> 290
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (59)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (230)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (250)
<223> n equals a,t,g, or c

<220>
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<222> (262)

<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (264)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (290)
<223> n equals a,t,g, or c

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aacgggaccg tccttctcgc tccgccccgc gggggtcccc tcgtctctcc tctccccgcc 120
cgccggcggt gcgtgtggga aggcgtgggg tgcggacccc ggcccgacct cgccgtcccg 180
cccgccgcct tctgcgtcgc gggtgcgggc cggcggggtc ctctgacgcn gcagacagcc 240
ctcgctgtcn cctccagtgg angncgactt gcgggcggta ctcctacgan 290

<210> 828
<211> 420
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (149)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (334)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (382)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (396)
<223> n equals a,t,g, or c

<220>
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<222> (403)
<223> n equals a,t,g, or c

<220>
<221> misc feature

<222> (405)
<223> n equals a,t,g, or c

<400> 828
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agcgtgcacc aagggcttgg tctgcggggg ccttggagct cctgctcttc tcccgcacct 120
ccatggatgc actgctgccg agcagagcng cctctgccag gccccgccct gggattccta 180
gagactagct tcagttttgc tatttttttt aagtgggaga agggtgggca gttatcactg 240
gggaagagag gaccggccac ctgtccagca tgggctccag agccttcctc tctcacaggg 300
cagagtcttg tcggcaaggc agcctcctgg ccantttctc tgctcatgtt tctggttagc 360
agagttcaga gccaattgtt tnacttcttg gttgtncccg tgnangaagc ctttcaaaac 420

<210> 829
<211> 298
<212> DNA
<213> Homo sapiens

<220>
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<222> (19)
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<220>
<221> misc feature
<222> (20)
<223> n equals a,t,g, or c

<220>
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<222> (30)
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<220>
<221> misc feature
<222> (56)
<223> n equals a,t,g, or c

<220>
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<222> (57)
<223> n equals a,t,g, or c

<220>
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<222> (109)
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<222> (125)
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<222> (129)
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<221> misc feature
<222> (171)
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<222> (181)
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<220>
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<222> (191)
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<220>
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<222> (267)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (268)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (269)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (281)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (287)
<223> n equals a,t,g, or c

<400> 829
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tggagagtga caaaatggtg acaggtagct ggggacctag gctatctcnc catgaaggtt 120
gttcngctna ttgtatatct gtgtatgtag tgtaactata ttgtacaatg ngaagactgt 180
naactactat ntagggttgt tgcagattga aatttagttg tctcattggc tgtctgagga 240

agtgtggact tctatatata gatctannnt gaaaactgct ncatgantga aaaccaca 298

<210> 830
<211> 516
<212> DNA
<213> Homo sapiens

<220>
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<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (5)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (10)
<223> n equals a,t,g, or c

<220>
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<222> (408)
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<220>
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<222> (475)
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<220>
<221> misc feature
<222> (477)
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<220>
<221> misc feature
<222> (497)
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<220>
<221> misc feature
<222> (513)
<223> n equals a,t,g, or c

<220>
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<222> (515)
<223> n equals a,t,g, or c

<400> 830
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cgggggcatc cccttgtccc caagagaccc gacgcttgct tcatggccta cacgttcgag 120
agagagtctt cgggagagga ggaggagtag ggccgcctcg gggctgggca tccggcccct 180
ggggccaccc cttgtcagcc gggtgggtag gaaccgtaga ctcgctcatc tcgcctgggt 240
ttgtccgcat gttgtaatcg tgcaaataaa cgctcactcc gaattagcgg tgtatttctt 300
gaagtttaat attgtgtttg tgatactgaa gtatttgctt taattctaaa taaaaattta 360
tattttactt ttttattgct ggtttaagat gattcagatt atccttgnac tttgaggaga 420
agtttcttat ttggagcttt tggaaacagc ttaagctttt aacttggaaa gatangnatt 480
aatccccttc attggtntcc aaaagccaat aangng 516

<210> 831
<211> 636
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (414)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (453)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (530)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (617)
<223> n equals a,t,g, or c

<400> 831
ggaaaaaaat gagttccatt taaaattttg gcatatggca ttttctaact taggaagcca 60
caatgttctt ggcccatcat gacattgggt agcattaact gtaagttttg tgcttccaaa 120
tcactttttg gtttttaaga atttcttgat actcttatag cctgccttca attttgatcc 180

tttattcttt ctatttgtca ggtgcacaag attaccttcc tgttttagcc ttctgtcttg 240
tcaccaacca ttcttacttg gtggccatgt acttggaaaa aggccgcatg atctttctgg 300
ctccactcag tgtctaaggc accctgcttc ctttgcttgc atcccacaga ctatttccct 360
catcctattt actgcagcaa atctctcctt agttgatgag actgtgttta tctnccttta 420
aaaccctacc tatcctgaat ggtctgtcat tgnctgcctt taaaatcctt cctctttctt 480
cctcctctat tctctaaata atgatggggc ttaagttata cccaaagctn actttacaaa 540
atatttcctc aagactttgc agaaacacca acaaaatgcc atttaaaaaa ggggattttc 600
tttaaaggaa ctctaanaca ggcaaggttc tgatgt 636

<210> 832
<211> 466
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (421)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (443)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (446)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (453)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (466)
<223> n equals a,t,g, or c

<400> 832
gatcagatta tgagttactg tttaaaagaa aaatgctgtt tattcatgct gaggtgattc 60
agttccctcc ttcttacaga agtattttaa ttcaccccac actagaaatg cagcatcttt 120
gtggacgtct ttttcacaag cctccaaggc tccttagatt gggtcgttac taaaagtaca 180
ttaaaacact cttgtttatc gaagtatatt gatgtattct aaagctagta aacttcccta 240
acgtttaatt gccctacaga tgcttctctt gctgtgggtt ttcttttgtt agtggtctga 300
aataattatt ttcctgttct attaatacat aagtgtattt tgcacaaaaa aattaacctg 360
gtcaaatagt gattaccaaa atatatatta ataatcttgg gcaaattttt gccatttata 420
ngaaaacatt tttaacccac ggntangttc tanatttatt ctttcn 466

<210> 833
<211> 405

<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (237)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (278)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (335)
<223> n equals a,t,g, or c

<400> 833
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gggaggagtc tgtgcagttt ctgacacttg ttgttgaaca tggctaaata caatgggtat 120
cgctgagact aagttgtaaa aaattaacaa atgtgctgct tggttaaaat ggctacactc 180
atctgactca ttctttattc tattttagtt ggtttgtatc ttgcctaagg tgcgtantcc 240
aactcttggt attaccctcc taatagtcat actagtantc atactccctg gtgttatgta 300
ttctctaaaa gctttaaatg tctgcattgc aaccngccat caaatattga atgggctctc 360
ttttggctgg aattacaaac tcaaaaaatg tttctcagga aaaaa                 405
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<210> 834
<211> 402
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (277)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (332)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (354)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (359)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (390)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (400)
<223> n equals a,t,g, or c

<400> 834
gcaaacccac aggtcctaaa ctaccaaacc tgcattaaaa atttcggttg gggcgacctc 60
ggagcagaac ccaacctccg agcagtacat gctaagactt caccagtcaa agcgaactac 120
tatactcaat tgatccaata acttgaccaa cggaacaagt taccctaggg ataacagcgc 180
aatcctattc tagagtccat atcaacaata gggtttacga cctcgatgtt ggatcaggac 240
atcccgatgg tgcagccgct attaaaggtt cgtttgntca acgattaaag tcctacgtga 300
tctgagttca gaccggagta atccaggtcg gnttctatct acttcaaatt cctncctgna 360
cgaaaggaca agagaaataa gggctacttn acaaagcgcn tt 402

<210> 835
<211> 121
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (1)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (4)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (40)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (77)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (100)
<223> n equals a,t,g, or c

<220>

<221> misc feature
<222> (110)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (117)
<223> n equals a,t,g, or c

<400> 835
nttnaaaaaa aaaaaaaaaa aaaaaaaaaa aagaaaaaan aaaaaaaaaa aaaaaaaaaa 60
aaaaagggcg gccgttntaa aggatccaag cttacgtacn cgtgcatgcn acgtcanagc 120
t 121

<210> 836
<211> 411
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (340)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (344)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (357)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (386)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (408)
<223> n equals a,t,g, or c

<400> 836
agtaagcctg ccagacacgc tgtggcggct gcctgaagct agtgagtcgc ggcgccgcgc 60
acttgtggtt gggtcagtgc cgcgcgccgc tcggtcgtta ccgcgaggcg ctggtggcct 120
tcaggctgga cggcgcgggt cagccctggt ttgccggctt ctgggtcttt gaacagccgc 180
gatgtcgatc ttcaccccca ccaaccagat ccgcctaacc aatgtggccg tggtacggat 240
gaagcgcgcc aggaagcgct tcgaaatcgc ttgctacaga aacaagtcgt cggctggcgg 300
agggctttgg aaaaagactt gatgaatttt gcagacccan caangtttgt aaagttncca 360

aagtcagttt ccaaaaggaa attcancagg ggtttggaaa atgccaanga a 411

<210> 837
<211> 386
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (381)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (383)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (384)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (385)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (386)
<223> n equals a,t,g, or c

<400> 837
gcggcagctc agcaagtggt ggaccaggcc acagaggcgg ggcagaaagc catggaccag 60
ctggccaaga ccacccagga aaccatcgac aagactgcta accaggcctc tgacaccttc 120
tctgggatcg ggaaaaaatt cggcctcctg aaatgacagc agggagactt gggtcggcct 180
cctgaaatga tagcagggag acttgggtga cccccccttcc aggcgccatc tagcacagcc 240
tggccctgat ctccgggcag ccaccacctc ctcggtctgc cccctcatta aaattcacgt 300
tcccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 360
aaaaaaaaaa aaaaaaaaaa ngnnnn 386

<210> 838
<211> 124
<212> DNA
<213> Homo sapiens

<400> 838
gctttcaata gatcgcagcg agggagctgc tctgctacgt acgaaacccc gacccagaag 60
caggtcgtct acgaatggtt tagcgccagg ttccccacga acgtgcggtg cgtgacgggc 120
gagg 124

<210> 839
<211> 270
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (26)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (56)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (107)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (130)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (175)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (178)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (250)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (260)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (261)
<223> n equals a,t,g, or c

<400> 839

atctggttgt ggttacaatg aaaatnagaa gcattattga tggattcgca taagcncaat 60
gtgatgtcct gcgccgttct gccccctctc ccttccaggg tgagggnctg gggtgagggt 120
taatgttcgn accagtgctg gctgttcccc tcaccctaac cctctcccca aaggncgnag 180
gggcccggtt acccaattcg ccctatagtg agtcgtatta caattcactg gccgtcgttt 240
tacaagacgn agggaggagn ntgatgaaaa 270

<210> 840
<211> 430
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (210)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (262)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (263)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (348)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (369)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (390)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (395)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (409)
<223> n equals a,t,g, or c

<400> 840
ctctacatca ccgccccgac cttagctctc accatcgctc ttctactatg aacccccctc 60
cccataccca accccctggt caacctcaac ctaggcctcc tatttattct agccacctct 120
agcctagccg tttactcaat cctctgatca gggtgagcat caaactcaaa ctacgccctg 180
atcggcgcac tgcgagcagt agcccaaacn atctcatatg aagtcaccct agccatcatt 240
cctactatca acattactaa tnngttggct cctttaacct ctccaccctt atcacaacac 300
aagaacactc ctgaatatcc tgccatcata accctttggc catatatnat tatcttccac 360
actagggana acaacgaacc cccttcgaan cttgngaaag ggaatttcna ataatcttca 420
ggttcaaatt 430

<210> 841
<211> 650
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (519)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (555)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (564)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (573)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (589)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (634)
<223> n equals a,t,g, or c

<400> 841
gccgtcatct actctaccat ctttgcaggc acactcatca cagcgctaag ctcgcactga 60
ttttttacct gagtaggcct agaaataaac atgctagctt ttattccagt tctaaccaaa 120
aaaataaacc ctcgttccac agaagctgcc atcaagtatt tcctcacgca agcaaccgca 180
tccataatcc ttctaatagc tatcctcttc aacaatatac tctccggaca atgaaccata 240
accaataata ccaatcaata ctcatcatta ataatcataa tggctatagc aataaaacta 300

ggaatagccc cctttcactt ctgagtccca gaggttaccc aaggcacccc tctgacatcc 360
ggcctgcttc ttctcacatg acaaaaacta gcccccatct caatcatata ccaaatctct 420
ccctcactag acgtaagcct tctcctcact ctctcaatct tatccatcat agtaggcagt 480
tgagggtgga ttaaaccaaa acccagctac gcaaaatcnt agcatacttc ctcaattacc 540
cacataggat gaatnaatag cagnttctac cgnacaaccc ttacataanc atttcttaaa 600
ttaactaatt atattaatcc taactactac ggantctact actaacttaa 650

<210> 842
<211> 509
<212> DNA
<213> Homo sapiens

<220>
<221> misc feature
<222> (438)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (455)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (462)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (468)
<223> n equals a,t,g, or c

<220>
<221> misc feature
<222> (482)
<223> n equals a,t,g, or c

<400> 842
gcctgtgtct gctaaaaaag aaaagaaagt ttcctgcatg ttcattcctg atgggcgggt 60
gtctgtctct gctcgaattg acagaaaagg attctgtgaa ggtgatgaga tttccatcca 120
tgctgacttt gagaatacat gttcccgaat tgtggtcccc aaagctgcca ttgtggcccg 180
ccacacttac cttgccaatg gccagaccaa ggtgctgact cagaagttgt catcagtcag 240
aggcaatcat attatctcag ggacatgcgc atcatggcgt ggcaagagcc ttcgggttca 300
gaagatcagg ccttctatcc tgggctgcaa catccttcga gttgaatatt ccttactgat 360
ctatgttagc gttcctggat ccaagaaggt catccttgac ctgcccctgg taattggcag 420
cagatcaggt ctaagcanca gaacatccag ctggncagcc cnaaccanct ctgaagatga 480
gntgggtaga tctgaacatc ctgataccc 509

<210> 843
<211> 158
<212> PRT

<213> Homo sapiens

<400> 843

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Lys Arg Asp Trp Val Ile Pro Pro Ile Ser Cys Pro Glu Asn Glu Lys
  1               5                  10                  15

Gly Pro Phe Pro Lys Asn Leu Val Gln Ile Lys Ser Asn Lys Asp Lys
             20                  25                  30

Glu Gly Lys Val Phe Tyr Ser Ile Thr Gly Gln Gly Ala Asp Thr Pro
         35                  40                  45

Pro Val Gly Val Phe Ile Ile Glu Arg Glu Thr Gly Trp Leu Lys Val
     50                  55                  60

Thr Glu Pro Leu Asp Arg Glu Arg Ile Ala Thr Tyr Thr Leu Phe Ser
 65                  70                  75                  80

His Ala Val Ser Ser Asn Gly Asn Ala Val Glu Asp Pro Met Glu Ile
                 85                  90                  95

Leu Ile Thr Val Thr Asp Gln Asn Asp Asn Lys Pro Glu Phe Thr Gln
            100                 105                 110

Glu Val Phe Lys Gly Ser Val Met Glu Gly Ala Leu Pro Gly Thr Ser
        115                 120                 125

Val Met Glu Val Thr Ala Thr Asp Ala Asp Asp Gly Cys Gly Thr Pro
    130                 135                 140

Thr Met Pro Pro Ser Leu Thr Pro Ser Ser Ala Gln Asp Pro
145                 150                 155
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<210> 844
<211> 601
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (64)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (106)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (152)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (358)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (383)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 844
Thr Glu Leu Leu Lys Ser Ala Ala Arg His Gly Thr Ala Glu Ser Ala
1 5 10 15

Pro Trp Pro Arg Gly Gln Gly Trp Gln Gln Trp Gln Gln Gln Trp Arg
20 25 30

Arg Arg Trp Xaa Ser Trp Arg Lys Asp Arg Ala Arg Thr Arg Arg Gln
35 40 45

Glu Glu Leu Ala Leu Ser Gln Glu Pro Lys Ser Ser Ser Arg Gly Xaa
50 55 60

Ser Pro Gly Ala Ser Pro Ala Ser Pro Thr Ser Gln Gln Phe Cys Cys
65 70 75 80

Phe Arg Leu Asp Gln Val Ile His Ser Asn Pro Ala Gly Ile Gln Gln
85 90 95

Ala Leu Ala Gln Leu Ser Xaa Arg Gln Xaa Ser Val Thr Ala Pro Gly
100 105 110

Gly His Pro Arg His Lys Pro Gly Pro Pro Gln Ala Pro Gln Gly Pro
115 120 125

Ser Pro Arg Pro Pro Thr Arg Tyr Glu Pro Gln Arg Val Asn Ser Gly
130 135 140

```
Leu Ser Ser Asp Pro His Phe Xaa Glu Pro Gly Pro Met Val Arg Gly
145                 150                 155                 160

Val Gly Gly Thr Pro Arg Asp Ser Ala Gly Val Ser Pro Phe Pro Pro
                165                 170                 175

Lys Arg Arg Glu Arg Pro Pro Arg Lys Pro Glu Leu Leu Gln Glu Glu
            180                 185                 190

Ser Leu Pro Pro Pro His Ser Ser Gly Phe Leu Gly Ser Lys Pro Glu
        195                 200                 205

Gly Pro Gly Pro Gln Ala Glu Ser Arg Asp Thr Gly Thr Glu Ala Leu
    210                 215                 220

Thr Pro His Ile Trp Asn Arg Leu His Thr Ala Thr Ser Arg Lys Ser
225                 230                 235                 240

Tyr Arg Pro Ser Ser Met Glu Pro Trp Met Glu Pro Leu Ser Pro Phe
                245                 250                 255

Glu Asp Val Ala Gly Thr Glu Met Ser Gln Ser Asp Ser Gly Val Asp
            260                 265                 270

Leu Ser Gly Asp Ser Gln Val Ser Ser Gly Pro Cys Ser Gln Arg Ser
        275                 280                 285

Ser Pro Asp Gly Gly Leu Lys Gly Ala Ala Glu Gly Pro Pro Lys Arg
    290                 295                 300

Pro Gly Gly Ser Ser Pro Leu Asn Ala Val Pro Cys Glu Gly Pro Pro
305                 310                 315                 320

Gly Ser Glu Pro Pro Arg Arg Pro Pro Pro Ala Pro His Asp Gly Asp
                325                 330                 335

Arg Lys Glu Leu Pro Arg Glu Gln Pro Leu Pro Pro Gly Pro Ile Gly
            340                 345                 350

Thr Glu Arg Ser Gln Xaa Thr Asp Arg Gly Thr Glu Pro Gly Pro Ile
        355                 360                 365

Arg Pro Ser His Arg Pro Gly Pro Pro Val Gln Phe Gly Thr Xaa Asp
    370                 375                 380

Lys Asp Ser Asp Leu Arg Leu Val Val Gly Asp Ser Leu Lys Ala Glu
385                 390                 395                 400

Lys Glu Leu Thr Ala Ser Val Thr Glu Ala Ile Pro Val Ser Arg Asp
                405                 410                 415
```

Trp Glu Leu Leu Pro Ser Ala Ala Ala Ser Ala Glu Pro Gln Ser Lys
420 425 430

Asn Leu Asp Ser Gly His Cys Val Pro Glu Pro Ser Ser Ser Gly Gln
435 440 445

Arg Leu Tyr Pro Glu Val Phe Tyr Gly Ser Ala Gly Pro Ser Ser Ser
450 455 460

Gln Ile Ser Gly Gly Ala Met Asp Ser Gln Leu His Pro Asn Ser Gly
465 470 475 480

Gly Phe Arg Pro Gly Thr Pro Ser Leu His Pro Tyr Arg Ser Gln Pro
485 490 495

Leu Tyr Leu Pro Pro Gly Pro Ala Pro Pro Ser Ala Leu Leu Ser Gly
500 505 510

Val Ala Leu Lys Gly Gln Phe Leu Asp Phe Ser Thr Met Gln Ala Thr
515 520 525

Glu Leu Gly Lys Leu Pro Ala Gly Gly Val Leu Tyr Pro Pro Pro Ser
530 535 540

Phe Leu Tyr Ser Pro Ala Phe Cys Pro Ser Pro Leu Pro Asp Thr Ser
545 550 555 560

Leu Leu Gln Val Arg Gln Asp Leu Pro Ser Pro Ser Asp Phe Tyr Ser
565 570 575

Thr Pro Leu Gln Pro Gly Gly Gln Ser Gly Phe Leu Pro Ser Gly Ala
580 585 590

Pro Ala Ser Arg Cys Phe Tyr Pro Trp
595 600

<210> 845
<211> 67
<212> PRT
<213> Homo sapiens

<400> 845
Thr Gln Lys Thr Ser Ser Leu Leu Pro Ala Leu Ser Leu Gln Leu Pro
1 5 10 15

Leu Leu Thr Arg Phe Ser Ile Met Cys Ser Val Lys Glu Glu Phe Trp
20 25 30

Arg Val Gln Ser Ile Ile Thr Glu Leu Val Leu Lys Gly Glu Phe Gly
35 40 45

Val Glu Glu Ala Met Lys Leu Ile Thr Gly Thr Glu Ala Lys Tyr Lys
50 55 60

Ser Ile Asp
65

<210> 846
<211> 146
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 846
Ser Gln Gly Pro Asp His Pro Ser Ser Gln Leu Gln Pro Leu Asn Xaa
1 5 10 15

Ser Leu Ser His Leu Leu Val Pro Cys Leu Ser Ile Met Ser Leu Leu
20 25 30

Asn Lys Pro Lys Ser Glu Met Thr Pro Glu Glu Leu Gln Lys Arg Glu
35 40 45

Glu Glu Glu Phe Asn Thr Gly Pro Leu Ser Val Leu Thr Gln Ser Val
50 55 60

Lys Asn Asn Thr Gln Val Leu Ile Asn Cys Arg Asn Asn Lys Lys Leu
65 70 75 80

Leu Gly Arg Val Lys Ala Phe Asp Arg His Cys Asn Met Val Leu Glu
85 90 95

Asn Val Lys Glu Met Trp Thr Glu Val Pro Lys Ser Gly Lys Gly Lys
100 105 110

Lys Lys Ser Lys Pro Val Asn Lys Asp Arg Tyr Ile Ser Lys Met Phe
115 120 125

Leu Arg Gly Asp Ser Val Ile Val Val Leu Arg Asn Pro Leu Ile Ala
130 135 140

Gly Lys
145

<210> 847
<211> 184
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (179)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 847

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Ala Arg Met Ala Ala Asp Lys Xaa Pro Ala Ala Gly Pro Arg Ser Arg
  1               5                  10                  15

Ala Ala Met Ala Gln Trp Arg Lys Lys Lys Gly Leu Arg Lys Arg Arg
             20                  25                  30

Gly Ala Ala Ser Gln Ala Arg Gly Ser Asn Ser Glu Asp Gly Glu Phe
         35                  40                  45

Glu Ile Gln Ala Glu Asp Asp Ala Arg Ala Arg Lys Leu Gly Pro Gly
     50                  55                  60

Arg Pro Leu Pro Thr Phe Pro Thr Ser Glu Cys Thr Ser Asp Val Glu
 65                  70                  75                  80

Pro Asp Thr Arg Glu Met Val Arg Ala Gln Asn Lys Lys Lys Lys Lys
                 85                  90                  95

Ser Gly Gly Phe Gln Ser Met Gly Leu Ser Tyr Pro Val Phe Lys Gly
            100                 105                 110

Ile Met Lys Lys Gly Tyr Lys Val Pro Thr Pro Ile Gln Arg Lys Thr
        115                 120                 125

Ile Pro Val Ile Leu Asp Gly Lys Asp Val Val Ala Met Ala Arg Thr
    130                 135                 140

Gly Ser Gly Lys Thr Ala Cys Phe Leu Leu Pro Met Phe Glu Arg Leu
145                 150                 155                 160

Lys Thr His Ser Ala Gln Thr Gly Ala Arg Ala Ser Ser Ser Arg Arg
                165                 170                 175
```

```
Pro Glu Xaa Trp Pro Cys Arg Pro
            180



<210> 848
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 848
Ala Arg Ala Ser Ser Glu Cys Ala Arg Cys Ala Ala Ala Val Arg Thr
  1               5                  10                  15

Cys Arg Arg Arg His Arg His His Ala Gln Leu Arg Arg His Leu Glu
             20                  25                  30

Asp Ala Xaa Ser Glu Asn Phe Asp Glu Leu Leu Lys Ala Leu Gly Val
         35                  40                  45

Asn Ala Met Leu Arg Lys Val Ala Val Ala Ala Ala Ser Lys Pro His
     50                  55                  60

Val Glu Ile Arg Gln Asp Gly Asp Gln Phe Tyr Ile Lys Thr Ser Thr
 65                  70                  75                  80

Thr Val Arg Thr Thr Glu Ile Asn Phe Lys Val Gly Glu Gly Phe Glu
                 85                  90                  95

Glu Glu Thr Val Asp Gly Arg Lys Cys Arg Ser Leu Ala Thr Trp Glu
            100                 105                 110

Asn Glu Asn Lys Ile His Cys Thr Gln Thr Leu Leu Glu Gly Asp Gly
        115                 120                 125

Pro Lys Thr Tyr Trp Thr Arg Glu Leu Ala Asn Asp Glu Leu Ile Leu
    130                 135                 140

Thr Phe Gly Ala Asp Asp Val Val Cys Thr Arg Ile Tyr Val Arg Glu
145                 150                 155                 160
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<210> 849
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (50)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 849
Val Gln Asn Val Gly Tyr Gln Ser Lys His Cys Gly Ala Val Xaa Tyr
1 5 10 15

Ala Arg Leu Pro Cys Glu Met Ile Gln Asp Gln Asn Lys Ala Leu Asp
20 25 30

Cys Ser Lys Thr Gln Asn Ser Ser Arg Ala Glu Gly Gly Arg Leu Ile
35 40 45

Trp Xaa Glu Gly Pro Lys Tyr Lys Thr Asp Gly Leu Arg Leu Glu Thr
50 55 60

Arg Gly Leu Arg Trp Lys Ala His Val Pro Arg
65 70 75

<210> 850
<211> 383
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (299)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 850
Ser Thr His Ala Ser Ala His Ala Ser Val Ala Asn Glu Val Ile Lys
1 5 10 15

Cys Lys Ala Ala Val Ala Trp Glu Ala Gly Lys Pro Leu Ser Ile Glu
20 25 30

```
Glu Ile Glu Val Ala Pro Pro Lys Ala His Glu Val Arg Ile Lys Ile
        35                  40                  45

Ile Ala Thr Ala Val Cys His Thr Asp Ala Tyr Thr Leu Ser Gly Ala
    50                  55                  60

Asp Pro Glu Gly Cys Phe Pro Val Ile Leu Gly His Glu Gly Ala Gly
65                  70                  75                  80

Ile Val Glu Ser Val Gly Glu Gly Val Thr Lys Leu Lys Ala Gly Asp
                85                  90                  95

Thr Val Ile Pro Leu Tyr Ile Pro Gln Cys Gly Glu Cys Lys Phe Cys
            100                 105                 110

Leu Asn Pro Lys Thr Asn Leu Cys Gln Lys Ile Arg Val Thr Gln Gly
        115                 120                 125

Lys Gly Leu Met Pro Asp Gly Thr Ser Arg Phe Thr Cys Lys Gly Lys
    130                 135                 140

Thr Ile Leu His Tyr Met Gly Thr Ser Thr Phe Ser Glu Tyr Thr Val
145                 150                 155                 160

Val Ala Asp Ile Ser Val Ala Lys Ile Asp Pro Leu Ala Pro Leu Asp
                165                 170                 175

Lys Val Cys Leu Leu Gly Cys Gly Ile Ser Thr Gly Tyr Gly Ala Ala
            180                 185                 190

Val Asn Thr Ala Lys Leu Glu Pro Gly Ser Val Cys Ala Val Phe Gly
        195                 200                 205

Leu Gly Gly Val Gly Leu Ala Val Ile Met Gly Cys Lys Val Ala Gly
    210                 215                 220

Ala Ser Arg Ile Ile Gly Val Asp Ile Asn Lys Asp Lys Phe Ala Arg
225                 230                 235                 240

Ala Lys Glu Phe Gly Ala Thr Glu Cys Ile Asn Pro Gln Asp Phe Ser
                245                 250                 255

Lys Pro Ile Gln Glu Val Leu Ile Glu Met Thr Asp Gly Gly Val Asp
            260                 265                 270

Tyr Ser Phe Glu Cys Ile Gly Asn Val Lys Val Met Arg Ala Ala Leu
        275                 280                 285

Glu Ala Cys His Lys Gly Trp Gly Val Thr Xaa Val Val Gly Val Ala
    290                 295                 300
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Ala Ser Gly Glu Glu Ile Ala Thr Arg Pro Phe Gln Leu Val Thr Gly
305 310 315 320

Arg Thr Trp Lys Gly Thr Ala Phe Gly Gly Trp Lys Ser Val Glu Ser
325 330 335

Val Pro Lys Leu Val Ser Glu Tyr Met Ser Lys Lys Ile Lys Val Asp
340 345 350

Glu Phe Val Thr His Asn Leu Ser Phe Asp Glu Ile Asn Lys Ala Phe
355 360 365

Glu Leu Met His Ser Gly Lys Ser Ile Arg Thr Val Val Lys Ile
370 375 380

<210> 851
<211> 154
<212> PRT
<213> Homo sapiens

<400> 851
Ala Arg Ala Pro Arg Ala Thr Leu Asn Gly Pro Gly Ala Arg Gly Arg
1 5 10 15

Val Gly Val Val Val Leu Arg Pro Arg Pro Arg Gly Leu Arg Phe Pro
20 25 30

Trp Cys Pro Gly Arg Pro Ala Ser Gly Ala Val Ser Tyr Glu Ser Ala
35 40 45

His Ala Ala Ser Val Arg Leu Thr Leu Arg Thr Met Glu Gly Gly Phe
50 55 60

Gly Ser Asp Phe Gly Gly Ser Gly Ser Gly Lys Leu Asp Pro Gly Leu
65 70 75 80

Ile Met Glu Gln Val Lys Val Gln Ile Ala Val Ala Asn Ala Gln Glu
85 90 95

Leu Leu Gln Arg Met Thr Asp Lys Cys Phe Arg Lys Cys Ile Gly Lys
100 105 110

Pro Gly Gly Ser Leu Asp Asn Ser Glu Gln Lys Cys Ile Ala Met Cys
115 120 125

Met Asp Arg Tyr Met Asp Ala Trp Asn Thr Val Ser Arg Ala Tyr Asn
130 135 140

Ser Arg Leu Gln Arg Glu Arg Ala Asn Met

145 150

<210> 852
<211> 396
<212> PRT
<213> Homo sapiens

<400> 852
Asp Ser Arg Val Asp Pro Arg Val Arg Ala Ile Ile Ala Lys Thr Phe
1 5 10 15

Lys Gly Arg Gly Ile Thr Gly Val Glu Asp Lys Glu Ser Trp His Gly
20 25 30

Lys Pro Leu Pro Lys Asn Met Ala Glu Gln Ile Ile Gln Glu Ile Tyr
35 40 45

Ser Gln Ile Gln Ser Lys Lys Lys Ile Leu Ala Thr Pro Pro Gln Glu
50 55 60

Asp Ala Pro Ser Val Asp Ile Ala Asn Ile Arg Met Pro Ser Leu Pro
65 70 75 80

Ser Tyr Lys Val Gly Asp Lys Ile Ala Thr Arg Lys Ala Tyr Gly Gln
85 90 95

Ala Leu Ala Lys Leu Gly His Ala Ser Asp Arg Ile Ile Ala Leu Asp
100 105 110

Gly Asp Thr Lys Asn Ser Thr Phe Ser Glu Ile Phe Lys Lys Glu His
115 120 125

Pro Asp Arg Phe Ile Glu Cys Tyr Ile Ala Glu Gln Asn Met Val Ser
130 135 140

Ile Ala Val Gly Cys Ala Thr Arg Asn Arg Thr Val Pro Phe Cys Ser
145 150 155 160

Thr Phe Ala Ala Phe Phe Thr Arg Ala Phe Asp Gln Ile Arg Met Ala
165 170 175

Ala Ile Ser Glu Ser Asn Ile Asn Leu Cys Gly Ser His Cys Gly Val
180 185 190

Ser Ile Gly Glu Asp Gly Pro Ser Gln Met Ala Leu Glu Asp Leu Ala
195 200 205

Met Phe Arg Ser Val Pro Thr Ser Thr Val Phe Tyr Pro Ser Asp Gly
210 215 220

Val Ala Thr Glu Lys Ala Val Glu Leu Ala Ala Asn Thr Lys Gly Ile
225 230 235 240

Cys Phe Ile Arg Thr Ser Arg Pro Glu Asn Ala Ile Ile Tyr Asn Asn
245 250 255

Asn Glu Asp Phe Gln Val Gly Gln Ala Lys Val Val Leu Lys Ser Lys
260 265 270

Asp Asp Gln Val Thr Val Ile Gly Ala Gly Val Thr Leu His Glu Ala
275 280 285

Leu Ala Ala Ala Glu Leu Leu Lys Lys Glu Lys Ile Asn Ile Arg Val
290 295 300

Leu Asp Pro Phe Thr Ile Lys Pro Leu Asp Arg Lys Leu Ile Leu Asp
305 310 315 320

Ser Ala Arg Ala Thr Lys Gly Arg Ile Leu Thr Val Glu Asp His Tyr
325 330 335

Tyr Glu Gly Gly Ile Gly Glu Ala Val Ser Ser Ala Val Val Gly Glu
340 345 350

Pro Gly Ile Thr Val Thr His Leu Ala Val Asn Arg Val Pro Arg Ser
355 360 365

Gly Lys Pro Ala Glu Leu Leu Lys Met Phe Gly Ile Asp Arg Asp Ala
370 375 380

Ile Ala Gln Ala Val Arg Gly Leu Ile Thr Lys Ala
385 390 395

<210> 853
<211> 302
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (228)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 853
Ser Arg Leu Gly Leu Gln Ser Cys Gly Leu Ser Thr Gln Ala Ile Thr
1 5 10 15

Leu Ser Glu Thr Ala Ala Ala Leu Asp Cys Ser Leu Pro Arg Leu His

```
            20                  25                  30

Ala Arg Gln Ser Met Arg Val Thr Leu Ala Thr Ile Ala Trp Met Val
        35                  40                  45

Ser Phe Val Ser Asn Tyr Ser His Thr Ala Asn Ile Leu Pro Asp Ile
    50                  55                  60

Glu Asn Glu Asp Phe Ile Lys Asp Cys Val Arg Ile His Asn Lys Phe
65                  70                  75                  80

Arg Ser Glu Val Lys Pro Thr Ala Ser Asp Met Leu Tyr Met Thr Trp
                85                  90                  95

Asp Pro Ala Leu Ala Gln Ile Ala Lys Ala Trp Ala Ser Asn Cys Gln
            100                 105                 110

Phe Ser His Asn Thr Arg Leu Lys Pro Pro His Lys Leu His Pro Asn
        115                 120                 125

Phe Thr Ser Leu Gly Glu Asn Ile Trp Thr Gly Ser Val Pro Ile Phe
    130                 135                 140

Ser Val Ser Ser Ala Ile Thr Asn Trp Tyr Asp Glu Ile Gln Asp Tyr
145                 150                 155                 160

Asp Phe Lys Thr Arg Ile Cys Lys Lys Val Cys Gly His Tyr Thr Gln
                165                 170                 175

Val Val Trp Ala Asp Ser Tyr Lys Val Gly Cys Ala Val Gln Phe Cys
            180                 185                 190

Pro Lys Val Ser Gly Phe Asp Ala Leu Ser Asn Gly Ala His Phe Ile
        195                 200                 205

Cys Asn Tyr Gly Pro Gly Gly Asn Tyr Pro Thr Trp Pro Tyr Lys Arg
    210                 215                 220

Gly Ala Thr Xaa Ser Ala Cys Pro Asn Asn Asp Lys Cys Leu Asp Asn
225                 230                 235                 240

Leu Cys Val Asn Arg Gln Arg Asp Gln Val Lys Arg Tyr Tyr Ser Val
                245                 250                 255

Val Tyr Pro Gly Trp Pro Ile Tyr Pro Arg Asn Arg Tyr Thr Ser Leu
            260                 265                 270

Phe Leu Ile Val Asn Ser Val Ile Leu Ile Leu Ser Val Ile Ile Thr
        275                 280                 285

Ile Leu Val Gln His Lys Tyr Pro Asn Leu Val Leu Leu Asp
```

290 295 300

<210> 854
<211> 237
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (235)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 854
Val Pro Ala Ser Phe Ala Ala Ala Ser Ala Val Leu Ser Ala Val Phe
1 5 10 15

Pro Gln Glu Pro Ala Tyr Phe Leu Asn Met Glu Ser Val Val Arg Arg
20 25 30

Cys Pro Phe Leu Ser Arg Val Pro Gln Ala Phe Leu Gln Lys Ala Gly
35 40 45

Lys Ser Leu Leu Phe Tyr Ala Gln Asn Cys Pro Lys Met Met Glu Val
50 55 60

Gly Ala Lys Pro Ala Pro Arg Ala Leu Ser Thr Ala Ala Val His Tyr
65 70 75 80

Gln Gln Ile Lys Glu Thr Pro Pro Ala Ser Glu Lys Asp Lys Thr Ala
85 90 95

Lys Ala Lys Val Gln Gln Thr Pro Asp Gly Ser Gln Gln Ser Pro Asp
100 105 110

Gly Thr Gln Leu Pro Ser Gly His Pro Leu Pro Ala Thr Ser Gln Gly
115 120 125

Thr Ala Ser Lys Cys Pro Phe Leu Ala Ala Gln Met Asn Gln Arg Gly
130 135 140

Ser Ser Val Phe Cys Lys Ala Ser Leu Glu Leu Gln Glu Asp Val Gln
145 150 155 160

Glu Met Asn Ala Val Arg Lys Glu Val Ala Glu Thr Ser Ala Gly Pro
165 170 175

Ser Val Val Ser Val Lys Thr Asp Gly Gly Asp Pro Ser Gly Leu Leu
180 185 190

Lys Asn Phe Gln Asp Ile Met Gln Lys Gln Arg Pro Glu Arg Val Ser
195 200 205

His Leu Leu Gln Asp Asn Leu Pro Lys Ser Val Ser Thr Phe Gln Tyr
210 215 220

Asp Arg Phe Phe Glu Lys Lys Ile Asp Glu Xaa Lys Glu
225 230 235

<210> 855
<211> 272
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (202)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 855
Thr Pro Gly Ile Phe Thr Glu Gln Ser Met Ile Thr Phe Leu Pro Leu
1 5 10 15

Leu Leu Gly Leu Ser Leu Gly Cys Thr Gly Ala Gly Gly Phe Val Ala
20 25 30

His Val Glu Ser Thr Cys Leu Leu Asp Asp Ala Gly Thr Pro Lys Asp
35 40 45

Phe Thr Tyr Cys Ile Ser Phe Asn Lys Asp Leu Leu Thr Cys Trp Asp
50 55 60

Pro Glu Glu Asn Lys Met Ala Pro Cys Glu Phe Gly Val Leu Asn Ser
65 70 75 80

Leu Ala Asn Val Leu Ser Gln His Leu Asn Gln Lys Asp Thr Leu Met
85 90 95

Gln Arg Leu Arg Asn Gly Leu Gln Asn Cys Ala Thr His Thr Gln Pro
100 105 110

Phe Trp Gly Ser Leu Thr Asn Arg Thr Arg Pro Pro Ser Val Gln Val
115 120 125

Ala Lys Thr Thr Pro Phe Asn Thr Arg Glu Pro Val Met Leu Ala Cys
130 135 140

Tyr Val Trp Gly Phe Tyr Pro Ala Glu Val Thr Ile Thr Trp Arg Lys
145 150 155 160

Asn Gly Lys Leu Val Met Pro His Ser Ser Ala His Lys Thr Ala Gln
165 170 175

Pro Asn Gly Asp Trp Thr Tyr Gln Thr Leu Ser His Leu Ala Leu Thr
180 185 190

Pro Ser Tyr Gly Asp Thr Tyr Thr Cys Xaa Val Glu His Ile Gly Ala
195 200 205

Pro Glu Pro Ile Leu Arg Asp Trp Thr Pro Gly Leu Ser Pro Met Gln
210 215 220

Thr Leu Lys Val Ser Val Ser Ala Val Thr Leu Gly Leu Gly Leu Ile
225 230 235 240

Ile Phe Ser Leu Gly Val Ile Ser Trp Arg Arg Ala Gly His Ser Ser
245 250 255

Tyr Thr Pro Leu Pro Gly Ser Asn Tyr Ser Glu Gly Trp His Ile Ser
260 265 270

<210> 856
<211> 153
<212> PRT
<213> Homo sapiens

<400> 856
Val Val Ala Arg Phe Ile Arg Ile Tyr Pro Leu Thr Trp Asn Gly Ser
1 5 10 15

Leu Cys Met Arg Leu Glu Val Leu Gly Cys Ser Val Ala Pro Val Tyr
20 25 30

Ser Tyr Tyr Ala Gln Asn Glu Val Val Ala Thr Asp Asp Leu Asp Phe
35 40 45

Arg His His Ser Tyr Lys Asp Met Arg Gln Leu Met Lys Val Val Asn
50 55 60

Glu Glu Cys Pro Thr Ile Thr Arg Thr Tyr Ser Leu Gly Lys Ser Ser
65 70 75 80

Arg Gly Leu Lys Ile Tyr Ala Met Glu Ile Ser Asp Asn Pro Gly Glu
85 90 95

His Glu Leu Gly Glu Pro Glu Phe Arg Tyr Thr Ala Gly Ile His Gly
100 105 110

Asn Glu Val Leu Gly Arg Glu Leu Leu Leu Leu Leu Met Gln Tyr Leu
115 120 125

Cys Arg Glu Tyr Arg Asp Gly Asn Pro Arg Val Arg Ser Trp Cys Arg
130 135 140

Thr His Ala Ser Thr Trp Cys Pro His
145 150

<210> 857
<211> 258
<212> PRT
<213> Homo sapiens

<400> 857
Cys Leu Ser Gln Lys Ala Val Arg Ala Pro Arg Phe Leu Arg Gly Leu
1 5 10 15

Pro Ser Gly Arg Val Asn Cys Phe Leu Gln Ala Gly His Gly Ala Ser
20 25 30

Arg Ser Gln Gly Ser Gly Leu Cys Gln Met Leu Lys Glu Gly Ala Lys
35 40 45

His Phe Ser Gly Leu Glu Glu Ala Val Tyr Arg Asn Ile Gln Ala Cys
50 55 60

Lys Glu Leu Ala Gln Thr Thr Arg Thr Ala Tyr Gly Pro Asn Gly Met
65 70 75 80

Asn Lys Met Val Ile Asn His Leu Glu Lys Leu Phe Val Thr Asn Asp
85 90 95

Ala Ala Thr Ile Leu Arg Glu Leu Glu Val Gln His Pro Ala Ala Lys
100 105 110

Met Ile Val Met Ala Ser His Met Gln Glu Gln Glu Val Gly Asp Gly
115 120 125

Thr Asn Phe Val Leu Val Phe Ala Gly Ala Leu Leu Glu Leu Ala Glu
130 135 140

Glu Leu Leu Arg Ile Gly Leu Ser Val Ser Glu Val Ile Glu Gly Tyr
145 150 155 160

Glu Ile Ala Cys Arg Lys Ala His Glu Ile Leu Pro Asn Leu Val Cys

165 170 175

Cys Ser Ala Lys Asn Leu Arg Asp Ile Asp Glu Val Ser Ser Leu Leu
180 185 190

Arg Thr Ser Ile Met Ser Lys Gln Tyr Gly Asn Glu Val Phe Leu Ala
195 200 205

Lys Leu Ile Ala Gln Ala Cys Val Ser Ile Phe Pro Asp Ser Gly His
210 215 220

Phe Asn Val Asp Asn Ile Arg Val Cys Lys Ile Leu Gly Ser Gly Ile
225 230 235 240

Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys Lys Glu Thr Glu
245 250 255

Val Met

<210> 858
<211> 143
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (14)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (135)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 858
Pro Asp Ser Leu Pro Pro Pro Ser Pro Arg Leu Pro Ala Xaa Gly Pro
1 5 10 15

Glu Phe Pro Gly Arg Pro Thr Arg Pro Glu Arg Ser Pro Ser Leu Gly
20 25 30

Ile Pro Lys Cys Phe His Ser Val Ile Arg Thr Glu His Arg Gly Leu
35 40 45

Thr Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys
50 55 60

Gly Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val

65 70 75 80

Lys Pro Gly Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr
85 90 95

Phe Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly
100 105 110

Leu Glu Trp Val Gly Arg Ile Lys Ser Lys Thr Asp Gly Gly Thr Thr
115 120 125

Asp Tyr Ala Ala Pro Val Xaa Arg Gln Ile His His Leu Lys Arg
130 135 140

<210> 859
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (132)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (133)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 859
Val Thr Met Ala Gln Gln Ala Ala Asp Lys Tyr Leu Tyr Val Asp Lys
1 5 10 15

Asn Phe Ile Asn Asn Pro Leu Ala Gln Ala Asp Trp Ala Ala Lys Lys
20 25 30

Leu Val Trp Val Pro Ser Asp Lys Ser Gly Phe Glu Pro Ala Ser Leu
35 40 45

Lys Glu Glu Val Gly Glu Glu Ala Ile Val Glu Leu Val Glu Asn Gly
50 55 60

Lys Lys Val Lys Val Asn Lys Asp Asp Ile Gln Lys Met Asn Pro Pro
65 70 75 80

Lys Phe Ser Lys Val Glu Asp Met Ala Glu Leu Thr Cys Leu Asn Glu
85 90 95

Ala Ser Val Leu His Asn Leu Lys Glu Arg Tyr Tyr Ser Gly Leu Ile

```
            100                 105                 110

Tyr Val Ser Gly Cys Arg Gly Thr Pro Gln Ala Gly Ser Glu Gly Ser
        115                 120                 125

Glu Val Gly Xaa Xaa Ala Gly
    130                 135



<210> 860
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 860
Ala Xaa Leu Ile Lys Thr Arg Val Leu Ile Tyr Asn Lys Ser Asn Phe
  1               5                  10                  15

Ser Leu Ser Leu Gly Thr Ser Asn Cys Thr Pro Gln Ile Thr Asp Thr
             20                  25                  30

Ser Glu Phe Phe Met Val Lys Lys Ala Pro Thr Leu Thr Tyr Lys Cys
         35                  40                  45

Gly Pro Arg Asn
     50



<210> 861
<211> 321
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (18)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 861
Ala His Gly Val Thr Ser Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser
  1               5                  10                  15

Thr Xaa Pro Pro Val His Asn Val Thr Ser Ala Ser Gly Ser Ala Ser
             20                  25                  30
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Gly Ser Ala Ser Thr Leu Val His Asn Gly Thr Ser Ala Arg Ala Thr
        35                  40                  45

Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser His His
    50                  55                  60

Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr Asp Ala
65                  70                  75                  80

Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser Asn His
                85                  90                  95

Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser
            100                 105                 110

Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser
        115                 120                 125

Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu
    130                 135                 140

Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe
145                 150                 155                 160

Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
                165                 170                 175

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
            180                 185                 190

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
        195                 200                 205

Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly Val Pro Gly
    210                 215                 220

Trp Gly Ile Ala Leu Leu Val Leu Val Cys Val Leu Val Ala Leu Ala
225                 230                 235                 240

Ile Val Tyr Leu Ile Ala Leu Ala Val Cys Gln Cys Arg Arg Lys Asn
                245                 250                 255

Tyr Gly Gln Leu Asp Ile Phe Pro Ala Arg Asp Thr Tyr His Pro Met
            260                 265                 270

Ser Glu Tyr Pro Thr Tyr His Thr His Gly Arg Tyr Val Pro Pro Ser
        275                 280                 285

Ser Thr Asp Arg Ser Pro Tyr Glu Lys Val Ser Ala Gly Asn Gly Gly
    290                 295                 300
```

Ser Ser Leu Ser Tyr Thr Asn Pro Ala Val Ala Ala Thr Ser Ala Asn
305 310 315 320

Leu

<210> 862
<211> 327
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (307)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 862
Phe Gly Thr Ser Leu Thr Gln Val Leu Leu Gly Ala Gly Glu Asn Thr
1 5 10 15

Lys Thr Asn Leu Glu Ser Ile Leu Ser Tyr Pro Lys Asp Phe Thr Cys
20 25 30

Val His Gln Ala Leu Lys Gly Phe Thr Thr Lys Gly Val Thr Ser Val
35 40 45

Ser Gln Ile Phe His Ser Pro Asp Leu Ala Ile Arg Asp Thr Phe Val
50 55 60

Asn Ala Ser Arg Thr Leu Tyr Ser Ser Ser Pro Arg Val Leu Ser Asn
65 70 75 80

Asn Ser Asp Ala Asn Leu Glu Leu Ile Asn Thr Trp Val Ala Lys Asn
85 90 95

Thr Asn Asn Lys Ile Ser Arg Leu Leu Asp Ser Leu Pro Ser Asp Thr
100 105 110

Arg Leu Val Leu Leu Asn Ala Ile Tyr Leu Ser Ala Lys Trp Lys Thr
115 120 125

Thr Phe Asp Pro Lys Lys Thr Arg Met Glu Pro Phe His Phe Lys Asn
130 135 140

Ser Val Ile Lys Val Pro Met Met Asn Ser Lys Lys Tyr Pro Val Ala
145 150 155 160

His Phe Ile Asp Gln Thr Leu Lys Ala Lys Val Gly Gln Leu Gln Leu

165 170 175

Ser His Asn Leu Ser Leu Val Ile Leu Val Pro Gln Asn Leu Lys His
180 185 190

Arg Leu Glu Asp Met Glu Gln Ala Leu Ser Pro Ser Val Phe Lys Ala
195 200 205

Ile Met Glu Lys Leu Glu Met Ser Lys Phe Gln Pro Thr Leu Leu Thr
210 215 220

Leu Pro Arg Ile Lys Val Thr Thr Ser Gln Asp Met Leu Ser Ile Met
225 230 235 240

Glu Lys Leu Glu Phe Phe Asp Phe Ser Tyr Asp Leu Asn Leu Cys Gly
245 250 255

Leu Thr Glu Asp Pro Asp Leu Gln Val Ser Ala Met Gln His Gln Thr
260 265 270

Val Leu Glu Leu Thr Glu Thr Gly Val Glu Ala Ala Ala Ala Ser Ala
275 280 285

Ile Ser Val Ala Arg Thr Leu Leu Val Phe Glu Val Gln Gln Pro Phe
290 295 300

Leu Phe Xaa Leu Trp Asp Gln Gln His Lys Phe Pro Val Phe Met Gly
305 310 315 320

Arg Val Tyr Asp Pro Arg Ala
325

<210> 863
<211> 86
<212> PRT
<213> Homo sapiens

<400> 863
Tyr Tyr Ile Val His Leu Lys Leu Thr Glu Arg Val Asn Leu Lys Cys
1 5 10 15

Ser His His Thr Asn Pro Lys Val Thr Met Phe Ser Pro His Lys Pro
20 25 30

Lys Gly Asn Tyr Val Leu Ile Ser Leu Ile Val Val Thr Ile Ser Gln
35 40 45

Cys Ile His Leu Pro Lys His Tyr Val Val Tyr Leu Glu Tyr Ile Ile
50 55 60

Leu Phe Ile Asn Tyr Thr Ser Ile Lys Leu Lys Glu Gly Ile Thr Asn
65 70 75 80

Ser His Lys Ile Gln Ile
85

<210> 864
<211> 130
<212> PRT
<213> Homo sapiens

<400> 864
Leu Thr Gln Gln Gln Gln Pro Ala Thr Gly Pro Gln Pro Ser Leu Gly
1 5 10 15

Val Ser Phe Gly Thr Pro Phe Gly Ser Gly Ile Gly Thr Gly Leu Gln
20 25 30

Ser Ser Gly Leu Gly Ser Ser Asn Leu Gly Gly Phe Gly Thr Ser Ser
35 40 45

Gly Phe Gly Cys Ser Thr Thr Gly Ala Ser Thr Phe Gly Phe Gly Thr
50 55 60

Thr Asn Lys Pro Ser Gly Ser Leu Ser Ala Gly Phe Gly Ser Ser Ser
65 70 75 80

Thr Ser Gly Phe Asn Phe Ser Asn Pro Gly Ile Thr Ala Ser Ala Gly
85 90 95

Leu Thr Phe Gly Val Ser Asn Pro Ala Ser Ala Gly Phe Gly Thr Gly
100 105 110

Gly Gln Leu Leu Gln Leu Lys Lys Pro Pro Ala Gly Asn Lys Arg Gly
115 120 125

Lys Arg
130

<210> 865
<211> 78
<212> PRT
<213> Homo sapiens

<400> 865
Ser Glu Trp Lys Ile Lys Gly Pro Ser Ser Pro Leu Ala Ser Leu Pro

1 5 10 15

Gly Arg Arg His Gly Gly Ser Ser Ala Thr Gly Ala Cys Gly Glu Ala
20 25 30

Met Ala Ala Ala Glu Gly Ser Ser Gly Pro Ala Gly Leu Thr Leu Gly
35 40 45

Arg Ser Phe Ser Asn Tyr Arg Pro Phe Glu Pro Gln Ala Leu Gly Leu
50 55 60

Ser Pro Ser Trp Arg Leu Thr Gly Phe Ser Gly Met Lys Gly
65 70 75

<210> 866
<211> 529
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (517)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 866
Pro Pro Pro Glu Pro Arg Ala Xaa Met Ala Glu Asn Pro Ser Leu Glu
1 5 10 15

Asn His Arg Ile Lys Ser Phe Lys Asn Lys Gly Arg Asp Val Glu Thr
20 25 30

Met Arg Arg His Arg Asn Glu Val Thr Val Glu Leu Arg Lys Asn Lys
35 40 45

Arg Asp Glu His Leu Leu Lys Lys Arg Asn Val Pro Gln Glu Glu Ser
50 55 60

Leu Glu Asp Ser Asp Val Asp Ala Asp Phe Lys Ala Gln Asn Val Thr
65 70 75 80

Leu Glu Ala Ile Leu Gln Asn Ala Thr Ser Asp Asn Pro Val Val Gln
85 90 95

Leu Ser Ala Val Gln Ala Ala Arg Lys Leu Leu Ser Ser Asp Arg Asn

100 105 110

Pro Pro Ile Asp Asp Leu Ile Lys Ser Gly Ile Leu Pro Ile Leu Val
115 120 125

Lys Cys Leu Glu Arg Asp Asp Asn Pro Ser Leu Gln Phe Glu Ala Ala
130 135 140

Trp Ala Leu Thr Asn Ile Ala Ser Gly Thr Ser Ala Gln Thr Gln Ala
145 150 155 160

Val Val Gln Ser Asn Ala Val Pro Leu Phe Leu Arg Leu Leu Arg Ser
165 170 175

Pro His Gln Asn Val Cys Glu Gln Ala Val Trp Ala Leu Gly Asn Ile
180 185 190

Ile Gly Asp Gly Pro Gln Cys Arg Asp Tyr Val Ile Ser Leu Gly Val
195 200 205

Val Lys Pro Leu Leu Ser Phe Ile Ser Pro Ser Ile Pro Ile Thr Phe
210 215 220

Leu Arg Asn Val Thr Trp Val Ile Val Asn Leu Cys Arg Asn Lys Asp
225 230 235 240

Pro Pro Pro Pro Met Glu Thr Val Gln Glu Ile Leu Pro Ala Leu Cys
245 250 255

Val Leu Ile Tyr His Thr Asp Ile Asn Ile Leu Val Asp Thr Val Trp
260 265 270

Ala Leu Ser Tyr Leu Thr Asp Gly Gly Asn Glu Gln Ile Gln Met Val
275 280 285

Ile Asp Ser Gly Val Val Pro Phe Leu Val Pro Leu Leu Ser His Gln
290 295 300

Glu Val Lys Val Gln Thr Ala Ala Leu Arg Ala Val Gly Asn Ile Val
305 310 315 320

Thr Gly Thr Asp Glu Gln Thr Gln Val Val Leu Asn Cys Asp Val Leu
325 330 335

Ser His Phe Pro Asn Leu Leu Ser His Pro Lys Glu Lys Ile Asn Lys
340 345 350

Glu Ala Val Trp Phe Leu Ser Asn Ile Thr Ala Gly Asn Gln Gln Gln
355 360 365

Val Gln Ala Val Ile Asp Ala Gly Leu Ile Pro Met Ile Ile His Gln

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    370                 375                 380

Leu Ala Lys Gly Asp Phe Gly Thr Gln Lys Glu Ala Ala Trp Ala Ile
385                 390                 395                 400

Ser Asn Leu Thr Ile Ser Gly Arg Lys Asp Gln Val Glu Tyr Leu Val
                405                 410                 415

Gln Gln Asn Val Ile Pro Pro Phe Cys Asn Leu Leu Ser Val Lys Asp
            420                 425                 430

Ser Gln Val Val Gln Val Val Leu Asp Gly Leu Lys Asn Ile Leu Ile
        435                 440                 445

Met Ala Gly Asp Glu Ala Ser Thr Ile Ala Glu Ile Ile Glu Glu Cys
    450                 455                 460

Gly Gly Leu Glu Lys Ile Glu Val Leu Gln Gln His Glu Asn Glu Asp
465                 470                 475                 480

Ile Tyr Lys Leu Ala Phe Glu Ile Ile Asp Gln Tyr Phe Ser Gly Asp
                485                 490                 495

Asp Ile Asp Glu Asp Pro Cys Leu Ile Pro Glu Ala Thr Gln Gly Gly
            500                 505                 510

Thr Tyr Asn Phe Xaa Pro Thr Ala Asn Leu Gln Thr Lys Glu Phe Asn
        515                 520                 525

Phe



<210> 867
<211> 237
<212> PRT
<213> Homo sapiens

<400> 867
Arg Pro Gly Pro Val Arg Arg Arg Gly Lys Val Glu Leu Ile Lys Phe
  1               5                  10                  15

Val Arg Val Gln Trp Arg Arg Pro Gln Val Glu Trp Arg Arg Arg Arg
             20                  25                  30

Trp Gly Pro Gly Pro Gly Ala Ser Met Ala Gly Ser Glu Glu Leu Gly
         35                  40                  45

Leu Arg Glu Asp Thr Leu Arg Val Leu Ala Ala Phe Leu Arg Arg Gly
     50                  55                  60
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Glu Ala Ala Gly Ser Pro Val Pro Thr Pro Pro Arg Ser Pro Ala Gln
65 70 75 80

Glu Glu Pro Thr Asp Phe Leu Ser Arg Leu Arg Arg Cys Leu Pro Cys
85 90 95

Ser Leu Gly Arg Gly Ala Ala Pro Ser Glu Ser Pro Arg Pro Cys Ser
100 105 110

Leu Pro Ile Arg Pro Cys Tyr Gly Leu Glu Pro Gly Pro Ala Thr Pro
115 120 125

Asp Phe Tyr Ala Leu Val Ala Gln Arg Leu Glu Gln Leu Val Gln Glu
130 135 140

Gln Leu Lys Ser Pro Pro Ser Pro Glu Leu Gln Gly Pro Pro Ser Thr
145 150 155 160

Glu Lys Glu Ala Ile Leu Arg Arg Leu Val Ala Leu Leu Glu Glu Glu
165 170 175

Ala Glu Val Ile Asn Gln Lys Leu Ala Ser Asp Pro Ala Leu Arg Thr
180 185 190

Ser Trp Ser Ala Cys Pro Pro Thr Leu Ser Pro Ala Trp Trp Ser Cys
195 200 205

Ser Val Ala Gly Met Thr Ala Leu Ala Gln Ala Glu His Ala Pro Gly
210 215 220

Pro Arg Leu Leu Pro Arg Ser Pro Trp Pro Ala Trp Pro
225 230 235

<210> 868
<211> 196
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 868
Leu Ser Val Ser Ala Xaa Ala Ala Xaa Val Ala Ala Ala Ala Ile His
1 5 10 15

Ser Asp Ser Ala Ala Ala Pro Gly Gly Gly Gly Ala Ala Arg Asp Phe
20 25 30

Phe Phe Phe Gln Thr Asp Arg Gly Ala Ala Ala Asp Met Ser Thr Pro
35 40 45

Ala Arg Arg Arg Leu Met Arg Asp Phe Lys Arg Leu Gln Glu Asp Pro
50 55 60

Pro Val Gly Val Ser Gly Ala Pro Ser Glu Asn Asn Ile Met Gln Trp
65 70 75 80

Asn Ala Val Ile Phe Gly Pro Glu Gly Thr Pro Phe Glu Asp Gly Thr
85 90 95

Phe Lys Leu Val Ile Glu Phe Ser Glu Glu Tyr Pro Asn Lys Pro Pro
100 105 110

Thr Val Arg Phe Leu Ser Lys Met Phe His Pro Asn Val Tyr Ala Asp
115 120 125

Gly Ser Ile Cys Leu Asp Ile Leu Gln Asn Arg Trp Ser Pro Thr Tyr
130 135 140

Asp Val Ser Ser Ile Leu Thr Ser Ile Gln Ser Leu Leu Asp Glu Pro
145 150 155 160

Asn Pro Asn Ser Pro Ala Asn Ser Gln Ala Ala Gln Leu Tyr Gln Glu
165 170 175

Asn Lys Arg Glu Tyr Glu Lys Arg Val Ser Ala Ile Val Glu Gln Ser
180 185 190

Trp Asn Asp Ser
195

<210> 869
<211> 544
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 869
Ala Asp Ala Trp Val Ala Xaa Ala Xaa Ala Ser Ser Gly Leu Val Val
1   5   10   15

Ala Arg Pro Thr Ser Ala Val Pro Ala Glu Pro Arg Pro Phe Arg Pro
            20   25   30

Ser Pro Pro His Leu Ala Ala Met Arg Leu Arg Arg Leu Ala Leu Phe
        35   40   45

Pro Gly Val Ala Leu Leu Leu Ala Ala Ala Arg Leu Ala Ala Ala Ser
    50   55   60

Asp Val Leu Glu Leu Thr Asp Asp Asn Phe Glu Ser Arg Ile Ser Asp
65   70   75   80

Thr Gly Ser Ala Gly Leu Met Leu Val Glu Phe Phe Ala Pro Trp Cys
                85   90   95

Gly His Cys Lys Arg Leu Ala Pro Glu Tyr Glu Ala Ala Ala Thr Arg
            100   105   110

Leu Lys Gly Ile Val Pro Leu Ala Lys Val Asp Cys Thr Ala Asn Thr
        115   120   125

Asn Thr Cys Asn Lys Tyr Gly Val Ser Gly Tyr Pro Thr Leu Lys Ile
    130   135   140

Phe Arg Asp Gly Glu Glu Ala Gly Ala Tyr Asp Gly Pro Arg Thr Ala
145   150   155   160

Asp Gly Ile Val Ser His Leu Lys Lys Gln Ala Gly Pro Ala Ser Val
                165   170   175

Pro Leu Arg Thr Glu Glu Glu Phe Lys Lys Phe Ile Ser Asp Lys Asp
            180   185   190

Ala Ser Ile Val Gly Phe Phe Asp Asp Ser Phe Ser Glu Ala His Ser
        195   200   205

Glu Phe Leu Lys Ala Ala Ser Asn Leu Arg Asp Asn Tyr Arg Phe Ala
    210   215   220

His Thr Asn Val Glu Ser Leu Val Asn Glu Tyr Asp Asp Asn Gly Glu
225   230   235   240

Gly Ile Ile Leu Phe Arg Pro Ser His Leu Thr Asn Lys Phe Glu Asp
245 250 255

Lys Thr Val Ala Tyr Thr Glu Gln Lys Met Thr Ser Gly Lys Ile Lys
260 265 270

Lys Phe Ile Gln Glu Asn Ile Phe Gly Ile Cys Pro His Met Thr Glu
275 280 285

Asp Asn Lys Asp Leu Ile Gln Gly Lys Asp Leu Leu Ile Ala Tyr Tyr
290 295 300

Asp Val Asp Tyr Glu Lys Asn Ala Lys Gly Ser Asn Tyr Trp Arg Asn
305 310 315 320

Arg Val Met Met Val Ala Lys Lys Phe Leu Asp Ala Gly His Lys Leu
325 330 335

Asn Phe Ala Val Ala Ser Arg Lys Thr Phe Ser His Glu Leu Ser Asp
340 345 350

Phe Gly Leu Glu Ser Thr Ala Gly Glu Ile Pro Val Val Ala Ile Arg
355 360 365

Thr Ala Lys Gly Glu Lys Phe Val Met Gln Glu Glu Phe Ser Arg Asp
370 375 380

Gly Lys Ala Leu Glu Arg Phe Leu Gln Asp Tyr Phe Asp Gly Asn Leu
385 390 395 400

Lys Arg Tyr Leu Lys Ser Glu Pro Ile Pro Glu Ser Asn Asp Gly Pro
405 410 415

Val Lys Val Val Val Ala Glu Asn Phe Asp Glu Ile Val Asn Asn Glu
420 425 430

Asn Lys Asp Val Leu Ile Glu Phe Tyr Ala Pro Trp Cys Gly His Cys
435 440 445

Lys Asn Leu Glu Pro Lys Tyr Lys Glu Leu Gly Glu Lys Leu Ser Lys
450 455 460

Asp Pro Asn Ile Val Ile Ala Lys Met Asp Ala Thr Ala Asn Asp Val
465 470 475 480

Pro Ser Pro Tyr Glu Val Arg Gly Phe Pro Thr Ile Tyr Phe Ser Pro
485 490 495

Ala Asn Lys Lys Leu Asn Pro Lys Lys Tyr Glu Gly Gly Arg Glu Leu
500 505 510

```
Ser Asp Phe Ile Ser Tyr Leu Gln Arg Glu Ala Thr Asn Pro Pro Val
        515                 520                 525

Ile Gln Glu Glu Lys Pro Lys Lys Lys Lys Lys Ala Gln Glu Asp Leu
    530                 535                 540
```

<210> 870
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 870

```
Arg Arg Xaa Ala Ile Phe Thr Cys Glu Val Pro Gly Val Tyr Tyr Phe
  1               5                  10                  15

Xaa Tyr His Val His Cys Lys Gly Gly Asn Val Trp Val Ala Leu Phe
             20                  25                  30

Lys Asn Asn Glu Pro Val Met Tyr Thr Tyr Asp Glu Tyr Lys Lys Gly
         35                  40                  45

Phe Leu Asp Gln Ala Ser Gly Ser Ala Val Leu Leu Leu Arg Pro Gly
     50                  55                  60

Asp Arg Cys Ser Ser Arg Cys Pro Gln Asn Arg Leu Gln Asp Cys Met
 65                  70                  75                  80

Pro Gly Ser Met Ser Thr Pro Pro Phe Gln Asp Ile Tyr Cys Ile Pro
                 85                  90                  95

Cys Lys Asn Lys Lys Thr Lys Asn Lys Glu Lys Lys Glu Ile Leu
            100                 105                 110
```

<210> 871
<211> 124
<212> PRT
<213> Homo sapiens

<400> 871
Gly Lys Thr Glu Val Asn Tyr Thr Gln Leu Val Asp Leu His Ala Arg
1   5   10   15

Tyr Ala Glu Cys Gly Leu Arg Ile Leu Ala Phe Pro Cys Asn Gln Phe
            20   25   30

Gly Lys Gln Glu Pro Gly Ser Asn Glu Glu Ile Lys Glu Phe Ala Ala
        35   40   45

Gly Tyr Asn Val Lys Phe Asp Met Phe Ser Lys Ile Cys Val Asn Gly
    50   55   60

Asp Asp Ala His Pro Leu Trp Lys Trp Met Lys Ile Gln Pro Lys Gly
65   70   75   80

Lys Gly Ile Leu Gly Asn Ala Ile Lys Trp Asn Phe Thr Lys Phe Leu
                85   90   95

Ile Asp Lys Asn Gly Cys Val Val Lys Arg Tyr Gly Pro Met Glu Glu
            100   105   110

Pro Leu Val Ile Glu Lys Asp Leu Pro His Tyr Phe
        115   120

<210> 872
<211> 35
<212> PRT
<213> Homo sapiens

<400> 872
Ser Gln His Phe Gly Arg Pro Arg Gln Ala Glu His Leu Lys Glu Phe
1   5   10   15

Lys Thr Ser Val Ala Asn Val Val Asn Pro Val Ser Thr Lys Asn Thr
            20   25   30

Lys Ile Val
        35

<210> 873
<211> 420

<212> PRT
<213> Homo sapiens

<400> 873
```
Val Cys Leu Gln Leu Cys Gln Ser Thr Val Ser Cys Pro Leu Gly Tyr
  1               5                  10                  15

Leu Ala Ser Thr Ala Thr Asn Asp Cys Gly Cys Thr Thr Thr Thr Cys
             20                  25                  30

Leu Pro Asp Lys Val Cys Val His Arg Ser Thr Ile Tyr Pro Val Gly
         35                  40                  45

Gln Phe Trp Glu Glu Gly Cys Asp Val Cys Thr Cys Thr Asp Met Glu
     50                  55                  60

Asp Ala Val Met Gly Leu Arg Val Ala Gln Cys Ser Gln Lys Pro Cys
 65                  70                  75                  80

Glu Asp Ser Cys Arg Ser Gly Phe Thr Tyr Val Leu His Glu Gly Glu
                 85                  90                  95

Cys Cys Gly Arg Cys Leu Pro Ser Ala Cys Glu Val Val Thr Gly Ser
            100                 105                 110

Pro Arg Gly Asp Ser Gln Ser Ser Trp Lys Ser Val Gly Ser Gln Trp
        115                 120                 125

Ala Ser Pro Glu Asn Pro Cys Leu Ile Asn Glu Cys Val Arg Val Lys
    130                 135                 140

Glu Glu Val Phe Ile Gln Gln Arg Asn Val Ser Cys Pro Gln Leu Glu
145                 150                 155                 160

Val Pro Val Cys Pro Ser Gly Phe Gln Leu Ser Cys Lys Thr Ser Ala
                165                 170                 175

Cys Cys Pro Ser Cys Arg Cys Glu Arg Met Glu Ala Cys Met Leu Asn
            180                 185                 190

Gly Thr Val Ile Gly Pro Gly Lys Thr Val Met Ile Asp Val Cys Thr
        195                 200                 205

Thr Cys Arg Cys Met Val Gln Val Gly Val Ile Ser Gly Phe Lys Leu
    210                 215                 220

Glu Cys Arg Lys Thr Thr Cys Asn Pro Cys Pro Leu Gly Tyr Lys Glu
225                 230                 235                 240

Glu Asn Asn Thr Gly Glu Cys Cys Gly Arg Cys Leu Pro Thr Ala Cys
                245                 250                 255
```

Thr Ile Gln Leu Arg Gly Gly Gln Ile Met Thr Leu Lys Arg Asp Glu
260 265 270

Thr Leu Gln Asp Gly Cys Asp Thr His Phe Cys Lys Val Asn Glu Arg
275 280 285

Gly Glu Tyr Phe Trp Glu Lys Arg Val Thr Gly Cys Pro Pro Phe Asp
290 295 300

Glu His Lys Cys Leu Ala Glu Gly Gly Lys Ile Met Lys Ile Pro Gly
305 310 315 320

Thr Cys Cys Asp Thr Cys Glu Glu Pro Glu Cys Asn Asp Ile Thr Ala
325 330 335

Arg Leu Gln Tyr Val Lys Val Gly Ser Cys Lys Ser Glu Val Glu Val
340 345 350

Asp Ile His Tyr Cys Gln Gly Lys Cys Ala Ser Lys Ala Met Tyr Ser
355 360 365

Ile Asp Ile Asn Asp Val Gln Asp Gln Cys Ser Cys Cys Ser Pro Thr
370 375 380

Arg Thr Glu Pro Met Gln Val Ala Leu His Cys Thr Asn Gly Ser Val
385 390 395 400

Val Tyr His Glu Val Leu Asn Ala Met Glu Cys Lys Cys Ser Pro Arg
405 410 415

Lys Cys Ser Lys
420

<210> 874
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (90)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (143)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 874
Arg Gln Val Pro His Glu Arg Ala Val Arg Asp Gly Arg Gly Gly Gly
1 5 10 15

Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met Arg Arg His Ser
20 25 30

Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala Val Val Leu Gln
35 40 45

Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala
50 55 60

Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr
65 70 75 80

Asp Ser Pro Phe Pro Asn Ser Cys Ala Xaa Gly Met Ala Asn Gly Asp
85 90 95

Ala Pro Cys Met Gly Ala Xaa Lys Arg Gly Gly Cys Gly Gly Tyr Ala
100 105 110

Gln Trp Thr Arg Tyr Thr Cys Gln Arg Pro Ser Ala Arg Ser Phe Arg
115 120 125

Phe Leu Pro Phe Leu Ser Arg His Val Arg Arg Leu Ser Pro Xaa Ser
130 135 140

Ser Lys Ser Val Gly Ser Leu
145 150

<210> 875
<211> 95
<212> PRT
<213> Homo sapiens

<400> 875
Ala Leu Asn Leu Asn Ser Gln Leu Asn Ile Pro Lys Asp Thr Ser Gln
1 5 10 15

Leu Lys Lys His Ile Thr Leu Leu Cys Asp Arg Leu Ser Lys Gly Gly
20 25 30

Arg Leu Cys Leu Ser Thr Asp Ala Ala Ala Pro Gln Thr Met Val Met

35 40 45

Pro Gly Gly Cys Thr Thr Ile Pro Glu Ser Asp Leu Glu Glu Arg Ser
50 55 60

Val Glu Gln Asp Ser Thr Glu Leu Phe Thr Asn His Arg His Leu Thr
65 70 75 80

Ala Glu Thr Pro Arg Pro Val Ser Pro Leu Gln Gly Val Ser Glu
85 90 95

<210> 876
<211> 238
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (20)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 876
Thr Lys Lys Ala Leu Glu Xaa Ser Asn Xaa Arg Phe Ala Ala Xaa Phe
1 5 10 15

Phe Arg Thr Xaa Trp Asn Pro Pro Gly Ala Phe Lys Glu Phe Gly Thr
20 25 30

Ser Leu Leu Arg Arg Arg Arg Gly Ser Gly Ala Asn Met Pro Val Ala
35 40 45

Arg Ser Trp Val Cys Arg Lys Thr Tyr Val Thr Pro Arg Arg Pro Phe
50 55 60

Glu Lys Ser Arg Leu Asp Gln Glu Leu Lys Leu Ile Gly Glu Tyr Gly
65 70 75 80

Leu Arg Asn Lys Arg Glu Val Trp Arg Val Lys Phe Thr Leu Ala Lys
85 90 95

Ile Arg Lys Ala Ala Arg Glu Leu Leu Thr Leu Asp Glu Lys Asp Pro
100 105 110

Arg Arg Leu Phe Glu Gly Asn Ala Leu Leu Arg Arg Leu Val Arg Ile
115 120 125

Gly Val Leu Asp Glu Gly Lys Met Lys Leu Asp Tyr Ile Leu Gly Leu
130 135 140

Lys Ile Glu Asp Phe Leu Glu Arg Arg Leu Gln Thr Gln Val Phe Lys
145 150 155 160

Leu Gly Leu Ala Lys Ser Ile His His Ala Arg Val Leu Ile Arg Gln
165 170 175

Arg His Ile Arg Val Arg Lys Gln Val Val Asn Ile Pro Ser Phe Ile
180 185 190

Val Arg Leu Asp Ser Gln Lys His Ile Asp Phe Ser Leu Arg Ser Pro
195 200 205

Tyr Gly Gly Gly Arg Pro Gly Arg Val Lys Arg Lys Asn Ala Lys Lys
210 215 220

Gly Gln Gly Gly Ala Gly Ala Gly Asp Asp Glu Glu Glu Asp
225 230 235

<210> 877
<211> 79
<212> PRT
<213> Homo sapiens

<400> 877
Ala Gly Ile Arg His Glu Pro Ser Ala Ala Ala Met Ser Ser Gly Ala
1 5 10 15

Ser Ala Ser Ala Leu Gln Arg Leu Val Glu Gln Leu Lys Leu Glu Ala
20 25 30

Gly Val Glu Arg Ile Lys Val Ser Gln Ala Ala Ala Glu Leu Gln Gln
35 40 45

Tyr Cys Met Gln Asn Ala Cys Lys Asp Ala Leu Leu Val Gly Val Pro

50 55 60

Ala Gly Ser Asn Pro Phe Arg Glu Pro Arg Ser Cys Ala Leu Leu
65 70 75

<210> 878
<211> 136
<212> PRT
<213> Homo sapiens

<400> 878
Ile Ala Ile Met Asn Asp Thr Val Thr Ile Arg Thr Arg Lys Phe Met
1 5 10 15

Thr Asn Arg Leu Leu Gln Arg Lys Gln Met Val Ile Asp Val Leu His
20 25 30

Pro Gly Lys Ala Thr Val Pro Lys Thr Glu Ile Arg Glu Lys Leu Ala
35 40 45

Lys Met Tyr Lys Thr Thr Pro Asp Val Ile Phe Val Phe Gly Phe Arg
50 55 60

Thr His Phe Gly Gly Gly Lys Thr Thr Gly Phe Gly Met Ile Tyr Asp
65 70 75 80

Ser Leu Asp Tyr Ala Lys Lys Asn Glu Pro Lys His Arg Leu Ala Arg
85 90 95

His Gly Leu Tyr Glu Lys Lys Lys Thr Ser Arg Lys Gln Arg Lys Glu
100 105 110

Arg Lys Asn Arg Met Lys Lys Val Arg Gly Thr Ala Lys Ala Asn Val
115 120 125

Gly Ala Gly Lys Lys Pro Lys Glu
130 135

<210> 879
<211> 141
<212> PRT
<213> Homo sapiens

<400> 879
Gly Cys Val Gly Val Arg Pro Ser Leu His Pro Ala Thr Ser Thr Ala
1 5 10 15

```
Ser Gly Ser Ala Ser Pro Thr Leu Ala Arg Ala Met Ala Ser Val Ser
            20                  25                  30

Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu His Asp Asp Glu Val
        35                  40                  45

Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile Lys Ala Ala Gly Val
    50                  55                  60

Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala Lys Ala Leu Ala Asn
65                  70                  75                  80

Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly Ala Gly Gly Pro Ala
                85                  90                  95

Pro Ala Ala Gly Ala Ala Pro Ala Gly Gly Pro Ala Pro Ser Thr Ala
            100                 105                 110

Ala Ala Pro Ala Glu Glu Lys Lys Val Glu Ala Lys Lys Glu Glu Ser
        115                 120                 125

Glu Glu Ser Asp Asp Asp Met Gly Phe Gly Leu Phe Asp
    130                 135                 140
```

<210> 880
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (14)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (128)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (130)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (131)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 880
Ser Ala Gly Ala His Ala His Gly Ala Arg Glu Leu Ala Xaa Phe Leu
1   5   10   15

Thr Pro Xaa Pro Gly Ala Glu Ala Lys Glu Val Glu Glu Thr Ile Glu
            20   25   30

Gly Met Leu Leu Arg Leu Glu Glu Phe Cys Ser Leu Ala Asp Leu Ile
        35   40   45

Arg Ser Asp Thr Ser Gln Ile Leu Glu Glu Asn Ile Pro Val Leu Lys
    50   55   60

Ala Lys Leu Thr Glu Met Arg Gly Ile Tyr Ala Lys Val Asp Arg Leu
65   70   75   80

Glu Ala Phe Val Lys Met Val Gly His His Val Ala Phe Leu Glu Ala
                85   90   95

Asp Val Leu Gln Ala Glu Arg Asp His Gly Ala Phe Pro Gln Ala Leu
            100   105   110

Arg Arg Trp Leu Gly Ser Ala Gly Ser Pro Pro Ser Gly Thr Ser Xaa
        115   120   125

Leu Xaa Xaa Cys Pro
    130

<210> 881
<211> 260
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (14)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (124)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (171)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 881
```
Ile Glu Glu Pro Arg Asp Thr Arg Leu Gln Val Cys Ser Xaa Val His
  1               5                  10                  15

Ile Trp Cys Leu Asp Lys Phe Lys Met Arg Lys His Arg His Leu Pro
             20                  25                  30

Leu Val Ala Val Phe Cys Leu Phe Leu Ser Gly Phe Pro Thr Thr His
         35                  40                  45

Ala Gln Gln Gln Gln Ala Val Ile Glu Val Asn Lys Arg Asp Ile Val
     50                  55                  60

Phe Leu Val Asp Gly Ser Ser Ala Leu Gly Leu Ala Asn Phe Asn Ala
 65                  70                  75                  80

Ile Arg Asp Phe Ile Ala Lys Val Ile Gln Arg Leu Glu Ile Gly Gln
                 85                  90                  95

Asp Leu Ile Gln Val Ala Val Ala Gln Tyr Ala Asp Thr Val Arg Pro
            100                 105                 110

Glu Phe Tyr Phe Asn Thr His Pro Thr Lys Arg Xaa Val Ile Thr Ala
        115                 120                 125

Val Arg Lys Met Lys Pro Leu Xaa Gly Ser Ala Leu Tyr Thr Gly Ser
    130                 135                 140

Ala Leu Asp Phe Val Arg Asn Asn Leu Phe Thr Ser Ser Ala Gly Tyr
145                 150                 155                 160

Arg Ala Ala Glu Gly Ile Pro Lys Leu Leu Xaa Leu Ile Thr Gly Gly
                165                 170                 175

Lys Ser Leu Asp Glu Ile Ser Gln Pro Ala Gln Glu Leu Lys Arg Ser
            180                 185                 190

Ser Ile Met Ala Phe Ala Ile Gly Asn Lys Gly Ala Asp Gln Ala Glu
        195                 200                 205

Leu Glu Glu Ile Ala Phe Asp Ser Ser Leu Val Phe Ile Pro Ala Glu
    210                 215                 220
```

Phe Arg Ala Ala Pro Leu Gln Gly Met Leu Pro Gly Leu Leu Ala Pro
225 230 235 240

Leu Arg Thr Leu Ser Gly Thr Pro Glu Val His Ser Asn Lys Arg Asp
245 250 255

Ile Ile Phe Leu
260

<210> 882
<211> 149
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 882
Xaa Xaa Glu Ser Glu Xaa Ser Phe Xaa Cys Arg Lys Xaa Ile Ile Xaa
1 5 10 15

Phe Leu Xaa Tyr Lys Arg Val Val Phe Leu Lys Gln Leu Ala Ser Gly
20 25 30

Leu Leu Leu Val Thr Gly Pro Leu Val Leu Asn Arg Val Pro Leu Arg
35 40 45

Arg Thr His Gln Lys Phe Val Ile Ala Thr Ser Thr Lys Ile Asp Ile
50 55 60

Ser Asn Val Lys Ile Pro Lys His Leu Thr Asp Ala Tyr Phe Lys Lys
65 70 75 80

Lys Lys Leu Arg Lys Pro Arg His Gln Glu Gly Glu Ile Phe Asp Thr
85 90 95

Glu Lys Glu Lys Tyr Glu Ile Thr Glu Gln Arg Lys Ile Asp Gln Lys
100 105 110

Ala Val Asp Ser Gln Ile Leu Pro Lys Ile Lys Ala Ile Pro Gln Leu
115 120 125

Gln Gly Tyr Leu Arg Ser Val Phe Ala Leu Thr Asn Gly Ile Tyr Pro
130 135 140

His Lys Leu Val Phe
145

<210> 883
<211> 256
<212> PRT
<213> Homo sapiens

<400> 883
Trp Lys Ser Val Val Val Leu Ala Val Ser Ala Gly Ala Gly Ser Ala
1 5 10 15

His Pro Arg Gln Asn Lys Tyr Ser Val Leu Leu Pro Thr Tyr Asn Glu
20 25 30

Arg Glu Asn Leu Pro Leu Ile Val Trp Leu Leu Val Lys Ser Phe Ser
35 40 45

Glu Ser Gly Ile Asn Tyr Glu Ile Ile Ile Ile Asp Asp Gly Ser Pro
50 55 60

Asp Gly Thr Arg Asp Val Ala Glu Gln Leu Glu Lys Ile Tyr Gly Ser
65 70 75 80

Asp Arg Ile Leu Leu Arg Pro Arg Glu Lys Lys Leu Gly Leu Gly Thr
85 90 95

Ala Tyr Ile His Gly Met Lys His Ala Thr Gly Asn Tyr Ile Ile Ile
100 105 110

Met Asp Ala Asp Leu Ser His His Pro Lys Phe Ile Pro Glu Phe Ile
115 120 125

Arg Lys Gln Lys Glu Gly Asn Phe Asp Ile Val Ser Gly Thr Arg Tyr
130 135 140

Lys Gly Asn Gly Gly Val Tyr Gly Trp Asp Leu Lys Arg Lys Ile Ile
145 150 155 160

Ser Arg Gly Ala Asn Phe Leu Thr Gln Ile Leu Leu Arg Pro Gly Ala
165 170 175

Ser Asp Leu Thr Gly Ser Phe Arg Leu Tyr Arg Lys Glu Val Leu Glu
180 185 190

Lys Leu Ile Glu Lys Cys Val Ser Lys Gly Tyr Val Phe Gln Met Glu
195 200 205

Met Ile Val Arg Ala Arg Gln Leu Asn Tyr Thr Ile Gly Glu Val Pro
210 215 220

Ile Ser Phe Val Asp Arg Val Tyr Gly Glu Ser Lys Leu Gly Gly Asn
225 230 235 240

Glu Ile Val Ser Phe Leu Lys Gly Leu Leu Thr Leu Phe Ala Thr Thr
245 250 255

<210> 884
<211> 449
<212> PRT
<213> Homo sapiens

<400> 884
Gly Gly Ser Trp Cys Arg Ser Ser Pro Gly Arg Asp Gly Ser Pro Gly
1 5 10 15

Ala Lys Gly Asp Arg Gly Glu Thr Gly Pro Ala Gly Pro Pro Gly Ala
20 25 30

Pro Gly Ala Pro Gly Ala Pro Gly Pro Val Gly Pro Ala Gly Lys Ser
35 40 45

Gly Asp Arg Gly Glu Thr Gly Pro Ala Gly Pro Ala Gly Pro Val Gly
50 55 60

Pro Val Gly Ala Arg Gly Pro Ala Gly Pro Gln Gly Pro Arg Gly Asp
65 70 75 80

Lys Gly Glu Thr Gly Glu Gln Gly Asp Arg Gly Ile Lys Gly His Arg
85 90 95

Gly Phe Ser Gly Leu Gln Gly Pro Pro Gly Pro Pro Gly Ser Pro Gly
100 105 110

Glu Gln Gly Pro Ser Gly Ala Ser Gly Pro Ala Gly Pro Arg Gly Pro
115 120 125

Pro Gly Ser Ala Gly Ala Pro Gly Lys Asp Gly Leu Asn Gly Leu Pro
130 135 140

Gly Pro Ile Gly Pro Pro Gly Pro Arg Gly Arg Thr Gly Asp Ala Gly
145 150 155 160

Pro Val Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro Pro Gly Pro
165 170 175

Pro Ser Ala Gly Phe Asp Phe Ser Phe Leu Pro Gln Pro Pro Gln Glu
180 185 190

Lys Ala His Asp Gly Gly Arg Tyr Tyr Arg Ala Asp Asp Ala Asn Val
195 200 205

Val Arg Asp Arg Asp Leu Glu Val Asp Thr Thr Leu Lys Ser Leu Ser
210 215 220

Gln Gln Ile Glu Asn Ile Arg Ser Pro Glu Gly Ser Arg Lys Asn Pro
225 230 235 240

Ala Arg Thr Cys Arg Asp Leu Lys Met Cys His Ser Asp Trp Lys Ser
245 250 255

Gly Glu Tyr Trp Ile Asp Pro Asn Gln Gly Cys Asn Leu Asp Ala Ile
260 265 270

Lys Val Phe Cys Asn Met Glu Thr Gly Glu Thr Cys Val Tyr Pro Thr
275 280 285

Gln Pro Ser Val Ala Gln Lys Asn Trp Tyr Ile Ser Lys Asn Pro Lys
290 295 300

Asp Lys Arg His Val Trp Phe Gly Glu Ser Met Thr Asp Gly Phe Gln
305 310 315 320

Phe Glu Tyr Gly Gly Gln Gly Ser Asp Pro Ala Asp Val Ala Ile Gln
325 330 335

Leu Thr Phe Leu Arg Leu Met Ser Thr Glu Ala Ser Gln Asn Ile Thr
340 345 350

Tyr His Cys Lys Asn Ser Val Ala Tyr Met Asp Gln Gln Thr Gly Asn
355 360 365

Leu Lys Lys Ala Leu Leu Leu Gln Gly Ser Asn Glu Ile Glu Ile Arg
370 375 380

Ala Glu Gly Asn Ser Arg Phe Thr Tyr Ser Val Thr Val Asp Gly Cys
385 390 395 400

Thr Ser His Thr Gly Ala Trp Gly Lys Thr Val Ile Glu Tyr Lys Thr
405 410 415

Thr Lys Thr Ser Arg Leu Pro Ile Ile Asp Val Ala Pro Leu Asp Val
420 425 430

Gly Ala Pro Asp Gln Glu Phe Gly Phe Asp Val Gly Pro Val Cys Phe
435 440 445

Leu

<210> 885
<211> 64
<212> PRT
<213> Homo sapiens

<400> 885
Gly Lys Leu Val Thr Leu Gln Val Pro Val Arg Asn Ser Arg Val Asp
1 5 10 15

Pro Arg Val Arg Trp Gly Phe Thr Lys Phe Asn Ala Asp Glu Phe Glu
20 25 30

Asp Met Val Ala Glu Lys Arg Leu Ile Pro Asp Gly Cys Gly Val Lys
35 40 45

Tyr Ile Pro Ser Arg Gly Pro Leu Asp Lys Trp Arg Ala Leu His Ser

50 55 60

<210> 886
<211> 132
<212> PRT
<213> Homo sapiens

<400> 886
Thr Thr Leu Arg Ala Leu Ala Leu Asn Leu Trp Pro Pro Lys Ser Arg
1 5 10 15

Ser Leu Ile Ser Ser Trp Gln Ser Cys Gly Gln Glu Val Leu Lys Gly
20 25 30

Lys Thr His Ser Asp Asn Cys Ser Pro Ile Tyr Gln Pro Ser Ala Gly
35 40 45

Val Ser Asp Arg Gly Pro Leu Pro Pro Leu Glu Cys Ala Thr Tyr Glu
50 55 60

Glu Cys Pro Met Gly Lys Arg Arg Leu Ser Cys Pro Leu Ala Ala Cys
65 70 75 80

Ala Ser Ile Pro Gly Gln Lys Phe Pro Gln Glu Pro Leu Ala Leu Ala
85 90 95

Gln Ser His Cys Glu Arg Arg Trp Glu Pro Thr Pro Leu Gly Glu Gly
100 105 110

Ala Val Leu Leu Gly Thr Ser Gln His Gln Val Arg Ser Leu Lys Leu
115 120 125

Lys Asn Val Asn
130

<210> 887
<211> 70
<212> PRT
<213> Homo sapiens

<400> 887
Gly Leu Ser Ser Glu Ala Arg Glu Lys Ser Ser Glu Pro Gln Glu Arg
1 5 10 15

Ser Ser Glu Pro Trp Glu Arg Ser Ser Glu Pro Trp Glu Gly Leu Val
20 25 30

Thr Phe Glu Asp Val Ala Val Glu Phe Thr Gln Glu Glu Trp Ala Leu
35 40 45

Leu Asp Pro Ala Gln Arg Thr Leu Tyr Arg Asp Val Met Leu Glu Asn
50 55 60

Cys Arg Thr Trp Pro His
65 70

<210> 888
<211> 373
<212> PRT
<213> Homo sapiens

<400> 888
Val Asp Pro Arg Val Arg Phe Arg Glu Glu Phe Leu Phe Ser Ser Leu
1 5 10 15

Gln Glu Gly Arg Asp Lys Asp Thr Phe Ser Lys Met Ala Met Val Ser
20 25 30

Glu Phe Leu Lys Gln Ala Trp Phe Ile Glu Asn Glu Glu Gln Glu Tyr
35 40 45

Val Gln Thr Val Lys Ser Ser Lys Gly Gly Pro Gly Ser Ala Val Ser
50 55 60

Pro Tyr Pro Thr Phe Asn Pro Ser Ser Asp Val Ala Ala Leu His Lys
65 70 75 80

Ala Ile Met Val Lys Gly Val Asp Glu Ala Thr Ile Ile Asp Ile Leu
85 90 95

Thr Lys Arg Asn Asn Ala Gln Arg Gln Gln Ile Lys Ala Ala Tyr Leu
100 105 110

Gln Glu Thr Gly Lys Pro Leu Asp Glu Thr Leu Lys Lys Ala Leu Thr
115 120 125

Gly His Leu Glu Glu Val Val Leu Ala Leu Leu Lys Thr Pro Ala Gln
130 135 140

Phe Asp Ala Asp Glu Leu Arg Ala Ala Met Lys Gly Leu Gly Thr Asp
145 150 155 160

Glu Asp Thr Leu Ile Glu Ile Leu Ala Ser Arg Thr Asn Lys Glu Ile

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            165                 170                 175
Arg Asp Ile Asn Arg Val Tyr Arg Glu Glu Leu Lys Arg Asp Leu Ala
        180                 185                 190
Lys Asp Ile Thr Ser Asp Thr Ser Gly Asp Phe Arg Asn Ala Leu Leu
    195                 200                 205
Ser Leu Ala Lys Gly Asp Arg Ser Glu Asp Phe Gly Val Asn Glu Asp
210                 215                 220
Leu Ala Asp Ser Asp Ala Arg Ala Leu Tyr Glu Ala Gly Glu Arg Arg
225                 230                 235                 240
Lys Gly Thr Asp Val Asn Val Phe Asn Thr Ile Leu Thr Thr Arg Ser
                245                 250                 255
Tyr Pro Gln Leu Arg Arg Val Phe Gln Lys Tyr Thr Lys Tyr Ser Lys
            260                 265                 270
His Asp Met Asn Lys Val Leu Asp Leu Glu Leu Lys Gly Asp Ile Glu
        275                 280                 285
Lys Cys Leu Thr Ala Ile Val Lys Cys Ala Thr Ser Lys Pro Ala Phe
    290                 295                 300
Phe Ala Glu Lys Leu His Gln Ala Met Lys Gly Val Gly Thr Arg His
305                 310                 315                 320
Lys Ala Leu Ile Arg Ile Met Val Ser Arg Ser Glu Ile Asp Met Asn
                325                 330                 335
Asp Ile Lys Ala Phe Tyr Gln Lys Met Tyr Gly Ile Ser Leu Cys Gln
            340                 345                 350
Ala Ile Leu Asp Glu Thr Lys Gly Asp Tyr Glu Lys Ile Leu Val Ala
        355                 360                 365
Leu Cys Gly Gly Asn
    370
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<210> 889
<211> 336
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (51)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (60)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (100)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (183)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 889
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Gly Arg Lys Lys His Leu Xaa Ala Arg Leu Val Thr Glu Met Asp Ser
 1               5                  10                  15

Lys Tyr Gln Cys Val Lys Leu Asn Asp Gly His Phe Met Pro Val Leu
            20                  25                  30

Gly Phe Gly Thr Tyr Ala Pro Ala Glu Val Pro Lys Ser Lys Ala Leu
        35                  40                  45

Glu Ala Xaa Lys Leu Ala Ile Glu Ala Gly Phe Xaa His Ile Asp Ser
    50                  55                  60

Ala His Xaa Tyr Asn Asn Glu Glu Gln Val Gly Leu Ala Ile Arg Ser
65                  70                  75                  80

Lys Ile Ala Asp Gly Ser Val Lys Arg Glu Asp Ile Phe Tyr Thr Ser
                85                  90                  95

Lys Leu Trp Xaa Asn Ser His Arg Pro Glu Leu Val Arg Pro Ala Leu
            100                 105                 110

Glu Arg Ser Leu Lys Asn Leu Gln Leu Asp Tyr Val Asp Leu Tyr Leu
        115                 120                 125
```

Ile His Phe Pro Val Ser Val Lys Pro Gly Glu Glu Val Ile Pro Lys
130 135 140

Asp Glu Asn Gly Lys Ile Leu Phe Asp Thr Val Asp Leu Cys Ala Thr
145 150 155 160

Trp Glu Ala Val Glu Lys Cys Lys Asp Ala Gly Leu Ala Lys Ser Ile
165 170 175

Gly Val Ser Asn Phe Asn Xaa Arg Gln Leu Glu Met Ile Leu Asn Lys
180 185 190

Pro Gly Leu Lys Tyr Lys Pro Val Cys Asn Gln Val Glu Cys His Pro
195 200 205

Tyr Phe Asn Gln Arg Lys Leu Leu Asp Phe Cys Lys Ser Lys Asp Ile
210 215 220

Val Leu Val Ala Tyr Ser Ala Leu Gly Ser His Arg Glu Glu Pro Trp
225 230 235 240

Val Asp Pro Asn Ser Pro Val Leu Leu Glu Asp Pro Val Leu Cys Ala
245 250 255

Leu Ala Lys Lys His Lys Arg Thr Pro Ala Leu Ile Ala Leu Arg Tyr
260 265 270

Gln Leu Gln Arg Gly Val Val Val Leu Ala Lys Ser Tyr Asn Glu Gln
275 280 285

Arg Ile Arg Gln Asn Val Gln Val Phe Glu Phe Gln Leu Thr Ser Glu
290 295 300

Glu Met Lys Ala Ile Asp Gly Leu Asn Arg Asn Val Arg Tyr Leu Thr
305 310 315 320

Leu Asp Ile Phe Ala Gly Pro Pro Asn Tyr Pro Phe Ser Asp Glu Tyr
325 330 335

<210> 890
<211> 195
<212> PRT
<213> Homo sapiens

<400> 890

Arg Ser Ser Glu Val Tyr Ala Gln Leu Cys Asn Val Ala Arg Ile Glu
1 5 10 15

Ala Glu Arg Glu Ala Gly Val His Phe Arg Pro Gly Tyr Glu Tyr Gly
20 25 30

Pro Gly Pro Asp Asp Leu His Tyr Ser Ile Tyr Gly Pro Asp Gly Ala
35 40 45

Pro Phe Tyr Asn Tyr Leu Gly Pro Glu Asp Thr Val Pro Glu Pro Ala
50 55 60

Phe Pro Asn Thr Ala Gly His Ser Ala Asp Arg Thr Pro Ile Leu Glu
65 70 75 80

Ser Pro Leu Gln Pro Ser Glu Leu Gln Pro His Tyr Val Ala Ser His
85 90 95

Pro Glu Pro Pro Ala Gly Phe Glu Gly Leu Gln Ala Glu Glu Cys Gly
100 105 110

Ile Leu Asn Gly Cys Glu Asn Gly Arg Cys Val Arg Val Arg Glu Gly
115 120 125

Tyr Thr Cys Asp Cys Phe Glu Gly Phe Gln Leu Asp Ala Ala His Met
130 135 140

Ala Cys Val Asp Val Asn Glu Cys Asp Asp Leu Asn Gly Pro Ala Val
145 150 155 160

Leu Cys Val His Gly Tyr Cys Glu Asn Thr Glu Gly Ser Tyr Arg Cys
165 170 175

His Cys Ser Pro Gly Tyr Val Ala Glu Ala Gly Pro Pro His Cys Thr
180 185 190

Ala Lys Glu
195

<210> 891
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (109)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 891
Ser Ala Gly Leu Thr Gly Arg Ile Ala Phe Ala Ala Ala Arg Pro Gln
1 5 10 15

Thr Phe Val Pro Gly Pro Ser Ser Pro Pro Pro Pro Pro Pro Pro Arg
20 25 30

Pro Ala Glu Leu Ala Pro Ser Pro Pro Ala Asp Met Ser Glu Ser Lys
35 40 45

Ser Gly Pro Glu Tyr Ala Ser Phe Phe Ala Val Met Gly Ala Ser Ala
50 55 60

Ala Met Val Phe Ser Ala Leu Gly Ala Ala Tyr Gly Thr Ala Lys Ser
65 70 75 80

Gly Thr Gly Ile Ala Ala Met Ser Val Met Arg Pro Glu Gln Ile Met
85 90 95

Lys Ser Ile Ile Pro Val Val Met Ala Gly Ile Xaa Xaa Ile Tyr Gly
100 105 110

Leu Val Val Ala Val Leu Ile Ala Asn Ser Leu Asn Asp Asp Ile Ser
115 120 125

Leu Tyr Lys Ser Phe Leu Gln Leu Gly Ala Gly Leu Ser Val Gly Leu
130 135 140

Ser Gly Leu Ala Ala Gly Phe Ala Ile Gly Ile Val Gly Asp Ala Gly
145 150 155 160

Val Arg Gly Asn Ala Gln Gln Pro Arg Leu Phe Val Gly Met Ile Leu
165 170 175

Ile Leu Ile Phe Ala Glu Val Leu Gly Leu Tyr Gly Leu Ile Val Ala
180 185 190

Leu Ile Leu Ser Thr Lys
195

<210> 892
<211> 95
<212> PRT
<213> Homo sapiens

<400> 892
Asp Ala Trp Ala Pro Ser Glu Ser Arg Glu Ala Leu Leu Thr Pro Pro
1 5 10 15

Pro His Arg Arg His Thr Ala Ala Ala Ser Val Met Pro Lys His Glu
20 25 30

Phe Ser Val Asp Met Thr Cys Gly Gly Cys Ala Glu Ala Val Ser Arg
35 40 45

Val Leu Asn Lys Leu Gly Gly Val Lys Tyr Asp Ile Asp Leu Pro Asn
50 55 60

Lys Lys Val Cys Ile Glu Ser Glu His Ser Met Asp Thr Leu Leu Ala
65 70 75 80

Thr Leu Lys Lys Thr Gly Lys Thr Val Ser Tyr Leu Gly Leu Glu
85 90 95

<210> 893
<211> 123
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (111)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (117)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 893
Gly Glu His Pro Arg Gln Pro Ala Gly Asn Asn Ile Leu Ala Val Leu
1 5 10 15

Thr Cys Cys Gln Gln Ile His Arg Thr Trp Met Lys Phe Pro Phe Pro
20 25 30

Leu Val Ser Ser Cys Ser Thr Pro Leu Leu Asp Pro Lys Ser Leu Thr
35 40 45

Lys Ala Leu Asn Thr Val Lys Met Phe Tyr Ile Pro Phe His Leu Cys
50 55 60

Cys Phe Phe Asn Cys Ile Leu Pro Asp Val Leu Met Leu Ser Leu Met

65 70 75 80

Leu Ile Val Ile Pro Val Arg Val His Phe Ile Phe Met Leu Phe Gln
85 90 95

Pro Cys Ile Asn Ile His Leu Thr Lys Ile Thr Gln Leu Ile Xaa Lys
100 105 110

Lys Lys Lys Asn Xaa Gly Gly Gly Pro Gly Thr
115 120

<210> 894
<211> 172
<212> PRT
<213> Homo sapiens

<400> 894
Gln Phe Val Tyr Cys Gly Lys Lys Ala Gln Leu Asn Ile Gly Asn Val
1 5 10 15

Leu Pro Val Gly Thr Met Pro Glu Gly Thr Ile Val Cys Cys Leu Glu
20 25 30

Glu Lys Pro Gly Asp Arg Gly Lys Leu Ala Arg Ala Ser Gly Asn Tyr
35 40 45

Ala Thr Val Ile Ser His Asn Pro Glu Thr Lys Lys Thr Arg Val Lys
50 55 60

Leu Pro Ser Gly Ser Lys Lys Val Ile Ser Ser Ala Asn Arg Ala Val
65 70 75 80

Val Gly Val Val Ala Gly Gly Gly Arg Ile Asp Lys Pro Ile Leu Lys
85 90 95

Ala Gly Arg Ala Tyr His Lys Tyr Lys Ala Lys Arg Asn Cys Trp Pro
100 105 110

Arg Val Arg Gly Val Ala Met Asn Pro Val Glu His Pro Phe Gly Gly
115 120 125

Gly Asn His Gln His Ile Gly Lys Pro Ser Thr Ile Arg Arg Asp Ala
130 135 140

Pro Ala Gly Arg Lys Val Gly Leu Ile Ala Ala Arg Arg Thr Gly Arg
145 150 155 160

Leu Arg Gly Thr Lys Thr Val Gln Glu Lys Glu Asn
165 170

<210> 895
<211> 171
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (37)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 895
Asn Arg Glu Gly Ser Lys Gly Val Glu Thr Arg Arg Val Leu Val Gly
1 5 10 15

Glu Gln Gln Gln Cys Xaa Asp Ala Lys Ser Gln Gln Lys Glu Gln Met
20 25 30

Leu Leu Leu Glu Xaa Lys Ser Ala Ala Tyr Ser Gln Val Leu Leu Arg
35 40 45

Cys Leu Thr Leu Leu Gln Arg Leu Leu Gln Glu His Arg Leu Lys Thr
50 55 60

Gln Ser Glu Leu Asp Arg Ile Asn Ala Gln Tyr Leu Glu Val Lys Cys
65 70 75 80

Gly Ala Met Ile Leu Lys Leu Arg Met Glu Glu Leu Lys Ile Leu Ser
85 90 95

Asp Thr Tyr Thr Val Glu Lys Val Glu Val His Arg Leu Ile Arg Asp
100 105 110

Arg Leu Glu Gly Ala Ile His Leu Gln Glu Gln Asp Met Glu Asn Ser
115 120 125

Arg Gln Val Leu Asn Ser Tyr Glu Val Leu Gly Glu Glu Phe Asp Arg
130 135 140

Leu Val Lys Glu Tyr Thr Val Leu Lys Gln Ala Thr Glu Asn Lys Arg
145 150 155 160

Trp Ala Leu Gln Glu Phe Ser Lys Val Tyr Arg
165 170

<210> 896
<211> 99
<212> PRT
<213> Homo sapiens

<400> 896
Arg Glu Val Met Lys Leu Tyr Leu Phe Gln Trp Ala Leu Phe His Phe
1 5 10 15

Thr Thr Val Pro Leu Phe Gly Ser Trp Ser Tyr Thr Leu Ile Phe Ser
20 25 30

Ile Leu Leu Leu Asn Tyr Gln His Lys Ala Ile Tyr Leu Lys Asp Ser
35 40 45

Val Tyr Pro Ala Ile Ala Leu Lys Ser Ser Arg Lys Arg Asn Pro Leu
50 55 60

Thr Cys Ile Ser Phe Cys Arg Ala Ser Leu Phe Ser Phe Val Leu Cys
65 70 75 80

Phe Leu Pro Phe Glu Ser Asp Ser Val Leu Val Arg Lys Thr Ser Trp
85 90 95

Asp His Ser

<210> 897
<211> 289
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (255)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 897
Ala Pro Glu Phe Pro Gly Arg Pro Thr Arg Pro Pro Thr Arg Arg Pro
1 5 10 15

Arg Val Arg Gly Arg Ser Gln Leu Ser Ala His Gly Pro Ala Ser Phe
20 25 30

Lys Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly
35 40 45

```
Asp His Ser Thr Pro Pro Ser Ala Tyr Gly Ser Val Lys Ala Tyr Thr
     50                  55                  60

Asn Phe Asp Ala Glu Arg Asp Ala Leu Asn Ile Glu Thr Ala Ile Lys
 65                  70                  75                  80

Thr Lys Gly Val Asp Glu Val Thr Ile Val Asn Ile Leu Thr Asn Arg
                 85                  90                  95

Ser Asn Ala Gln Arg Gln Asp Ile Ala Phe Ala Tyr Gln Arg Arg Thr
            100                 105                 110

Lys Lys Glu Leu Ala Ser Ala Leu Lys Ser Ala Leu Ser Gly His Leu
        115                 120                 125

Glu Thr Val Ile Leu Gly Leu Leu Lys Thr Pro Ala Gln Tyr Asp Ala
    130                 135                 140

Ser Glu Leu Lys Ala Ser Met Lys Gly Leu Gly Thr Asp Glu Asp Ser
145                 150                 155                 160

Leu Ile Glu Ile Ile Cys Ser Arg Thr Asn Gln Glu Leu Gln Glu Ile
                165                 170                 175

Asn Arg Val Tyr Lys Glu Met Tyr Lys Thr Asp Leu Glu Lys Asp Ile
            180                 185                 190

Ile Ser Asp Thr Ser Gly Asp Phe Arg Lys Leu Met Val Ala Leu Ala
        195                 200                 205

Lys Gly Arg Arg Ala Glu Asp Gly Ser Val Ile Asp Tyr Glu Leu Ile
    210                 215                 220

Asp Gln Asp Ala Arg Asp Leu Tyr Asp Ala Gly Val Lys Arg Lys Gly
225                 230                 235                 240

Thr Asp Val Pro Lys Trp Ile Ser Ile Met Thr Glu Arg Ser Xaa Pro
                245                 250                 255

Thr Ser Arg Lys Tyr Leu Ile Gly Thr Arg Val Thr Ala Leu Met Thr
            260                 265                 270

Cys Trp Lys Ala Ser Gly Lys Arg Leu Lys Glu Thr Trp Lys Met Leu
        275                 280                 285

Ser
```

<210> 898
<211> 232
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (205)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 898
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Asn Pro Arg Gly Lys Val Ala Gly Phe Asp Leu Asp Gly Thr Leu Ile
  1               5                  10                  15

Thr Thr Arg Ser Gly Lys Val Phe Pro Thr Gly Pro Ser Asp Trp Arg
             20                  25                  30

Ile Leu Tyr Pro Glu Ile Pro Arg Lys Leu Arg Glu Leu Glu Ala Glu
         35                  40                  45

Gly Tyr Lys Leu Val Ile Phe Thr Asn Gln Met Ser Ile Gly Arg Gly
     50                  55                  60

Lys Leu Pro Ala Glu Glu Phe Lys Ala Lys Val Glu Ala Val Val Glu
 65                  70                  75                  80

Lys Leu Gly Val Pro Phe Gln Val Leu Val Ala Thr His Ala Gly Leu
                 85                  90                  95

Tyr Arg Lys Pro Val Thr Gly Met Trp Asp His Leu Gln Glu Gln Ala
            100                 105                 110

Asn Asp Gly Thr Pro Ile Ser Ile Gly Asp Ser Ile Phe Val Gly Asp
        115                 120                 125

Ala Ala Gly Arg Pro Ala Asn Trp Ala Pro Gly Arg Lys Lys Lys Asp
    130                 135                 140

Phe Ser Cys Ala Asp Arg Leu Phe Ala Leu Asn Leu Gly Leu Pro Phe
145                 150                 155                 160

Ala Thr Pro Glu Glu Phe Phe Leu Lys Trp Pro Ala Ala Gly Phe Glu
                165                 170                 175

Leu Pro Ala Phe Asp Pro Arg Thr Val Ser Arg Ser Gly Pro Leu Cys
            180                 185                 190

Leu Pro Glu Ser Arg Ala Leu Leu Ser Ala Thr Arg Xaa Trp Leu Ser
        195                 200                 205

Gln Trp Asp Ser Leu Gly Pro Gly Ser Pro Pro Phe Ser Arg Ser Thr
```

210 215 220

Ser Cys Arg Pro Asp Met Ser Thr
225 230

<210> 899
<211> 218
<212> PRT
<213> Homo sapiens

<400> 899
Leu Arg Val Ala Arg Pro Asp Ala Ala Arg Ala Ala Pro Leu Ala Pro
1 5 10 15

Ala Ala Ala Met Lys Ala Val Val Gln Arg Val Thr Arg Ala Ser Val
20 25 30

Thr Val Gly Gly Glu Gln Ile Ser Ala Ile Gly Arg Gly Ile Cys Val
35 40 45

Leu Leu Gly Ile Ser Leu Glu Asp Thr Gln Lys Glu Leu Glu His Met
50 55 60

Val Arg Lys Ile Leu Asn Leu Arg Val Phe Glu Asp Glu Ser Gly Lys
65 70 75 80

His Trp Ser Lys Ser Val Met Asp Lys Gln Tyr Glu Ile Leu Cys Val
85 90 95

Ser Gln Phe Thr Leu Gln Cys Val Leu Lys Gly Asn Lys Pro Asp Phe
100 105 110

His Leu Ala Met Pro Thr Glu Gln Ala Glu Gly Phe Tyr Asn Ser Phe
115 120 125

Leu Glu Gln Leu Arg Lys Thr Tyr Arg Pro Glu Leu Ile Lys Asp Gly
130 135 140

Lys Phe Gly Ala Tyr Met Gln Val His Ile Gln Asn Asp Gly Pro Val
145 150 155 160

Thr Ile Glu Leu Glu Ser Pro Ala Pro Gly Thr Ala Thr Ser Asp Pro
165 170 175

Lys Gln Leu Ser Lys Leu Glu Lys Gln Gln Gln Arg Lys Glu Lys Thr
180 185 190

Arg Ala Lys Gly Pro Ser Glu Phe Lys Gln Gly Lys Lys His Ser Pro
195 200 205

Lys Arg Arg Pro Gln Cys Gln Gln Arg Gly
210 215

<210> 900
<211> 152
<212> PRT
<213> Homo sapiens

<400> 900
Ser Lys Arg Gly His Val Pro Trp Gly Leu Glu Glu Ile Leu Asp Val
1 5 10 15

Ile Glu Pro Ser Gln Phe Val Lys Ile Gln Glu Pro Leu Phe Lys Gln
20 25 30

Ile Ala Lys Cys Val Ser Ser Pro His Phe Gln Val Ala Glu Arg Ala
35 40 45

Leu Tyr Tyr Trp Asn Asn Glu Tyr Ile Met Ser Leu Ile Glu Glu Asn
50 55 60

Ser Asn Val Ile Leu Pro Ile Met Phe Ser Ser Leu Tyr Arg Ile Ser
65 70 75 80

Lys Glu His Trp Asn Pro Ala Ile Val Ala Leu Val Tyr Asn Val Leu
85 90 95

Lys Ala Phe Met Glu Met Asn Ser Thr Met Phe Asp Glu Leu Thr Ala
100 105 110

Thr Tyr Lys Ser Asp Arg Gln Arg Glu Lys Lys Lys Glu Lys Glu Arg
115 120 125

Glu Glu Leu Trp Lys Lys Leu Glu Asp Leu Glu Leu Lys Arg Gly Leu
130 135 140

Arg Arg Asp Gly Ile Ile Pro Thr
145 150

<210> 901
<211> 261
<212> PRT
<213> Homo sapiens

<400> 901
Gly Leu Arg Glu Ile Ser Gly Arg Leu Ala Glu Met Pro Ala Asp Ser

```
1               5                   10                  15

Gly Tyr Pro Ala Tyr Leu Gly Ala Arg Leu Ala Ser Phe Tyr Glu Arg
            20                  25                  30

Ala Gly Arg Val Lys Cys Leu Gly Asn Pro Glu Arg Glu Gly Ser Val
        35                  40                  45

Ser Ile Val Gly Ala Val Ser Pro Pro Gly Gly Asp Phe Ser Asp Pro
    50                  55                  60

Val Thr Ser Ala Thr Leu Gly Ile Val Gln Val Phe Trp Gly Leu Asp
65                  70                  75                  80

Lys Lys Leu Ala Gln Arg Lys His Phe Pro Ser Val Asn Trp Leu Ile
                85                  90                  95

Ser Tyr Ser Lys Tyr Met Arg Ala Leu Asp Glu Tyr Tyr Asp Lys His
            100                 105                 110

Phe Thr Glu Phe Val Pro Leu Arg Thr Lys Ala Lys Glu Ile Leu Gln
        115                 120                 125

Glu Glu Glu Asp Leu Ala Glu Ile Val Gln Leu Val Gly Lys Ala Ser
    130                 135                 140

Leu Ala Glu Thr Asp Lys Ile Thr Leu Glu Val Ala Lys Leu Ile Lys
145                 150                 155                 160

Asp Asp Phe Leu Gln Gln Asn Gly Tyr Thr Pro Tyr Asp Arg Phe Cys
                165                 170                 175

Pro Phe Tyr Lys Thr Val Gly Met Leu Ser Asn Met Ile Ala Phe Tyr
            180                 185                 190

Asp Met Ala Arg Arg Val Phe Glu Thr Thr Ala Gln Ser Asp Asn Lys
        195                 200                 205

Ile Thr Trp Ser Ile Ile Arg Glu His Met Gly Asp Ile Leu Tyr Lys
    210                 215                 220

Leu Ser Ser Met Lys Phe Lys Asp Pro Leu Lys Asp Gly Glu Ala Lys
225                 230                 235                 240

Ile Lys Ser Asp Tyr Ala Gln Leu Leu Glu Asp Met Gln Asn Ala Phe
                245                 250                 255

Arg Ser Leu Glu Asp
            260
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<210> 902
<211> 169
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (33)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 902
Phe Pro Gly Arg Pro Thr Arg Pro Arg Gly Ile Ser Val Ser Gly Gly
1 5 10 15

Glu Ala Val Cys Pro Val Gln Trp Arg Leu Arg Lys Leu Ala Ala Ala
20 25 30

Xaa Gly Lys Gly Gln Glu Val Glu Thr Ser Val Thr Tyr Tyr Arg Leu
35 40 45

Glu Glu Val Ala Lys Arg Asn Ser Leu Lys Glu Leu Trp Leu Val Ile
50 55 60

His Gly Arg Val Tyr Asp Val Thr Arg Phe Leu Asn Glu His Pro Gly
65 70 75 80

Gly Glu Glu Val Leu Leu Glu Gln Ala Gly Val Asp Ala Ser Glu Ser
85 90 95

Phe Glu Asp Val Gly His Ser Ser Asp Ala Arg Glu Met Leu Lys Gln
100 105 110

Tyr Tyr Ile Gly Asp Ile His Pro Ser Asp Leu Lys Pro Glu Ser Gly
115 120 125

Ser Lys Asp Pro Ser Lys Asn Asp Thr Cys Lys Ser Cys Trp Ala Tyr
130 135 140

Trp Ile Leu Pro Ile Ile Gly Ala Val Leu Leu Gly Phe Leu Tyr Arg
145 150 155 160

Tyr Tyr Thr Ser Glu Ser Lys Ser Ser
165

<210> 903
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 903
Pro Leu Cys Leu Ala Lys Asn Lys Asn Phe Leu Ile Leu Arg Xaa Asn
1   5   10   15

Ile Gln Xaa Ile His Ile Lys Ser Leu Glu Asn Ile Ile Pro Phe Asp
            20   25   30

Ser Leu Ile Thr Leu Leu Glu Tyr Lys Glu Met Ile Leu Asn Ile Tyr
        35   40   45

Val Val Leu Trp Ser
    50

<210> 904
<211> 329
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 904
Arg Arg Xaa Ala Xaa Pro Arg Val Arg Trp Lys Ile Cys Gly Leu Ser
1   5   10   15

Pro Thr Thr Thr Leu Ala Ile Tyr Phe Glu Val Val Asn Gln His Asn

20 25 30

Ala Pro Ile Xaa Gln Gly Gly Arg Gly Ala Ile Gln Phe Val Thr Gln
35 40 45

Tyr Gln His Ser Ser Gly Gln Arg Arg Ile Arg Val Thr Thr Ile Ala
50 55 60

Arg Asn Trp Ala Asp Ala Gln Thr Gln Ile Gln Asn Ile Ala Ala Ser
65 70 75 80

Phe Asp Gln Glu Ala Ala Ala Ile Leu Met Ala Arg Leu Ala Ile Tyr
85 90 95

Arg Ala Glu Thr Glu Glu Gly Pro Asp Val Leu Arg Trp Leu Asp Arg
100 105 110

Gln Leu Ile Arg Leu Cys Gln Lys Phe Gly Glu Tyr His Lys Asp Asp
115 120 125

Pro Ser Ser Phe Arg Phe Ser Glu Thr Phe Ser Leu Tyr Pro Gln Phe
130 135 140

Met Phe His Leu Arg Arg Ser Ser Phe Leu Gln Val Phe Asn Asn Ser
145 150 155 160

Pro Asp Glu Ser Ser Tyr Tyr Arg His His Phe Met Arg Gln Asp Leu
165 170 175

Thr Gln Ser Leu Ile Met Ile Gln Pro Ile Leu Tyr Ala Tyr Ser Phe
180 185 190

Ser Gly Pro Pro Glu Pro Val Leu Leu Asp Ser Ser Ser Ile Leu Ala
195 200 205

Asp Arg Ile Leu Leu Met Asp Thr Phe Phe Gln Ile Leu Ile Tyr His
210 215 220

Gly Glu Thr Ile Ala Gln Trp Arg Lys Ser Gly Tyr Gln Asp Met Pro
225 230 235 240

Glu Tyr Glu Asn Phe Arg His Leu Leu Gln Ala Pro Val Asp Asp Ala
245 250 255

Gln Glu Ile Leu His Ser Arg Phe Pro Met Pro Arg Tyr Ile Asp Thr
260 265 270

Glu His Gly Gly Ser Gln Ala Arg Phe Leu Leu Ser Lys Val Asn Pro
275 280 285

Ser Gln Thr His Asn Asn Met Tyr Ala Trp Gly Gln Glu Ser Gly Ala

290 295 300

Pro Ile Leu Thr Asp Asp Val Ser Leu Gln Val Phe Met Asp His Leu
305 310 315 320

Lys Lys Leu Ala Val Ser Ser Ala Ala
325

<210> 905
<211> 264
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (48)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 905
Phe Leu Leu Pro Thr Leu Trp Phe Cys Ser Pro Ser Ala Lys Tyr Phe
1 5 10 15

Phe Lys Met Ala Phe Tyr Asn Gly Trp Ile Leu Phe Leu Ala Val Leu
20 25 30

Ala Ile Pro Val Cys Ala Val Arg Gly Arg Asn Val Glu Asn Met Xaa
35 40 45

Ile Leu Arg Leu Met Leu Leu His Ile Lys Tyr Leu Tyr Gly Ile Arg
50 55 60

Val Glu Val Arg Gly Ala His His Phe Pro Pro Ser Gln Pro Tyr Val
65 70 75 80

Val Val Ser Asn His Gln Ser Ser Leu Asp Leu Leu Gly Met Met Glu
85 90 95

Val Leu Pro Gly Arg Cys Val Pro Ile Ala Lys Arg Glu Leu Leu Trp
100 105 110

Ala Gly Ser Ala Gly Leu Ala Cys Trp Leu Ala Gly Val Ile Phe Ile
115 120 125

Asp Arg Lys Arg Thr Gly Asp Ala Ile Ser Val Met Ser Glu Val Ala
130 135 140

Gln Thr Leu Leu Thr Gln Asp Val Arg Val Trp Val Phe Pro Glu Gly
145 150 155 160

```
Thr Arg Asn His Asn Gly Ser Met Leu Pro Phe Lys Arg Gly Ala Phe
                165                 170                 175

His Leu Ala Val Gln Ala Gln Val Pro Ile Val Pro Ile Val Met Ser
            180                 185                 190

Ser Tyr Gln Asp Phe Tyr Cys Lys Lys Glu Arg Arg Phe Thr Ser Gly
        195                 200                 205

Gln Cys Gln Val Arg Val Leu Pro Pro Val Pro Thr Glu Gly Leu Thr
    210                 215                 220

Pro Asp Asp Val Pro Ala Leu Ala Asp Arg Val Arg His Ser Met Leu
225                 230                 235                 240

Thr Val Phe Arg Glu Ile Ser Thr Asp Gly Arg Gly Gly Gly Asp Tyr
                245                 250                 255

Leu Lys Lys Pro Gly Gly Gly Gly
            260



<210> 906
<211> 189
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 906
Xaa Xaa Pro Xaa Pro Glu Phe Pro Gly Arg Thr His Ala Ser Gly Leu
  1               5                  10                  15

Leu Arg Ser Arg Leu Ala Leu Arg Trp Leu Ser His Val Arg Arg Pro
             20                  25                  30

Ser Arg Arg Val Pro Arg Met Pro Arg Gly Ser Arg Ser Arg Thr Ser
```

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        35                  40                  45

Arg Met Ala Pro Pro Ala Ser Arg Ala Pro Gln Met Arg Ala Ala Pro
     50                  55                  60

Arg Pro Ala Pro Val Ala Gln Pro Pro Ala Ala Ala Pro Pro Ser Ala
 65                  70                  75                  80

Val Gly Ser Ser Ala Ala Ala Pro Arg Gln Pro Gly Leu Met Ala Gln
                 85                  90                  95

Met Ala Thr Thr Ala Ala Gly Val Ala Val Gly Ser Ala Val Gly His
            100                 105                 110

Thr Leu Gly His Ala Ile Thr Gly Gly Phe Ser Gly Gly Ser Asn Ala
        115                 120                 125

Glu Pro Ala Arg Pro Asp Ile Thr Tyr Gln Glu Pro Gln Gly Thr Gln
    130                 135                 140

Pro Ala Gln Gln Gln Gln Pro Cys Leu Tyr Glu Ile Lys Gln Phe Leu
145                 150                 155                 160

Glu Cys Ala Gln Asn Gln Gly Asp Ile Lys Leu Cys Glu Gly Phe Asn
                165                 170                 175

Glu Val Leu Lys Gln Cys Arg Leu Ala Asn Gly Leu Ala
            180                 185
```

<210> 907
<211> 638
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (43)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (52)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (73)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (427)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 907
```
Tyr Val Gln Gly Tyr Ser Leu Ser Gln Ala Asp Val Asp Ala Phe Arg
  1               5                  10                  15

Gln Leu Ser Ala Pro Pro Ala Asp Pro Gln Leu Phe His Val Ala Arg
             20                  25                  30

Trp Phe Arg His Ile Glu Ala Leu Leu Gly Xaa Pro Cys Gly Lys Gly
         35                  40                  45

Gln Pro Cys Xaa Leu Pro Ser Xaa Gln Arg Pro Ala Cys Ala Ala Pro
     50                  55                  60

Val Val Pro Ser Cys Trp Asp Pro Xaa Cys Arg Leu His Leu Tyr Asn
 65                  70                  75                  80

Ser Leu Thr Arg Asn Lys Glu Val Phe Ile Pro Gln Asp Gly Lys Lys
                 85                  90                  95

Val Thr Trp Tyr Cys Cys Gly Pro Thr Val Tyr Asp Ala Ser His Met
            100                 105                 110

Gly His Ala Arg Ser Tyr Ile Ser Phe Asp Ile Leu Arg Arg Val Leu
        115                 120                 125

Lys Asp Tyr Phe Lys Phe Asp Val Phe Tyr Cys Met Asn Ile Thr Asp
    130                 135                 140

Ile Asp Asp Lys Ile Ile Lys Arg Ala Arg Gln Asn His Leu Phe Glu
145                 150                 155                 160

Gln Tyr Arg Glu Lys Arg Pro Glu Ala Ala Gln Leu Leu Glu Asp Val
                165                 170                 175

Gln Ala Ala Leu Lys Pro Phe Ser Val Lys Leu Asn Glu Thr Thr Asp
            180                 185                 190

Pro Asp Lys Lys Gln Met Leu Glu Arg Ile Gln His Ala Val Gln Leu
        195                 200                 205

Ala Thr Glu Pro Leu Glu Lys Ala Val Gln Ser Arg Leu Thr Gly Glu
```

210 215 220

Glu Val Asn Ser Cys Val Glu Val Leu Leu Glu Glu Ala Lys Asp Leu
225 230 235 240

Leu Ser Asp Trp Leu Asp Ser Thr Leu Gly Cys Asp Val Thr Asp Asn
245 250 255

Ser Ile Phe Ser Lys Leu Pro Lys Phe Trp Glu Gly Asp Phe His Arg
260 265 270

Asp Met Glu Ala Leu Asn Val Leu Pro Pro Asp Val Leu Thr Arg Val
275 280 285

Ser Glu Tyr Val Pro Glu Ile Val Asn Phe Val Gln Lys Ile Val Asp
290 295 300

Asn Gly Tyr Gly Tyr Val Ser Asn Gly Ser Val Tyr Phe Asp Thr Ala
305 310 315 320

Lys Phe Ala Ser Ser Glu Lys His Ser Tyr Gly Lys Leu Val Pro Glu
325 330 335

Ala Val Gly Asp Gln Lys Ala Leu Gln Glu Gly Glu Gly Asp Leu Ser
340 345 350

Ile Ser Ala Asp Arg Leu Ser Glu Lys Arg Ser Pro Asn Asp Phe Ala
355 360 365

Leu Trp Lys Ala Ser Lys Pro Gly Glu Pro Ser Trp Pro Cys Pro Trp
370 375 380

Gly Lys Gly Arg Pro Gly Trp His Ile Glu Cys Ser Ala Met Ala Gly
385 390 395 400

Thr Leu Leu Gly Ala Ser Met Asp Ile His Gly Gly Gly Phe Asp Leu
405 410 415

Arg Phe Pro His His Asp Asn Glu Leu Ala Xaa Ser Glu Ala Tyr Phe
420 425 430

Glu Asn Asp Cys Trp Val Arg Tyr Phe Leu His Thr Gly His Leu Thr
435 440 445

Ile Ala Gly Cys Lys Met Ser Lys Ser Leu Lys Asn Phe Ile Thr Ile
450 455 460

Lys Asp Ala Leu Lys Lys His Ser Ala Arg Gln Leu Arg Leu Ala Phe
465 470 475 480

Leu Met His Ser Trp Lys Asp Thr Leu Asp Tyr Ser Ser Asn Thr Met

485 490 495

Glu Ser Ala Leu Gln Tyr Glu Lys Phe Leu Asn Glu Phe Phe Leu Asn
500 505 510

Val Lys Asp Ile Leu Arg Ala Pro Val Asp Ile Thr Gly Gln Phe Glu
515 520 525

Lys Trp Gly Glu Glu Glu Ala Glu Leu Asn Lys Asn Phe Tyr Asp Lys
530 535 540

Lys Thr Ala Ile His Lys Ala Leu Cys Asp Asn Val Asp Thr Arg Thr
545 550 555 560

Val Met Glu Glu Met Arg Ala Leu Val Ser Gln Cys Asn Leu Tyr Met
565 570 575

Ala Ala Arg Lys Ala Val Arg Lys Arg Pro Asn Gln Ala Leu Leu Glu
580 585 590

Asn Ile Ala Leu Tyr Leu Thr His Met Leu Lys Ile Phe Gly Ala Val
595 600 605

Glu Glu Asp Ser Ser Leu Gly Phe Pro Val Gly Gly Pro Gly Thr Ser
610 615 620

Leu Ser Leu Glu Ala Thr Val Met Pro Tyr Leu Gln Val Leu
625 630 635

<210> 908
<211> 248
<212> PRT
<213> Homo sapiens

<400> 908
Ser His Pro Leu Arg Ser Arg Leu Pro Ser Ala Thr Gly Val Gly His
1 5 10 15

Ala Leu Ala Arg Ser Phe Cys Arg His Leu Gly Ser Ala Phe Pro Ala
20 25 30

Gln Asn Ala Arg Arg Ser Thr Glu Thr Val Pro Ala Thr Glu Gln Glu
35 40 45

Leu Pro Gln Pro Gln Ala Glu Thr Gly Ser Gly Thr Glu Ser Asp Ser
50 55 60

Asp Glu Ser Val Pro Glu Leu Glu Glu Gln Asp Ser Thr Gln Ala Thr
65 70 75 80

```
Thr Gln Gln Ala Gln Leu Ala Ala Ala Ala Glu Ile Asp Glu Glu Pro
                85                  90                  95

Val Ser Lys Ala Lys Gln Ser Arg Ser Glu Lys Lys Ala Arg Lys Ala
            100                 105                 110

Met Ser Lys Leu Gly Leu Arg Gln Val Thr Gly Val Thr Arg Val Thr
        115                 120                 125

Ile Arg Lys Ser Lys Asn Ile Leu Phe Val Ile Thr Lys Pro Asp Val
    130                 135                 140

Tyr Lys Ser Pro Ala Ser Asp Thr Tyr Ile Val Phe Gly Glu Ala Lys
145                 150                 155                 160

Ile Glu Asp Leu Ser Gln Gln Ala Gln Leu Ala Ala Ala Glu Lys Phe
                165                 170                 175

Lys Val Gln Gly Glu Ala Val Ser Asn Ile Gln Glu Asn Thr Gln Thr
            180                 185                 190

Pro Thr Val Gln Glu Glu Ser Glu Glu Glu Glu Val Asp Glu Thr Gly
        195                 200                 205

Val Glu Val Lys Asp Ile Glu Leu Val Met Ser Gln Ala Asn Val Ser
    210                 215                 220

Arg Ala Lys Ala Val Arg Ala Leu Lys Asn Asn Ser Asn Asp Ile Val
225                 230                 235                 240

Asn Ala Ile Met Glu Leu Thr Met
                245
```

<210> 909
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (46)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (158)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 909
Gln Gly Cys Cys Tyr Gly Ala Gly Arg Arg Val Ala Arg Leu Leu Ala
1   5   10   15

Pro Leu Met Trp Arg Arg Ala Val Ser Ser Val Ala Gly Ser Ala Val
            20   25   30

Gly Ala Glu Pro Gly Leu Arg Leu Leu Ala Val Gln Arg Xaa Pro Val
        35   40   45

Glu Gln Arg Ser Ala Gly Leu Ala Arg Pro Gln Thr Leu Ser Ala Ala
    50   55   60

Cys Thr Ala Lys Pro Gly Leu Glu Glu Arg Ala Glu Gly Thr Val Asn
65   70   75   80

Glu Gly Arg Pro Glu Ser Asp Ala Ala Asp His Thr Gly Pro Lys Phe
                85   90   95

Asp Ile Asp Met Met Val Ser Leu Leu Arg Gln Glu Asn Ala Arg Asp
            100   105   110

Ile Cys Val Ile Gln Val Pro Pro Glu Met Arg Tyr Thr Asp Tyr Phe
        115   120   125

Val Ile Val Ser Gly Thr Ser Thr Arg His Leu His Ala Met Ala Phe
    130   135   140

Tyr Val Val Lys Met Tyr Lys His Leu Lys Cys Lys Arg Xaa Pro Ser
145   150   155   160

Cys

<210> 910
<211> 487
<212> PRT
<213> Homo sapiens

<400> 910
Lys Ala Ala Ser Gly Pro Ala Thr Ser Ile Thr Gly Val Thr Met Gly
1   5   10   15

Ala Val Leu Gly Val Phe Ser Leu Ala Ser Trp Val Pro Cys Leu Cys
            20   25   30

Ser Gly Ala Ser Cys Leu Leu Cys Ser Cys Cys Pro Asn Ser Lys Asn
        35   40   45

```
Ser Thr Val Thr Arg Leu Ile Tyr Ala Phe Ile Leu Leu Leu Ser Thr
     50                  55                  60

Val Val Ser Tyr Ile Met Gln Arg Lys Glu Met Glu Thr Tyr Leu Lys
 65                  70                  75                  80

Lys Ile Pro Gly Phe Cys Glu Gly Gly Phe Lys Ile His Glu Ala Asp
                 85                  90                  95

Ile Asn Ala Asp Lys Asp Cys Asp Val Leu Val Gly Tyr Lys Ala Val
            100                 105                 110

Tyr Arg Ile Ser Phe Ala Met Ala Ile Phe Phe Phe Val Phe Ser Leu
        115                 120                 125

Leu Met Phe Lys Val Lys Thr Ser Lys Asp Leu Arg Ala Ala Val His
    130                 135                 140

Asn Gly Phe Trp Phe Phe Lys Ile Ala Ala Leu Ile Gly Ile Met Val
145                 150                 155                 160

Gly Ser Phe Tyr Ile Pro Gly Gly Tyr Phe Ser Ser Val Trp Phe Val
                165                 170                 175

Val Gly Met Ile Gly Ala Ala Leu Phe Ile Leu Ile Gln Leu Val Leu
            180                 185                 190

Leu Val Asp Phe Ala His Ser Trp Asn Glu Ser Trp Val Asn Arg Met
        195                 200                 205

Glu Glu Gly Asn Pro Arg Leu Trp Tyr Ala Ala Leu Leu Ser Phe Thr
    210                 215                 220

Ser Ala Phe Tyr Ile Leu Ser Ile Ile Cys Val Gly Leu Leu Tyr Thr
225                 230                 235                 240

Tyr Tyr Thr Lys Pro Asp Gly Cys Thr Glu Asn Lys Phe Phe Ile Ser
                245                 250                 255

Ile Asn Leu Ile Leu Cys Val Val Ala Ser Ile Ile Ser Ile His Pro
            260                 265                 270

Lys Ile Gln Glu His Gln Pro Arg Ser Gly Leu Leu Gln Ser Ser Leu
        275                 280                 285

Ile Thr Leu Tyr Thr Met Tyr Leu Thr Trp Ser Ala Met Ser Asn Glu
    290                 295                 300

Pro Asp Arg Ser Cys Asn Pro Asn Leu Met Ser Phe Ile Thr Arg Ile
305                 310                 315                 320
```

Thr Ala Pro Thr Leu Ala Pro Gly Asn Ser Thr Ala Val Val Pro Thr
325 330 335

Pro Thr Pro Pro Ser Lys Ser Gly Ser Leu Leu Asp Ser Asp Asn Phe
340 345 350

Ile Gly Leu Phe Val Phe Val Leu Cys Leu Leu Tyr Ser Ser Ile Arg
355 360 365

Thr Ser Thr Asn Ser Gln Val Asp Lys Leu Thr Leu Ser Gly Ser Asp
370 375 380

Ser Val Ile Leu Gly Asp Thr Thr Thr Ser Gly Ala Ser Asp Glu Glu
385 390 395 400

Asp Gly Gln Pro Arg Arg Ala Val Asp Asn Glu Lys Glu Gly Val Gln
405 410 415

Tyr Ser Tyr Ser Leu Phe His Leu Met Leu Cys Leu Ala Ser Leu Tyr
420 425 430

Ile Met Met Thr Leu Thr Ser Trp Tyr Ser Pro Asp Ala Lys Phe Gln
435 440 445

Ser Met Thr Ser Lys Trp Pro Ala Val Trp Val Lys Ile Ser Ser Ser
450 455 460

Trp Val Cys Leu Leu Leu Tyr Val Trp Thr Leu Val Ala Pro Leu Val
465 470 475 480

Leu Thr Ser Arg Asp Phe Ser
485

<210> 911
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (69)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 911
Asp Pro Arg Val Arg His Arg Gly Asn Lys Val Val Lys Lys Lys Val
1 5 10 15

Leu Val Arg Cys Arg His Phe Ile Cys Pro His Ser Leu Arg Leu Ser
20 25 30

Gln Ser Phe Gln Gln Arg Tyr Val Gly Pro Glu His Pro Glu Phe Thr
35 40 45

Thr Ser Val Val Arg Arg Ala Thr Met Arg Arg Ala Leu Gly Arg Ile
50 55 60

Cys His Phe Gln Xaa Val Arg Gly Thr Ala Ser Leu Gly Glu Gly Ala
65 70 75 80

Leu Gly Cys Asp Ser Arg Thr Cys Lys Ala Ala Ser Gly Leu Trp Arg
85 90 95

Gly Arg

<210> 912
<211> 206
<212> PRT
<213> Homo sapiens

<400> 912
Phe Ser Leu Phe Pro Leu Ala Lys Ser Phe Asp Asp Gly Asp Tyr Phe
1 5 10 15

Pro Val Trp Gly Thr Cys Leu Gly Phe Glu Glu Leu Ser Leu Leu Ile
20 25 30

Ser Gly Glu Cys Leu Leu Thr Ala Thr Asp Thr Val Asp Val Ala Met
35 40 45

Pro Leu Asn Phe Thr Gly Gly Gln Leu His Ser Arg Met Phe Gln Asn
50 55 60

Phe Pro Thr Glu Leu Leu Leu Ser Leu Ala Val Glu Pro Leu Thr Ala
65 70 75 80

Asn Phe His Lys Trp Ser Leu Ser Val Lys Asn Phe Thr Met Asn Glu
85 90 95

Lys Leu Lys Lys Phe Phe Asn Val Leu Thr Thr Asn Thr Asp Gly Lys
100 105 110

Ile Glu Phe Ile Ser Thr Met Glu Gly Tyr Lys Tyr Pro Val Tyr Gly
115 120 125

Val Gln Trp His Pro Glu Lys Ala Pro Tyr Glu Trp Lys Asn Leu Asp
130 135 140

Gly Ile Ser His Ala Pro Asn Ala Val Lys Thr Ala Phe Tyr Leu Ala
145 150 155 160

Glu Phe Phe Val Asn Glu Ala Arg Lys Asn Asn His His Phe Lys Ser
165 170 175

Glu Ser Glu Glu Glu Lys Ala Leu Ile Tyr Gln Phe Ser Pro Ile Tyr
180 185 190

Thr Gly Asn Ile Ser Ser Phe Gln Gln Cys Tyr Ile Phe Asp
195 200 205

<210> 913
<211> 91
<212> PRT
<213> Homo sapiens

<400> 913
Phe Ser Gly Pro Cys Pro Val Asn Thr Leu Gly Trp Glu Val Ser Ser
1 5 10 15

Phe Ser Pro Leu Leu Ser Ser Cys Leu Asn Met Val Arg Thr Lys Ala
20 25 30

Asp Ser Val Pro Gly Thr Tyr Arg Lys Val Val Ala Ala Arg Ala Pro
35 40 45

Arg Lys Val Leu Gly Ser Ser Thr Ser Ala Thr Asn Ser Thr Ser Val
50 55 60

Ser Ser Arg Lys Glu His Val Leu Cys Asn Leu Ile Thr Gln Met Met
65 70 75 80

Lys Lys Asn Arg Thr Phe Ser Phe Ile Phe Glu
85 90

<210> 914
<211> 178
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (132)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (147)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (154)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 914
Arg Glu Leu Ser Thr Arg Gln Arg Ser Gln Ala Lys Pro Pro Ala Ser
1 5 10 15

Met Ala Ser Glu Phe Lys Lys Lys Leu Phe Trp Arg Ala Val Val Ala
20 25 30

Glu Phe Leu Ala Thr Thr Leu Phe Val Phe Ile Ser Ile Gly Ser Ala
35 40 45

Leu Gly Phe Lys Tyr Pro Val Gly Asn Asn Gln Thr Ala Val Gln Asp
50 55 60

Asn Val Lys Val Ser Leu Ala Phe Gly Leu Ser Ile Ala Thr Leu Ala
65 70 75 80

Gln Ser Val Gly His Ile Ser Gly Ala His Leu Asn Pro Ala Val Thr
85 90 95

Leu Gly Leu Leu Leu Ser Cys Gln Ile Ser Ile Phe Arg Ala Leu Met
100 105 110

Tyr Ile Ile Ala Gln Cys Val Gly Ala Ile Val Ala Thr Ala Ile Leu
115 120 125

Ser Gly Ile Xaa Ser Ser Leu Thr Gly Asn Ser Leu Gly Arg Asn Asp
130 135 140

Leu Ala Xaa Gly Val Asn Phe Gly Pro Xaa Pro Gly His Arg Asp His
145 150 155 160

Arg Asp Pro Pro Ala Gly Ala Met Arg Ala Gly Tyr Tyr Arg Pro Glu
165 170 175

Ala Pro

<210> 915
<211> 377
<212> PRT

<213> Homo sapiens

<220>
<221> SITE
<222> (355)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 915
Val Cys Ala His Gly Gln Gly Leu Leu Arg Tyr Phe Tyr Ser Arg Arg
1   5   10   15

Ile Asp Ile Thr Leu Ser Ser Val Lys Cys Phe His Lys Leu Ala Ser
            20   25   30

Ala Tyr Gly Ala Arg Gln Leu Gln Gly Tyr Cys Ala Ser Leu Phe Ala
        35   40   45

Ile Leu Leu Pro Gln Asp Pro Ser Phe Gln Met Pro Leu Asp Leu Tyr
    50   55   60

Ala Tyr Ala Val Ala Thr Gly Asp Ala Leu Leu Glu Lys Leu Cys Leu
65   70   75   80

Gln Phe Leu Ala Trp Asn Phe Glu Ala Leu Thr Gln Ala Glu Ala Trp
                85   90   95

Pro Ser Val Pro Thr Asp Leu Leu Gln Leu Leu Leu Pro Arg Ser Asp
            100   105   110

Leu Ala Val Pro Ser Glu Leu Ala Leu Leu Lys Ala Val Asp Thr Trp
        115   120   125

Ser Trp Gly Glu Arg Ala Ser His Glu Glu Val Glu Gly Leu Val Glu
    130   135   140

Lys Ile Arg Phe Pro Met Met Leu Pro Glu Glu Leu Phe Glu Leu Gln
145   150   155   160

Phe Asn Leu Ser Leu Tyr Trp Ser His Glu Ala Leu Phe Gln Lys Lys
                165   170   175

Thr Leu Gln Ala Leu Glu Phe His Thr Val Pro Phe Gln Leu Leu Ala
            180   185   190

Arg Tyr Lys Gly Leu Asn Leu Thr Glu Asp Thr Tyr Lys Pro Arg Ile
        195   200   205

Tyr Thr Ser Pro Thr Trp Ser Ala Phe Val Thr Asp Ser Ser Trp Ser
    210   215   220

Ala Arg Lys Ser Gln Leu Val Tyr Gln Ser Arg Arg Gly Pro Leu Val

225 230 235 240

Lys Tyr Ser Ser Asp Tyr Phe Gln Ala Pro Ser Asp Tyr Arg Tyr Tyr
245 250 255

Pro Tyr Gln Ser Phe Gln Thr Pro Gln His Pro Ser Phe Leu Phe Gln
260 265 270

Asp Lys Arg Val Ser Trp Ser Leu Val Tyr Leu Pro Thr Ile Gln Ser
275 280 285

Cys Trp Asn Tyr Gly Phe Ser Cys Ser Ser Asp Glu Leu Pro Val Leu
290 295 300

Gly Leu Thr Lys Ser Gly Gly Ser Asp Arg Thr Ile Ala Tyr Glu Asn
305 310 315 320

Lys Ala Leu Met Leu Cys Glu Gly Leu Phe Val Ala Asp Val Thr Asp
325 330 335

Phe Glu Gly Trp Lys Ala Ala Ile Pro Ser Ala Leu Asp Thr Asn Ser
340 345 350

Ser Lys Xaa Thr Ser Ser Phe Pro Cys Pro Ala Gly Thr Ser Thr Ala
355 360 365

Ser Ala Arg Ser Ser Ala Pro Ser Thr
370 375

<210> 916
<211> 100
<212> PRT
<213> Homo sapiens

<400> 916
Arg Val Gln Arg Asp Thr Cys Leu Pro Pro Met Ser Leu Ser Phe His
1 5 10 15

Leu Pro Ser Arg Arg Met Lys Asn Pro Ser Ile Val Gly Val Leu Cys
20 25 30

Thr Asp Ser Gln Gly Leu Asn Leu Gly Cys Arg Gly Thr Leu Ser Asp
35 40 45

Glu His Ala Gly Val Ile Ser Val Leu Ala Gln Gln Ala Ala Lys Leu
50 55 60

Thr Ser Asp Pro Thr Asp Ile Pro Val Val Cys Leu Glu Ser Asp Asn
65 70 75 80

Gly Asn Ile Met Ile Gln Lys His Asp Gly Ile Thr Val Ala Val His
85 90 95

Lys Met Ala Ser
100

<210> 917
<211> 245
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (44)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (64)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (87)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (172)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (240)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (242)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 917
Leu Pro Pro Arg Ser Val Gly Gly Leu Gln Lys Met Arg Arg Lys Leu
1 5 10 15

Gly Leu Val Gln Val Glu Leu Glu Glu Asp Gly Ala Leu Val Ser Lys
20 25 30

Leu Leu Glu Thr Met His Leu Thr Gly Ala Asp Xaa Thr Asn Thr Phe
35 40 45

Tyr Leu Leu Ser Ser Phe Pro Val Glu Leu Glu Ser Pro Gly Leu Xaa
50 55 60

Glu Phe Leu Ala Arg Leu Met Glu Gln Cys Ala Ser Leu Glu Glu Leu
65 70 75 80

Arg Leu Ala Phe Arg Pro Xaa Met Asp Pro Arg Gln Leu Ser Met Met
85 90 95

Leu Met Leu Ala Gln Ser Asn Pro Gln Leu Phe Ala Leu Met Gly Thr
100 105 110

Arg Ala Gly Ile Ala Arg Glu Leu Glu Arg Val Glu Gln Gln Ser Arg
115 120 125

Leu Glu Gln Leu Ser Ala Ala Glu Leu Gln Ser Arg Asn Gln Gly His
130 135 140

Trp Ala Asp Trp Leu Gln Ala Tyr Arg Ala Arg Leu Asp Lys Asp Leu
145 150 155 160

Glu Gly Ala Gly Asp Ala Ala Ala Trp Gln Ala Xaa Ala Arg Ala Arg
165 170 175

Asp Ala Arg Gln Gln Pro Glu Val Arg Ala Glu Glu Leu His Ser Arg
180 185 190

Arg Met Pro Phe Glu Val Ala Glu Arg Gly Asp Phe Ser Glu Val Arg
195 200 205

Arg Val Leu Lys Leu Phe Glu Thr Leu Tyr His Cys Glu Ala Gly Ala
210 215 220

Ala Thr Arg Arg Pro Arg Pro Arg Glu Ala Asp Gly Gly Gly Arg Xaa
225 230 235 240

Gly Xaa Phe Leu Thr
245

<210> 918
<211> 44
<212> PRT
<213> Homo sapiens

<400> 918
Asn Ser Ala Arg Arg Ile Ser Leu Lys Glu Gly Glu Gly Lys Thr Asp

```
  1               5                   10                  15

Phe Leu Cys Gly Thr Lys Thr Lys Pro Ser Val Ser Leu Cys Glu Gln
            20                  25                  30

Arg Cys Lys Lys Glu Glu Thr Gln Phe Thr His Gly
        35                  40
```

<210> 919
<211> 160
<212> PRT
<213> Homo sapiens

<400> 919

```
Phe Gly Thr Arg Val Thr Ser Gly Gly Ser Arg Asp Ala Val Pro Gly
  1               5                   10                  15

Ala Glu Pro Pro Lys Met Ala Val Cys Ile Ala Val Ile Ala Lys Glu
            20                  25                  30

Asn Tyr Pro Leu Tyr Ile Arg Ser Thr Pro Thr Glu Asn Glu Leu Lys
        35                  40                  45

Phe His Tyr Met Val His Thr Ser Leu Asp Val Val Asp Glu Lys Ile
    50                  55                  60

Ser Ala Met Gly Lys Ala Leu Val Asp Gln Arg Glu Leu Tyr Leu Gly
 65                  70                  75                  80

Leu Leu Tyr Pro Thr Glu Asp Tyr Lys Val Tyr Gly Tyr Val Thr Asn
                 85                  90                  95

Ser Lys Val Lys Phe Val Met Val Val Asp Ser Ser Asn Thr Ala Leu
            100                 105                 110

Arg Asp Asn Glu Ile Arg Ser Met Phe Arg Lys Leu His Asn Ser Tyr
        115                 120                 125

Thr Asp Val Met Cys Asn Pro Phe Tyr Asn Pro Gly Asp Arg Ile Gln
    130                 135                 140

Ser Arg Ala Phe Asp Asn Met Val Thr Ser Met Met Ile Gln Val Cys
145                 150                 155                 160
```

<210> 920
<211> 40
<212> PRT
<213> Homo sapiens

<400> 920

```
Leu Ala Phe Phe Leu Thr Ser Glu Gly Glu Lys Lys Val Ala Thr Tyr
 1               5                  10                  15

Met Phe Glu Lys Pro Leu Lys Ser Thr Gln Ser Lys Asp Phe Met Leu
            20                  25                  30

Gln Phe Gly His Met Leu Arg Val
        35                  40
```

<210> 921
<211> 372
<212> PRT
<213> Homo sapiens

<400> 921

```
Leu Leu Gly Pro Ala Gly Gln Arg Ser His Ala Ala Pro Met Arg Pro
 1               5                  10                  15

Leu Pro Pro Val Gly Asp Val Arg Leu Glu Leu Ser Pro Pro Pro Pro
            20                  25                  30

Leu Leu Pro Val Pro Val Val Ser Gly Ser Pro Val Gly Ser Ser Gly
        35                  40                  45

Arg Leu Met Ala Ser Ser Ser Ser Leu Val Pro Asp Arg Leu Arg Leu
    50                  55                  60

Pro Leu Cys Phe Leu Gly Val Phe Val Cys Tyr Phe Tyr Tyr Gly Ile
65                  70                  75                  80

Leu Gln Glu Lys Ile Thr Arg Gly Lys Tyr Gly Glu Gly Ala Lys Gln
                85                  90                  95

Glu Thr Phe Thr Phe Ala Leu Thr Leu Val Phe Ile Gln Cys Val Ile
            100                 105                 110

Asn Ala Val Phe Ala Lys Ile Leu Ile Gln Phe Phe Asp Thr Ala Arg
        115                 120                 125

Val Asp Arg Thr Arg Ser Trp Leu Tyr Ala Ala Cys Ser Ile Ser Tyr
    130                 135                 140

Leu Gly Ala Met Val Ser Ser Asn Ser Ala Leu Gln Phe Val Asn Tyr
```

145 150 155 160

Pro Thr Gln Val Leu Gly Lys Ser Cys Lys Pro Ile Pro Val Met Leu
165 170 175

Leu Gly Val Thr Leu Leu Lys Lys Lys Tyr Pro Leu Ala Lys Tyr Leu
180 185 190

Cys Val Leu Leu Ile Val Ala Gly Val Ala Leu Phe Met Tyr Lys Pro
195 200 205

Lys Lys Val Val Gly Ile Glu Glu His Thr Val Gly Tyr Gly Glu Leu
210 215 220

Leu Leu Leu Leu Ser Leu Thr Leu Asp Gly Leu Thr Gly Val Ser Gln
225 230 235 240

Asp His Met Arg Ala His Tyr Gln Thr Gly Ser Asn His Met Met Leu
245 250 255

Asn Ile Asn Leu Trp Ser Thr Leu Leu Leu Gly Met Gly Ile Leu Phe
260 265 270

Thr Gly Glu Leu Trp Glu Phe Leu Ser Phe Ala Glu Arg Tyr Pro Ala
275 280 285

Ile Ile Tyr Asn Ile Leu Leu Phe Gly Leu Thr Ser Ala Leu Gly Gln
290 295 300

Ser Phe Ile Phe Met Thr Val Val Tyr Phe Gly Pro Leu Thr Cys Ser
305 310 315 320

Ile Ile Thr Thr Thr Arg Lys Phe Phe Thr Ile Leu Ala Ser Val Ile
325 330 335

Leu Phe Ala Asn Pro Ile Ser Pro Met Gln Trp Val Gly Thr Val Leu
340 345 350

Val Phe Leu Gly Leu Gly Leu Asp Ala Lys Phe Gly Lys Gly Ala Lys
355 360 365

Lys Thr Ser His
370

<210> 922
<211> 363
<212> PRT
<213> Homo sapiens

<400> 922

```
Pro Ala Arg Thr Met Phe Tyr Ala His Phe Val Leu Ser Lys Arg Gly
1               5                   10                  15

Pro Leu Ala Lys Ile Trp Leu Ala Ala His Trp Asp Lys Lys Leu Thr
            20                  25                  30

Lys Ala His Val Phe Glu Cys Asn Leu Glu Ser Ser Val Glu Ser Ile
        35                  40                  45

Ile Ser Pro Lys Val Lys Met Ala Leu Arg Thr Ser Gly His Leu Leu
    50                  55                  60

Leu Gly Val Val Arg Ile Tyr His Arg Lys Ala Lys Tyr Leu Leu Ala
65                  70                  75                  80

Asp Cys Asn Glu Ala Phe Ile Lys Ile Lys Met Ala Phe Arg Pro Gly
                85                  90                  95

Val Val Asp Leu Pro Glu Glu Asn Arg Glu Ala Ala Tyr Asn Ala Ile
            100                 105                 110

Thr Leu Pro Glu Glu Phe His Asp Phe Asp Gln Pro Leu Pro Asp Leu
        115                 120                 125

Asp Asp Ile Asp Val Ala Gln Gln Phe Ser Leu Asn Gln Ser Arg Val
    130                 135                 140

Glu Glu Ile Thr Met Arg Glu Glu Val Gly Asn Ile Ser Ile Leu Gln
145                 150                 155                 160

Glu Asn Asp Phe Gly Asp Phe Gly Met Asp Asp Arg Glu Ile Met Arg
                165                 170                 175

Glu Gly Ser Ala Phe Glu Asp Asp Asp Met Leu Val Ser Thr Thr Thr
            180                 185                 190

Ser Asn Leu Leu Leu Glu Ser Glu Gln Ser Thr Ser Asn Leu Asn Glu
        195                 200                 205

Lys Ile Asn His Leu Glu Tyr Glu Asp Gln Tyr Lys Asp Asp Asn Phe
    210                 215                 220

Gly Glu Gly Asn Asp Gly Gly Ile Leu Asp Asp Lys Leu Ile Ser Asn
225                 230                 235                 240

Asn Asp Gly Gly Ile Phe Asp Asp Pro Pro Ala Leu Ser Glu Ala Gly
                245                 250                 255

Val Met Leu Pro Glu Gln Pro Ala His Asp Asp Met Asp Glu Asp Asp
            260                 265                 270
```

Asn Val Ser Met Gly Gly Pro Asp Ser Pro Asp Ser Val Asp Pro Val
275 280 285

Glu Pro Met Pro Thr Met Thr Asp Gln Thr Thr Leu Val Pro Asn Glu
290 295 300

Glu Glu Ala Phe Ala Leu Glu Pro Ile Asp Ile Thr Val Lys Glu Thr
305 310 315 320

Lys Ala Lys Arg Lys Arg Lys Leu Ile Val Asp Ser Val Lys Glu Leu
325 330 335

Asp Ser Lys Thr Ile Arg Ala Gln Leu Ser Asp Tyr Ser Asp Ile Val
340 345 350

Thr Thr Leu Asp Leu Ala Pro Pro Pro Arg Asn
355 360

<210> 923
<211> 296
<212> PRT
<213> Homo sapiens

<400> 923
Val Ala Val Ile Trp Ala Tyr Trp Leu Gly Leu Lys Val Arg Arg Glu
1 5 10 15

Tyr Arg Lys Phe Phe Arg Ala Asn Ala Gly Lys Lys Ile Tyr Glu Phe
20 25 30

Thr Leu Gln Arg Ile Val Gln Lys Tyr Phe Leu Glu Met Lys Asn Lys
35 40 45

Met Pro Ser Leu Ser Pro Ile Asp Lys Asn Trp Pro Ser Arg Pro Tyr
50 55 60

Leu Phe Leu Asp Ser Thr His Lys Glu Leu Lys Arg Ile Phe His Leu
65 70 75 80

Trp Arg Cys Lys Lys Tyr Arg Asp Gln Phe Thr Asp Gln Gln Lys Leu
85 90 95

Ile Tyr Glu Glu Lys Leu Glu Ala Ser Glu Leu Phe Lys Asp Lys Lys
100 105 110

Ala Leu Tyr Pro Ser Ser Val Gly Gln Pro Phe Gln Gly Ala Tyr Leu
115 120 125

Glu Ile Asn Lys Asn Pro Lys Tyr Lys Lys Leu Lys Asp Ala Ile Glu
130 135 140

Glu Lys Ile Ile Ile Ala Glu Val Val Asn Lys Ile Asn Arg Ala Asn
145 150 155 160

Gly Lys Ser Thr Ser Arg Ile Phe Leu Leu Thr Asn Asn Asn Leu Leu
165 170 175

Leu Ala Asp Gln Lys Ser Gly Gln Ile Lys Ser Glu Val Pro Leu Val
180 185 190

Asp Val Thr Lys Val Ser Met Ser Ser Gln Asn Asp Gly Phe Phe Ala
195 200 205

Val His Leu Lys Glu Gly Ser Glu Ala Ala Ser Lys Gly Asp Phe Leu
210 215 220

Phe Ser Ser Asp His Leu Ile Glu Met Ala Thr Lys Leu Tyr Arg Thr
225 230 235 240

Thr Leu Ser Gln Thr Lys Gln Lys Leu Asn Ile Glu Ile Ser Asp Glu
245 250 255

Phe Leu Val Gln Phe Arg Gln Asp Lys Val Cys Val Lys Phe Ile Gln
260 265 270

Gly Asn Gln Lys Asn Gly Ser Val Pro Thr Cys Lys Arg Lys Asn Asn
275 280 285

Arg Leu Leu Glu Val Ala Val Pro
290 295

<210> 924
<211> 91
<212> PRT
<213> Homo sapiens

<400> 924
His Phe Ser Ile Asn Tyr Asn Gln Lys Ser Asp Leu Leu Lys Glu Lys
1 5 10 15

Ser Asp Cys Lys Ser Phe Gln Gly Gln Thr Ala Thr Glu Pro Pro Thr
20 25 30

Pro Lys Gln Glu Thr Leu Val Lys Val Gln Glu Ala Arg Arg Phe Ser
35 40 45

Pro Thr Lys Val Gln Leu Gly Asn Asp Ala Glu Arg Met Thr Thr Thr

50 55 60

Cys Asn Ser Arg Lys Met Leu Ala Ser Arg Val Arg Val Thr Ser Glu
65 70 75 80

Cys His Lys Ser Ser Leu Ser His Cys Leu Ile
85 90

<210> 925
<211> 159
<212> PRT
<213> Homo sapiens

<400> 925
Asn Ser Ala Arg Ala Gly Gly Arg Ala Val Leu Ser Gly Glu Pro Glu
1 5 10 15

Ala Asn Met Asp Gln Glu Thr Val Gly Asn Val Val Leu Leu Ala Ile
20 25 30

Val Thr Leu Ile Ser Val Val Gln Asn Gly Phe Phe Ala His Lys Val
35 40 45

Glu His Glu Ser Arg Thr Gln Asn Gly Arg Ser Phe Gln Arg Thr Gly
50 55 60

Thr Leu Ala Phe Glu Arg Val Tyr Thr Ala Asn Gln Asn Cys Val Asp
65 70 75 80

Ala Tyr Pro Thr Phe Leu Ala Val Leu Trp Ser Ala Gly Leu Leu Cys
85 90 95

Ser Gln Val Pro Ala Ala Phe Ala Gly Leu Met Tyr Leu Phe Val Arg
100 105 110

Gln Lys Tyr Phe Val Gly Tyr Leu Gly Glu Arg Thr Gln Ser Thr Pro
115 120 125

Gly Tyr Ile Phe Gly Glu Thr His His Thr Leu Pro Val Pro His Val
130 135 140

Arg Cys Trp His Ile Gln Leu Leu Pro His Leu Leu Phe Arg Lys
145 150 155

<210> 926
<211> 303
<212> PRT

<213> Homo sapiens

<400> 926

```
Gly Ser Leu Ala Ser Pro Pro Ser Leu Gly Ser Met Gly Glu Lys Ser
  1               5                  10                  15

Glu Asn Cys Gly Val Pro Glu Asp Leu Leu Asn Gly Leu Lys Val Thr
             20                  25                  30

Asp Thr Gln Glu Ala Glu Cys Ala Gly Pro Pro Val Pro Asp Pro Lys
         35                  40                  45

Asn Gln His Ser Gln Ser Lys Leu Leu Arg Asp Asp Glu Ala His Leu
     50                  55                  60

Gln Glu Asp Gln Gly Glu Glu Glu Cys Phe His Asp Cys Ser Ala Ser
 65                  70                  75                  80

Phe Glu Glu Glu Pro Gly Ala Asp Lys Val Glu Asn Lys Ser Asn Glu
                 85                  90                  95

Asp Val Asn Ser Ser Glu Leu Asp Glu Glu Tyr Leu Ile Glu Leu Glu
            100                 105                 110

Lys Asn Met Ser Asp Glu Glu Lys Gln Lys Arg Arg Glu Glu Ser Thr
        115                 120                 125

Arg Leu Lys Glu Glu Gly Asn Glu Gln Phe Lys Lys Gly Asp Tyr Ile
    130                 135                 140

Glu Ala Glu Ser Ser Tyr Ser Arg Ala Leu Glu Met Cys Pro Ser Cys
145                 150                 155                 160

Phe Gln Lys Glu Arg Ser Ile Leu Phe Ser Asn Arg Ala Ala Ala Arg
                165                 170                 175

Met Lys Gln Asp Lys Lys Glu Met Ala Ile Asn Asp Cys Ser Lys Ala
            180                 185                 190

Ile Gln Leu Asn Pro Ser Tyr Ile Arg Ala Ile Leu Arg Arg Ala Glu
        195                 200                 205

Leu Tyr Glu Lys Thr Asp Lys Leu Asp Glu Ala Leu Glu Asp Tyr Lys
    210                 215                 220

Ser Ile Leu Glu Lys Asp Pro Ser Ile His Gln Ala Arg Glu Ala Cys
225                 230                 235                 240

Met Arg Leu Pro Lys Gln Ile Glu Glu Arg Asn Glu Arg Leu Lys Glu
                245                 250                 255
```

Glu Met Leu Gly Lys Leu Lys Asp Leu Gly Asn Leu Val Leu Arg Pro
260 265 270

Phe Gly Leu Ser Thr Glu Asn Phe Gln Ile Lys Gln Asp Ser Ser Thr
275 280 285

Gly Ser Tyr Ser Ile Asn Phe Val Gln Asn Pro Asn Asn Asn Arg
290 295 300

<210> 927
<211> 329
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 927
Xaa Gly Gly Cys Cys Ser Gly Pro Gly His Ser Lys Arg Arg Arg Gln
1 5 10 15

Ala Pro Gly Val Gly Ala Val Gly Gly Gly Ser Pro Glu Arg Glu Glu
20 25 30

Val Gly Ala Gly Tyr Asn Ser Glu Asp Glu Tyr Glu Ala Ala Ala Ala
35 40 45

Arg Ile Glu Ala Met Asp Pro Ala Thr Val Glu Gln Gln Glu His Trp
50 55 60

Phe Glu Lys Ala Leu Arg Asp Lys Lys Gly Phe Ile Ile Lys Gln Met
65 70 75 80

Lys Glu Asp Gly Ala Cys Leu Phe Arg Ala Val Ala Asp Gln Val Tyr
85 90 95

Gly Asp Gln Asp Met His Glu Val Val Arg Lys His Cys Met Asp Tyr
100 105 110

Leu Met Lys Asn Ala Asp Tyr Phe Ser Asn Tyr Val Thr Glu Asp Phe
115 120 125

Thr Thr Tyr Ile Asn Arg Lys Arg Lys Asn Asn Cys His Gly Asn His
130 135 140

Ile Glu Met Gln Ala Met Ala Glu Met Tyr Asn Arg Pro Val Glu Val
145 150 155 160

```
Tyr Gln Tyr Ser Thr Glu Pro Ile Asn Thr Phe His Gly Ile His Gln
                165                 170                 175

Asn Glu Asp Glu Pro Ile Arg Val Ser Tyr His Arg Asn Ile His Tyr
            180                 185                 190

Asn Ser Val Val Asn Pro Asn Lys Ala Thr Ile Gly Val Gly Leu Gly
        195                 200                 205

Leu Pro Ser Phe Lys Pro Gly Phe Ala Glu Gln Ser Leu Met Lys Asn
    210                 215                 220

Ala Ile Lys Thr Ser Glu Glu Ser Trp Ile Glu Gln Gln Met Leu Glu
225                 230                 235                 240

Asp Lys Lys Arg Ala Thr Asp Trp Glu Ala Thr Asn Glu Ala Ile Glu
                245                 250                 255

Glu Gln Val Ala Arg Glu Ser Tyr Leu Gln Trp Leu Arg Asp Gln Glu
            260                 265                 270

Lys Gln Ala Arg Gln Val Arg Gly Pro Ser Gln Pro Arg Lys Ala Ser
        275                 280                 285

Ala Thr Cys Ser Ser Ala Thr Ala Ala Ala Ser Ser Gly Leu Glu Glu
    290                 295                 300

Trp Thr Ser Arg Ser Pro Arg Gln Glu Phe Gln Pro Arg His Leu Ser
305                 310                 315                 320

Thr Leu Ser Cys Met Leu Asn Trp Ala
                325
```

<210> 928
<211> 436
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (210)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (217)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (262)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 928
Lys Arg Phe Leu Arg Asn Phe Lys Leu Leu Thr Lys Arg Glu Phe Trp
1 5 10 15

Lys Glu Asn Gln Glu His Tyr His Ile Val Gln Lys Phe Leu Ile Leu
20 25 30

Gly Asp Ile Asp Gly Leu Met Asp Glu Phe Ser Lys Trp Leu Ser Lys
35 40 45

Ser Arg Asn Asn Leu Pro Gly His Leu Leu Arg Phe Met Thr His Leu
50 55 60

Ile Leu Phe Phe Arg Thr Leu Gly Leu Gln Thr Lys Glu Glu Val Ser
65 70 75 80

Ile Glu Val Leu Lys Thr Tyr Ile Gln Leu Leu Ile Arg Glu Lys His
85 90 95

Thr Asn Leu Ile Ala Phe Tyr Thr Cys His Leu Pro Gln Asp Leu Ala
100 105 110

Val Ala Gln Tyr Ala Leu Phe Leu Glu Ser Val Thr Glu Phe Glu Gln
115 120 125

Arg His His Cys Leu Glu Leu Ala Lys Glu Ala Asp Leu Asp Val Ala
130 135 140

Thr Ile Thr Lys Thr Val Val Glu Asn Ile Arg Lys Lys Asp Asn Gly
145 150 155 160

Glu Phe Ser His His Asp Leu Ala Pro Ala Leu Asp Thr Gly Thr Thr
165 170 175

Glu Glu Asp Arg Leu Lys Ile Asp Val Ile Asp Trp Leu Val Phe Asp
180 185 190

Pro Ala Gln Arg Ala Glu Ala Leu Lys Gln Gly Asn Ala Ile Met Arg
195 200 205

Lys Xaa Leu Ala Ser Lys Lys His Xaa Ala Ala Lys Glu Val Phe Val
210 215 220

Lys Ile Pro Gln Asp Ser Ile Ala Glu Ile Tyr Asn Gln Cys Glu Glu
225 230 235 240

```
Gln Gly Met Glu Ser Pro Leu Pro Ala Glu Asp Asp Asn Ala Ile Arg
                245                 250                 255

Glu His Leu Cys Ile Xaa Ala Tyr Leu Glu Ala His Glu Thr Phe Asn
            260                 265                 270

Glu Trp Phe Lys His Met Asn Ser Val Pro Gln Lys Pro Ala Leu Ile
        275                 280                 285

Pro Gln Pro Thr Phe Thr Glu Lys Val Ala His Glu His Lys Glu Lys
    290                 295                 300

Lys Tyr Glu Met Asp Phe Gly Ile Trp Lys Gly His Leu Asp Ala Leu
305                 310                 315                 320

Thr Ala Asp Val Lys Glu Lys Met Tyr Asn Val Leu Leu Phe Val Asp
                325                 330                 335

Gly Gly Trp Met Val Asp Val Arg Glu Asp Ala Lys Glu Asp His Glu
            340                 345                 350

Arg Thr His Gln Met Val Leu Leu Arg Lys Leu Cys Leu Pro Met Leu
        355                 360                 365

Cys Phe Leu Leu His Thr Ile Leu His Ser Thr Gly Gln Tyr Gln Glu
    370                 375                 380

Cys Leu Gln Leu Ala Asp Met Val Ser Ser Glu Arg His Lys Leu Tyr
385                 390                 395                 400

Leu Val Phe Ser Lys Glu Glu Leu Arg Lys Leu Leu Gln Lys Leu Arg
                405                 410                 415

Glu Ser Ser Leu Met Leu Leu Asp Gln Gly Leu Asp Pro Leu Gly Tyr
            420                 425                 430

Glu Ile Gln Leu
        435
```

<210> 929
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (159)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 929

Asp Ala Asp Val Gln Phe Leu Ala Ser Val Leu Pro Pro Asp Thr Asp
1 5 10 15

Pro Ala Phe Phe Glu His Leu Arg Ala Leu Asp Cys Ser Glu Val Thr
20 25 30

Val Arg Ala Leu Pro Glu Gly Ser Leu Ala Phe Pro Gly Val Pro Leu
35 40 45

Leu Gln Val Ser Gly Pro Leu Leu Val Val Gln Leu Leu Glu Thr Pro
50 55 60

Leu Leu Cys Leu Val Ser Tyr Ala Ser Leu Val Ala Thr Asn Ala Ala
65 70 75 80

Arg Leu Arg Leu Ile Ala Gly Pro Glu Lys Arg Leu Leu Glu Met Gly
85 90 95

Leu Arg Arg Ala Gln Gly Pro Asp Gly Gly Leu Thr Ala Ser Thr Tyr
100 105 110

Ser Tyr Leu Gly Gly Phe Asp Ser Ser Ser Asn Val Leu Ala Gly Gln
115 120 125

Leu Arg Gly Val Pro Val Ala Gly Thr Leu Ala His Ser Phe Val Thr
130 135 140

Ser Phe Ser Gly Ser Glu Val Pro Leu Thr Arg Cys Trp Gly Xaa Ser
145 150 155 160

Leu

<210> 930
<211> 741
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

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<220>
<221> SITE
<222> (282)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 930
Leu Met Lys Ile Glu Ala Asn Xaa Asp His Met Gly Phe His Phe Thr
  1               5                  10                  15

Thr Gly Xaa Pro Ala Pro Ser Thr Glu Thr Glu Leu Asp Val Leu Leu
             20                  25                  30

Pro Thr Ala Thr Ser Leu Pro Ile Pro Arg Lys Ser Ala Thr Val Ile
         35                  40                  45

Pro Glu Ile Glu Gly Ile Lys Ala Glu Ala Lys Ala Leu Asp Asp Met
     50                  55                  60

Phe Glu Ser Ser Thr Leu Ser Asp Gly Gln Ala Ile Ala Asp Gln Ser
 65                  70                  75                  80

Glu Ile Ile Pro Thr Leu Gly Gln Phe Glu Arg Thr Gln Glu Glu Tyr
                 85                  90                  95

Glu Asp Lys Lys His Ala Gly Pro Ser Phe Gln Pro Glu Phe Ser Ser
            100                 105                 110

Gly Ala Glu Glu Ala Leu Val Asp His Thr Pro Tyr Leu Ser Ile Ala
        115                 120                 125

Thr Thr His Leu Met Asp Gln Ser Val Thr Glu Val Pro Asp Val Met
    130                 135                 140

Glu Gly Ser Asn Pro Pro Tyr Tyr Thr Asp Thr Thr Leu Ala Val Ser
145                 150                 155                 160

Thr Phe Ala Lys Leu Ser Ser Gln Thr Pro Ser Ser Pro Leu Thr Ile
                165                 170                 175

Tyr Ser Gly Ser Glu Ala Ser Gly His Thr Glu Ile Pro Gln Pro Ser
            180                 185                 190

Ala Leu Pro Gly Ile Asp Val Gly Ser Ser Val Met Ser Pro Gln Asp
        195                 200                 205

Ser Phe Lys Glu Ile His Val Asn Ile Glu Ala Thr Phe Lys Pro Ser
    210                 215                 220

Ser Glu Glu Tyr Leu His Ile Thr Glu Pro Pro Ser Leu Ser Pro Asp
225                 230                 235                 240
```

Thr Lys Leu Glu Pro Ser Glu Asp Asp Gly Lys Pro Glu Leu Leu Glu
245 250 255

Glu Met Glu Ala Ser Pro Thr Glu Leu Ile Ala Val Glu Gly Thr Glu
260 265 270

Ile Leu Gln Asp Phe Gln Asn Lys Thr Xaa Gly Gln Val Ser Gly Glu
275 280 285

Ala Ile Lys Met Phe Pro Thr Ile Lys Thr Pro Glu Ala Gly Thr Val
290 295 300

Ile Thr Thr Ala Asp Glu Ile Glu Leu Glu Gly Ala Thr Gln Trp Pro
305 310 315 320

His Ser Thr Ser Ala Ser Ala Thr Tyr Gly Val Glu Ala Gly Val Val
325 330 335

Pro Trp Leu Ser Pro Gln Thr Ser Glu Arg Pro Thr Leu Ser Ser Ser
340 345 350

Pro Glu Ile Asn Pro Glu Thr Gln Ala Ala Leu Ile Arg Gly Gln Asp
355 360 365

Ser Thr Ile Ala Ala Ser Glu Gln Gln Val Ala Ala Arg Ile Leu Asp
370 375 380

Ser Asn Asp Gln Ala Thr Val Asn Pro Val Glu Phe Asn Thr Glu Val
385 390 395 400

Ala Thr Pro Pro Phe Ser Leu Leu Glu Thr Ser Asn Glu Thr Asp Phe
405 410 415

Leu Ile Gly Ile Asn Glu Glu Ser Val Glu Gly Thr Ala Ile Tyr Leu
420 425 430

Pro Gly Pro Asp Arg Cys Lys Met Asn Pro Cys Leu Asn Gly Gly Thr
435 440 445

Cys Tyr Pro Thr Glu Thr Ser Tyr Val Cys Thr Cys Val Pro Gly Tyr
450 455 460

Ser Gly Asp Gln Cys Glu Leu Asp Phe Asp Glu Cys His Ser Asn Pro
465 470 475 480

Cys Arg Asn Gly Ala Thr Cys Val Asp Gly Phe Asn Thr Phe Arg Cys
485 490 495

Leu Cys Leu Pro Ser Tyr Val Gly Ala Leu Cys Glu Gln Asp Thr Glu
500 505 510

```
Thr Cys Asp Tyr Gly Trp His Lys Phe Gln Gly Gln Cys Tyr Lys Tyr
        515                 520                 525

Phe Ala His Arg Arg Thr Trp Asp Ala Ala Glu Arg Glu Cys Arg Leu
    530                 535                 540

Gln Gly Ala His Leu Thr Ser Ile Leu Ser His Glu Glu Gln Met Phe
545                 550                 555                 560

Val Asn Arg Val Gly His Asp Tyr Gln Trp Ile Gly Leu Asn Asp Lys
                565                 570                 575

Met Phe Glu His Asp Phe Arg Trp Thr Asp Gly Ser Thr Leu Gln Tyr
            580                 585                 590

Glu Asn Trp Arg Pro Asn Gln Pro Asp Ser Phe Phe Ser Ala Gly Glu
        595                 600                 605

Asp Cys Val Val Ile Ile Trp His Glu Asn Gly Gln Trp Asn Asp Val
    610                 615                 620

Pro Cys Asn Tyr His Leu Thr Tyr Thr Cys Lys Lys Gly Thr Val Ala
625                 630                 635                 640

Cys Gly Gln Pro Pro Val Val Glu Asn Ala Lys Thr Phe Gly Lys Met
                645                 650                 655

Lys Pro Arg Tyr Glu Ile Asn Ser Leu Ile Arg Tyr His Cys Lys Asp
            660                 665                 670

Gly Phe Ile Gln Arg His Leu Pro Thr Ile Arg Cys Leu Gly Asn Gly
        675                 680                 685

Arg Trp Ala Ile Pro Lys Ile Thr Cys Met Asn Pro Ser Ala Tyr Gln
    690                 695                 700

Arg Thr Tyr Ser Met Lys Tyr Phe Lys Asn Ser Ser Ser Ala Lys Asp
705                 710                 715                 720

Asn Ser Ile Asn Thr Ser Lys His Asp His Arg Trp Ser Arg Arg Trp
                725                 730                 735

Gln Glu Ser Arg Arg
            740
```

<210> 931
<211> 209
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (28)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 931
Gly Lys Ala Gly Asp Gln Leu Val Pro Asp Asn Leu Lys Glu Thr Asp
1   5   10   15

Lys Glu Lys Gly Asn Val Val Leu Lys Gly Glu Xaa Ser Ala Arg Met
            20   25   30

Lys Ile Pro Ser Asn Met Trp Val Glu Ala Trp Glu Thr Ala Lys Pro
        35   40   45

Ile Pro Ala Arg Arg Gln Arg Arg Leu Phe Asp Asp Thr Arg Glu Ala
    50   55   60

Glu Lys Val Leu His Tyr Leu Ala Ile Gln Lys Pro Ala Asp Leu Ala
65   70   75   80

Arg His Leu Leu Pro Cys Val Ile His Ala Ala Val Leu Lys Val Lys
                85   90   95

Glu Glu Glu Ser Leu Glu Asn Ile Ser Ser Val Lys Lys Ile Ile Lys
            100   105   110

Gln Ile Ile Ser His Ser Ser Lys Val Leu His Phe Pro Asn Pro Glu
        115   120   125

Asp Lys Lys Leu Glu Glu Ile Ile His Gln Ile Thr Asn Val Glu Ala
    130   135   140

Leu Ile Ala Arg Ala Arg Ser Leu Lys Ala Lys Phe Gly Thr Glu Lys
145   150   155   160

Cys Glu Gln Glu Glu Glu Lys Glu Asp Leu Glu Arg Phe Val Ser Cys
                165   170   175

Leu Leu Glu Gln Pro Glu Val Leu Val Thr Gly Ala Gly Arg Gly His
            180   185   190

Ala Gly Arg Ile Ile His Lys Leu Phe Val Asn Ala Gln Arg Cys Gln
        195   200   205

Leu

<210> 932
<211> 57
<212> PRT
<213> Homo sapiens

<400> 932
Leu Leu Glu Val Pro Glu Met Gly Leu Thr Phe Ile Lys Gln Ile Ala
1 5 10 15

Tyr Tyr Asp Leu Ala Ala Ala Thr Val Gln Leu His Ile Asn Ser Thr
20 25 30

Asp Gln Thr Ile Cys Ile Trp His His Leu Leu Thr His Asp Met Arg
35 40 45

Leu Phe Cys Ile Asn Cys Tyr Asp Gly
50 55

<210> 933
<211> 125
<212> PRT
<213> Homo sapiens

<400> 933
Ile Lys Glu Glu Ser Asp Tyr His Asp Leu Glu Ser Val Val Gln Gln
1 5 10 15

Val Glu Gln Asn Leu Glu Leu Met Thr Lys Arg Ala Val Lys Ala Glu
20 25 30

Asn His Val Val Lys Leu Lys Gln Glu Ile Ser Leu Leu Gln Ala Gln
35 40 45

Val Ser Asn Phe Gln Arg Glu Asn Glu Ala Leu Arg Cys Gly Gln Gly
50 55 60

Ala Ser Leu Thr Val Val Lys Gln Asn Ala Asp Val Ala Leu Gln Asn
65 70 75 80

Leu Arg Val Val Met Asn Ser Ala Gln Ala Ser Ile Lys Gln Leu Val
85 90 95

Ser Gly Ala Glu Thr Leu Asn Leu Val Ala Glu Ile Leu Lys Ser Ile
100 105 110

Asp Arg Ile Ser Glu Val Lys Asp Glu Glu Glu Asp Ser
115 120 125

<210> 934
<211> 306
<212> PRT
<213> Homo sapiens

<400> 934
Pro Thr Phe Ser Arg Ala Val Ala Thr Met Phe Ser Arg Ala Gly Val
1   5   10   15

Ala Gly Leu Ser Ala Trp Thr Leu Gln Pro Gln Trp Ile Gln Val Arg
            20   25   30

Asn Met Ala Thr Leu Lys Asp Ile Thr Arg Arg Leu Lys Ser Ile Lys
        35   40   45

Asn Ile Gln Lys Ile Thr Lys Ser Met Lys Met Val Ala Ala Ala Lys
    50   55   60

Tyr Ala Arg Ala Glu Arg Glu Leu Lys Pro Ala Arg Ile Tyr Gly Leu
65   70   75   80

Gly Ser Leu Ala Leu Tyr Glu Lys Ala Asp Ile Lys Gly Pro Glu Asp
                85   90   95

Lys Lys Lys His Leu Leu Ile Gly Val Ser Ser Asp Arg Gly Leu Cys
            100   105   110

Gly Ala Ile His Ser Ser Ile Ala Lys Gln Met Lys Ser Glu Val Ala
        115   120   125

Thr Leu Thr Ala Ala Gly Lys Glu Val Met Leu Val Gly Ile Gly Asp
    130   135   140

Lys Ile Arg Gly Ile Leu Tyr Arg Thr His Ser Asp Gln Phe Leu Val
145   150   155   160

Ala Phe Lys Glu Val Gly Arg Lys Pro Pro Thr Phe Gly Asp Ala Ser
                165   170   175

Val Ile Ala Leu Glu Leu Leu Asn Ser Gly Tyr Glu Phe Asp Glu Gly
            180   185   190

Ser Ile Ile Phe Asn Lys Phe Arg Ser Val Ile Ser Tyr Lys Thr Glu
        195   200   205

Glu Lys Pro Ile Phe Ser Leu Asn Thr Val Ala Ser Ala Asp Ser Met
    210   215   220

Ser Ile Tyr Asp Asp Ile Asp Ala Asp Val Leu Gln Asn Tyr Gln Glu
225   230   235   240

Tyr Asn Leu Ala Asn Ile Ile Tyr Tyr Ser Leu Lys Glu Ser Thr Thr
245 250 255

Ser Glu Gln Ser Ala Arg Met Thr Ala Met Asp Asn Ala Ser Lys Asn
260 265 270

Ala Ser Glu Met Ile Asp Lys Leu Thr Leu Thr Phe Asn Arg Thr Arg
275 280 285

Gln Ala Val Ile Thr Lys Glu Leu Ile Glu Ile Ile Ser Gly Ala Ala
290 295 300

Ala Leu
305

<210> 935
<211> 135
<212> PRT
<213> Homo sapiens

<400> 935
Gly Ala Leu Cys Ala Ala Ser Val Pro Arg Cys Val Trp Ser Ser Ala
1 5 10 15

Gly Val Val Ala Leu Phe Glu Glu His Cys Ala Pro Leu Val Trp Val
20 25 30

Tyr Thr Tyr Glu Cys Cys His Tyr Met Cys Ser Ala Leu Leu Ser Leu
35 40 45

Ser Cys Pro Cys Pro Ala Pro Ser Glu Arg Ala Ala Gly Leu Cys Cys
50 55 60

Arg Leu Val Val Pro Cys His Lys Gly Met Pro Arg Leu Thr Asp Leu
65 70 75 80

Ser Val Lys Thr Lys Asp Val Trp Glu Ile Pro Arg Glu Ser Leu Gln
85 90 95

Leu Ile Lys Arg Leu Gly Asn Gly Gln Phe Gly Glu Val Trp Met Gly
100 105 110

Met Leu Arg Leu Asn Tyr Ser Leu Ile Ser Phe Pro Val Trp Lys Ile
115 120 125

Pro Asn Thr Lys Asp Gly Arg
130 135

<210> 936
<211> 284
<212> PRT
<213> Homo sapiens

<400> 936
Leu Ser Gly Thr Thr Tyr Ala Arg Ala Cys Arg Ser Gln Cys Ala Ser
1   5   10   15

Ala Ala Gly Gly Cys Thr Gly Gly Ala Gly Gly Gly Gly Gly Gly Gly
            20   25   30

Gly Gly Trp Gly Gly Ala Gly Gly Lys Cys Cys Asp Ala Val Pro Gly
        35   40   45

Arg Gly Arg Arg Val Glu Ala Glu Tyr Gln Phe Pro Ser Gly Lys Ala
    50   55   60

Ala Met Ala Ile Phe Ser Val Tyr Val Val Asn Lys Ala Gly Gly Leu
65   70   75   80

Ile Tyr Gln Leu Asp Ser Tyr Ala Pro Arg Ala Glu Ala Glu Lys Thr
                85   90   95

Phe Ser Tyr Pro Leu Asp Leu Leu Leu Lys Leu His Asp Glu Arg Val
            100   105   110

Leu Val Ala Phe Gly Gln Arg Asp Gly Ile Arg Val Gly His Ala Val
        115   120   125

Leu Ala Ile Asn Gly Met Asp Val Asn Gly Arg Tyr Thr Ala Asp Gly
    130   135   140

Lys Glu Val Leu Glu Tyr Leu Gly Asn Pro Ala Asn Tyr Pro Val Ser
145   150   155   160

Ile Arg Phe Gly Arg Pro Arg Leu Thr Ser Asn Glu Lys Leu Met Leu
                165   170   175

Ala Ser Met Phe His Ser Leu Phe Ala Ile Gly Ser Gln Leu Ser Pro
            180   185   190

Glu Gln Gly Ser Ser Gly Ile Glu Met Leu Glu Thr Asp Thr Phe Lys
        195   200   205

Leu His Cys Tyr Gln Thr Leu Thr Gly Ile Lys Phe Val Val Leu Ala
    210   215   220

Asp Pro Arg Gln Ala Gly Ile Asp Ser Leu Leu Arg Lys Ile Tyr Glu

225 230 235 240

Ile Tyr Ser Asp Phe Ala Leu Lys Asn Pro Phe Tyr Ser Leu Glu Met
245 250 255

Pro Ile Arg Cys Glu Leu Phe Asp Gln Asn Leu Lys Leu Ala Leu Glu
260 265 270

Val Ala Glu Lys Ala Gly Thr Phe Gly Pro Gly Ser
275 280

<210> 937
<211> 338
<212> PRT
<213> Homo sapiens

<400> 937
Pro Val Ser Pro Leu His Arg Glu Glu Gly Asp Lys Trp Gly Glu Val
1 5 10 15

Trp Cys Gln Met Gly Trp Arg Arg Lys Arg Val Pro Gln Arg Gly Arg
20 25 30

Lys Ala Pro Pro Pro Gln Leu His Gly Asn Ile Asn Asn Leu Tyr Phe
35 40 45

Pro Ile Arg Trp Arg Asp Arg Leu His Trp Asp Ser Pro Asn Pro Ala
50 55 60

Ala Glu Cys Gln Arg Pro Arg Ser Thr Leu Val Ser Arg Lys Pro Gly
65 70 75 80

Pro Gly Arg Ile Thr Trp Asp Glu Leu Ala Ala Ser Gly Leu Pro Ser
85 90 95

Cys Asp Ala Ala Val Asn Leu Ala Gly Glu Asn Ile Leu Asn Pro Leu
100 105 110

Arg Arg Trp Asn Glu Thr Phe Gln Lys Glu Val Leu Gly Ser Arg Leu
115 120 125

Glu Thr Thr Gln Leu Leu Ala Lys Ala Ile Thr Lys Ala Pro Gln Pro
130 135 140

Pro Lys Ala Trp Val Leu Val Thr Gly Val Ala Tyr Tyr Gln Pro Ser
145 150 155 160

Leu Thr Ala Glu Tyr Asp Glu Asp Ser Pro Gly Gly Asp Phe Asp Phe
165 170 175

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Phe Ser Asn Leu Val Thr Lys Trp Glu Ala Ala Ala Arg Leu Pro Gly
            180                 185                 190

Asp Ser Thr Arg Gln Val Val Val Arg Ser Gly Val Val Leu Gly Arg
        195                 200                 205

Gly Gly Gly Ala Met Gly His Met Leu Leu Pro Phe Arg Leu Gly Leu
    210                 215                 220

Gly Gly Pro Ile Gly Ser Gly His Gln Phe Phe Pro Trp Ile His Ile
225                 230                 235                 240

Gly Asp Leu Ala Gly Ile Leu Thr His Ala Leu Glu Ala Asn His Val
                245                 250                 255

His Gly Val Leu Asn Gly Val Ala Pro Ser Ser Ala Thr Asn Ala Glu
            260                 265                 270

Phe Ala Gln Thr Phe Gly Ala Ala Leu Gly Arg Arg Ala Phe Ile Pro
        275                 280                 285

Leu Pro Ser Ala Val Val Gln Ala Val Phe Gly Arg Gln Arg Ala Ile
    290                 295                 300

Met Leu Leu Glu Gly Gln Lys Val Ile Pro Arg Arg Thr Leu Ala Thr
305                 310                 315                 320

Gly Tyr Gln Tyr Ser Phe Pro Glu Leu Gly Ala Ala Leu Lys Glu Ile
                325                 330                 335

Val Ala
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<210> 938
<211> 321
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (31)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (164)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (220)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (221)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (238)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (263)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (267)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (268)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 938
Cys Gln Glu Trp Val Pro Asp Arg Glu Ser Tyr Val Ser His Met Lys
1   5   10   15

Lys Ser His Gly Arg Thr Leu Lys Arg Tyr Pro Cys Arg Gln Xaa Glu
            20   25   30

Gln Ser Phe His Thr Pro Asn Ser Leu Arg Lys His Ile Arg Asn Asn
        35   40   45

His Asp Thr Val Lys Lys Phe Tyr Thr Cys Gly Tyr Cys Thr Glu Asp
    50   55   60

Ser Pro Ser Phe Pro Arg Pro Ser Leu Leu Glu Ser His Ile Ser Leu
65   70   75   80

Met His Gly Ile Arg Asn Pro Asp Leu Ser Gln Thr Ser Lys Val Lys
                85   90   95

Pro Pro Gly Gly His Ser Pro Gln Val Asn His Leu Lys Arg Pro Val
            100   105   110

Ser Gly Val Gly Asp Ala Pro Gly Thr Ser Asn Gly Ala Thr Val Ser
115 120 125

Ser Thr Lys Arg His Lys Ser Leu Phe Gln Cys Ala Lys Cys Ser Phe
130 135 140

Ala Thr Asp Ser Gly Leu Glu Phe Gln Ser His Ile Pro Gln His Gln
145 150 155 160

Val Gly Gln Xaa His Ser Pro Met Ser Pro Leu Trp Phe Val Leu His
165 170 175

Leu Cys Gln Leu Pro Gln Pro Pro Pro Leu His Cys Pro Gln Gly Glu
180 185 190

Arg Pro Gly Gly Gly Gly Gly Arg Gly Gly Gly Gly Thr Glu Met Ala
195 200 205

Val Glu Val Ala Glu Gln Arg Arg Ala Pro Gly Xaa Xaa Cys Pro Trp
210 215 220

Arg Leu Glu Arg Met Asp Trp Lys Asn Val Pro Val Ser Xaa Cys Gln
225 230 235 240

Leu Thr Gln Arg Arg Gly Asp Cys Trp Ala Arg Pro Leu Arg Thr Met
245 250 255

Val Ala Thr Met Ile Thr Xaa Asn His Arg Xaa Xaa Arg Thr Arg Thr
260 265 270

Ala Thr His Cys Pro Leu Arg Cys Asp Arg Arg Leu Cys Ser Val His
275 280 285

Gly Gln Gly Trp Cys Arg Ser Val Phe His Leu Pro Cys Gly Pro Trp
290 295 300

Lys Ile Lys Gly Ser Ala Pro Ser Val Ser Val Thr Gly Cys Thr Leu
305 310 315 320

Glu

<210> 939
<211> 151
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (44)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (71)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (81)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 939
Ala Ala Ser Xaa Gly Glu Gln Arg Glu Arg Ala Arg Leu Gln Thr Pro
1 5 10 15

Thr Arg Pro His Ser Thr Ser Ala Arg Pro Arg Arg Arg Gln Val Gln
20 25 30

Leu Leu Gln Leu Cys Gly Cys Ala Ala Lys Gly Xaa Ala His Gly Leu
35 40 45

Asp Val Thr Ser Pro Thr Val Ser Trp Leu Ala Cys Pro Cys Ala Arg
50 55 60

Pro Ser Xaa Ser Arg Gln Xaa Leu Gly Thr Ser Glu Glu Glu Pro Gly
65 70 75 80

Xaa Asn Gly Lys Gly Gly Ile Gly Val His His Ser Leu Leu Leu Trp
85 90 95

Ser Ser Thr Gly Gly Thr Xaa Met Glu Val Ser Cys Leu Thr Ser Leu
100 105 110

His Cys Thr Gly Pro Gly Met Pro Ile His Pro Leu Ala Glu Asp Thr
        115   120   125

His Gln Val Ile Cys Glu Glu Thr Leu Gly Ser His His Leu Lys Ala
    130   135   140

Arg Gly Ser Pro Ser His Arg
145   150

<210> 940
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 940
Arg Cys Gly Trp Ser Ser Arg Ser Arg Arg Ser Arg Cys Ala Arg Arg
  1   5   10   15

Cys Pro Pro Ser Pro Cys Pro Thr Pro Arg His Val Pro Ser Ser Arg
             20   25   30

His Pro Glu Val Cys Gly Leu Arg Thr Asn Ser His Arg Cys Leu Phe
         35   40   45

Arg Pro Gln Leu Gln Ala Met Pro Ala Ala Gly Gly Val Leu Tyr Gln
     50   55   60

Pro Ser Gly Pro Ala Ser Phe Pro Ser Thr Phe Ser Pro Ala Gly Ser
 65   70   75   80

Val Glu Gly Ser Pro Met His Gly Val Tyr Met Ser Gln Pro Val Pro
                 85   90   95

Ala Ala Gly Pro Tyr Pro Xaa
            100

<210> 941
<211> 136
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (123)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 941
Thr Ala Gly Arg Ser Asp Val Leu Pro Val Ala Gly Gly Glu Val Arg
1 5 10 15

Ala Leu Gln Glu Gly Gly Cys Gly Asp Lys Met Lys Ile Phe Val Gly
20 25 30

Asn Val Asp Gly Ala Asp Thr Thr Pro Glu Glu Leu Ala Ala Leu Phe
35 40 45

Ala Pro Tyr Gly Thr Val Met Ser Cys Ala Val Met Lys Gln Phe Ala
50 55 60

Phe Val His Met Arg Glu Asn Ala Gly Ala Leu Arg Ala Ile Glu Ala
65 70 75 80

Leu His Gly His Glu Leu Arg Pro Gly Arg Ala Leu Val Val Glu Met
85 90 95

Ser Arg Pro Arg Pro Leu Asn Thr Trp Lys Ile Phe Val Gly Asn Val
100 105 110

Ser Ala Ala Cys Thr Ser Gln Glu Leu Arg Xaa Ser Ser Ser Ala Ala
115 120 125

Asp Ala Ser Ser Ser Val Thr Trp
130 135

<210> 942
<211> 61
<212> PRT
<213> Homo sapiens

<400> 942
Ile Met Lys Glu Ser Ser Ser Val Leu Ala Lys Cys Ser Ser Ile Ala
1 5 10 15

Gly Tyr Ile Gln Trp Ser Ser Ile Asn Ser Tyr Leu Ser Gly Leu Asn
20 25 30

Gln Asn Cys Val Ser Leu Asn Ser Tyr His Thr Glu Gly Ala Ser Gln
35 40 45

Ile Thr Ile Phe Leu Ser Ala Val Phe Leu Gln Lys Ser
50 55 60

<210> 943
<211> 580
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (52)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (73)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 943
```
Gly Ala Gln Ala Gln Ala Ser Ala Arg Pro Leu Gln Ala Phe Gly Ala
  1               5                  10                  15

Arg Ala Arg Leu Gly Tyr Gly Pro Gly Arg Arg Arg Pro Pro Ser Ala
             20                  25                  30

Arg Cys Leu Ser Gly Thr Ala Asn Arg Arg Glu Arg Arg Arg Val Gly
         35                  40                  45

Leu Ser Ala Xaa Leu Gly Ala Gly Ala His Ala Arg Ala Pro Pro Gln
     50                  55                  60

Ala Gly Ala Met Ala Ser Gly Ser Xaa Ala Glu Cys Leu Gln Gln Glu
 65                  70                  75                  80

Thr Thr Cys Pro Val Cys Leu Gln Tyr Phe Ala Glu Pro Met Met Leu
                 85                  90                  95

Asp Cys Gly His Asn Ile Cys Cys Ala Cys Leu Ala Arg Cys Trp Gly
            100                 105                 110

Thr Ala Glu Thr Asn Val Ser Cys Pro Gln Cys Arg Glu Thr Phe Pro
        115                 120                 125

Gln Arg His Met Arg Pro Asn Arg His Leu Ala Asn Val Thr Gln Leu
    130                 135                 140

Val Lys Gln Leu Arg Thr Glu Arg Pro Ser Gly Pro Gly Gly Glu Met
145                 150                 155                 160

Gly Val Cys Glu Lys His Arg Glu Pro Leu Lys Leu Tyr Cys Glu Glu
                165                 170                 175
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Asp Gln Met Pro Ile Cys Val Val Cys Asp Arg Ser Arg Glu His Arg
            180                 185                 190

Gly His Ser Val Leu Pro Leu Glu Glu Ala Val Glu Gly Phe Lys Glu
        195                 200                 205

Gln Ile Gln Asn Gln Leu Asp His Leu Lys Arg Val Lys Asp Leu Lys
    210                 215                 220

Lys Arg Arg Arg Ala Gln Gly Glu Gln Ala Arg Ala Glu Leu Leu Ser
225                 230                 235                 240

Leu Thr Gln Met Glu Arg Glu Lys Ile Val Trp Glu Phe Glu Gln Leu
                245                 250                 255

Tyr His Ser Leu Lys Glu His Glu Tyr Arg Leu Leu Ala Arg Leu Glu
            260                 265                 270

Glu Leu Asp Leu Ala Ile Tyr Asn Ser Ile Asn Gly Ala Ile Thr Gln
        275                 280                 285

Phe Ser Cys Asn Ile Ser His Leu Ser Ser Leu Ile Ala Gln Leu Glu
    290                 295                 300

Glu Lys Gln Gln Gln Pro Thr Arg Glu Leu Leu Gln Asp Ile Gly Asp
305                 310                 315                 320

Thr Leu Ser Arg Ala Glu Arg Ile Arg Ile Pro Glu Pro Trp Ile Thr
                325                 330                 335

Pro Pro Asp Leu Gln Glu Lys Ile His Ile Phe Ala Gln Lys Cys Leu
            340                 345                 350

Phe Leu Thr Glu Ser Leu Lys Gln Phe Thr Glu Lys Met Gln Ser Asp
        355                 360                 365

Met Glu Lys Ile Gln Glu Leu Arg Glu Ala Gln Leu Tyr Ser Val Asp
    370                 375                 380

Val Thr Leu Asp Pro Asp Thr Ala Tyr Pro Ser Leu Ile Leu Ser Asp
385                 390                 395                 400

Asn Leu Arg Gln Val Arg Tyr Ser Tyr Leu Gln Gln Asp Leu Pro Asp
                405                 410                 415

Asn Pro Glu Arg Phe Asn Leu Phe Pro Cys Val Leu Gly Ser Pro Cys
            420                 425                 430

Phe Ile Ala Gly Arg His Tyr Trp Glu Val Glu Val Gly Asp Lys Ala
        435                 440                 445
```

Lys Trp Thr Ile Gly Val Cys Glu Asp Ser Val Cys Arg Lys Gly Gly
450 455 460

Val Thr Ser Ala Pro Gln Asn Gly Phe Trp Ala Val Ser Leu Trp Tyr
465 470 475 480

Gly Lys Glu Tyr Trp Ala Leu Thr Ser Pro Met Thr Ala Leu Pro Leu
485 490 495

Arg Thr Pro Leu Gln Arg Val Gly Ile Phe Leu Asp Tyr Asp Ala Gly
500 505 510

Glu Val Ser Phe Tyr Asn Val Thr Glu Arg Cys His Thr Phe Thr Phe
515 520 525

Ser His Ala Thr Phe Cys Gly Pro Val Arg Pro Tyr Phe Ser Leu Ser
530 535 540

Tyr Ser Gly Gly Lys Ser Ala Ala Pro Leu Ile Ile Cys Pro Met Ser
545 550 555 560

Gly Ile Asp Gly Phe Ser Gly His Val Gly Asn His Gly His Ser Met
565 570 575

Glu Thr Ser Pro
580

<210> 944
<211> 437
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (68)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (166)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (317)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 944

Ser Ala Thr Gly Ser Gly Glu Lys Glu Cys Gly Val Thr Ala Thr Phe
1 5 10 15

Asp Ala Ser Arg Thr Thr Phe Thr Arg Glu Gly Ser Phe Arg Val Thr
20 25 30

Thr Ala Thr Glu Gln Ala Glu Arg Glu Glu Ile Met Lys Gln Met Gln
35 40 45

Asp Ala Lys Lys Ala Glu Thr Asp Lys Ile Val Val Gly Ser Ser Val
50 55 60

Ala Pro Gly Xaa Thr Ala Pro Ser Pro Ser Ser Pro Thr Ser Pro Thr
65 70 75 80

Ser Asp Ala Thr Thr Ser Leu Glu Met Asn Asn Pro His Ala Ile Pro
85 90 95

Arg Arg His Ala Pro Ile Glu Gln Leu Ala Arg Gln Gly Ser Phe Arg
100 105 110

Gly Phe Pro Ala Leu Ser Gln Lys Met Ser Pro Phe Lys Arg Gln Leu
115 120 125

Ser Leu Arg Ile Asn Glu Leu Pro Ser Thr Met Gln Arg Lys Thr Asp
130 135 140

Phe Pro Ile Lys Asn Ala Val Pro Glu Val Glu Gly Glu Ala Glu Ser
145 150 155 160

Ile Ser Ser Leu Cys Xaa Gln Ile Thr Asn Ala Phe Ser Thr Pro Glu
165 170 175

Asp Pro Phe Ser Ser Ala Pro Met Thr Lys Pro Val Thr Val Val Ala
180 185 190

Pro Gln Ser Pro Thr Phe Gln Gly Thr Glu Trp Gly Gln Ser Ser Gly
195 200 205

Ala Ala Ser Pro Gly Leu Phe Gln Ala Gly His Arg Arg Thr Pro Ser
210 215 220

Glu Ala Asp Arg Trp Leu Glu Glu Val Ser Lys Ser Val Arg Ala Gln
225 230 235 240

Gln Pro Gln Ala Ser Ala Ala Pro Leu Gln Pro Val Leu Gln Pro Pro
245 250 255

Pro Pro Thr Ala Ile Ser Gln Pro Ala Ser Pro Phe Gln Gly Asn Ala
260 265 270

Phe Leu Thr Ser Gln Pro Val Pro Val Gly Val Val Pro Ala Leu Gln
275 280 285

Pro Ala Phe Val Pro Ala Gln Ser Tyr Pro Val Ala Asn Gly Met Pro
290 295 300

Tyr Pro Ala Pro Asn Val Pro Val Val Gly Ile Thr Xaa Ser Gln Met
305 310 315 320

Val Ala Asn Val Phe Gly Thr Ala Gly His Pro Gln Ala Ala His Pro
325 330 335

His Gln Ser Pro Ser Leu Val Arg Gln Gln Thr Phe Pro His Tyr Glu
340 345 350

Ala Ser Ser Ala Thr Thr Ser Pro Phe Phe Lys Pro Pro Ala Gln His
355 360 365

Leu Asn Gly Ser Ala Ala Phe Asn Gly Val Asp Asp Gly Arg Leu Ala
370 375 380

Ser Ala Asp Arg His Thr Glu Val Pro Thr Gly Thr Cys Pro Val Asp
385 390 395 400

Pro Phe Glu Ala Gln Trp Ala Ala Leu Glu Asn Lys Ser Lys Gln Arg
405 410 415

Thr Asn Pro Ser Pro Thr Asn Pro Phe Ser Ser Asp Leu Gln Lys Thr
420 425 430

Phe Glu Ile Glu Leu
435

<210> 945
<211> 160
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (119)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 945
His Gly Ser Met Arg Arg Leu Leu Ile Pro Leu Ala Leu Trp Leu Gly
1 5 10 15

Ala Val Gly Val Gly Val Ala Glu Leu Thr Glu Ala Gln Arg Arg Gly
20 25 30

```
Leu Gln Val Ala Leu Glu Glu Phe His Lys His Pro Pro Val Gln Trp
        35                  40                  45

Ala Phe Gln Glu Thr Ser Val Glu Ser Ala Val Asp Thr Pro Phe Pro
    50                  55                  60

Ala Gly Ile Phe Val Arg Leu Glu Phe Lys Leu Gln Gln Thr Ser Cys
65                  70                  75                  80

Arg Lys Arg Asp Trp Lys Lys Pro Glu Cys Lys Val Arg Pro Asn Gly
                85                  90                  95

Arg Lys Arg Lys Cys Leu Ala Cys Ile Lys Leu Gly Ser Glu Asp Lys
            100                 105                 110

Val Leu Gly Arg Leu Val Xaa Cys Pro Ile Glu Thr Gln Val Leu Arg
        115                 120                 125

Glu Thr Gln Cys Leu Arg Val Gln Arg Ala Gly Glu Asp Pro His Ser
    130                 135                 140

Phe Tyr Phe Pro Gly Gln Phe Ala Phe Ser Lys Ala Leu Pro Arg Ser
145                 150                 155                 160



<210> 946
<211> 221
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (198)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 946
Gly Gly Asp Pro Pro Gly Asp Leu Ser Ser Leu Ser Ser Lys Leu Leu
  1               5                  10                  15

Pro Gly Phe Thr Thr Leu Gly Phe Lys Asp Glu Arg Arg Asn Lys Val
            20                  25                  30

Thr Phe Leu Ser Ser Ala Thr Thr Ala Leu Ser Met Gln Asn Asn Ser
        35                  40                  45

Val Phe Gly Asp Leu Lys Ser Asp Glu Met Glu Leu Leu Tyr Ser Ala
```

50 55 60

Tyr Gly Asp Glu Thr Gly Val Gln Cys Ala Leu Ser Leu Gln Glu Phe
65 70 75 80

Val Lys Asp Ala Gly Ser Tyr Ser Lys Lys Val Val Asp Asp Leu Leu
85 90 95

Asp Gln Ile Thr Gly Gly Asp His Ser Arg Thr Leu Phe Gln Leu Lys
100 105 110

Gln Arg Arg Asn Val Pro Met Lys Pro Pro Asp Glu Ala Lys Val Gly
115 120 125

Asp Thr Leu Gly Asp Ser Ser Ser Ser Val Leu Glu Phe Met Ser Met
130 135 140

Lys Ser Tyr Pro Asp Val Ser Val Asp Ile Ser Met Leu Ser Ser Leu
145 150 155 160

Gly Lys Val Lys Lys Glu Leu Asp Pro Asp Asp Ser His Leu Asn Leu
165 170 175

Asp Glu Thr Thr Lys Leu Leu Gln Asp Leu His Glu Ala Gln Ala Asp
180 185 190

Ala Ala Ala Leu Gly Xaa Arg Pro Thr Ser Ala Pro Cys Pro Thr Pro
195 200 205

Pro Arg Gly Thr Ser Thr Thr Trp Glu Ala Leu Leu Ala
210 215 220

<210> 947
<211> 316
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (293)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (312)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 947
Glu Gln Tyr Val Cys Ala Gln Arg Asp Glu Tyr Leu Glu Ser Phe Cys

```
1               5                   10                  15
Lys Met Ala Thr Arg Lys Ile Ser Val Ile Thr Ile Phe Gly Pro Val
            20                  25                  30
Asn Asn Ser Thr Met Lys Ile Asp His Phe Gln Leu Asp Asn Glu Lys
        35                  40                  45
Pro Met Arg Val Val Asp Asp Glu Asp Leu Val Asp Gln Arg Leu Ile
    50                  55                  60
Ser Glu Leu Arg Lys Glu Tyr Gly Met Thr Tyr Asn Asp Phe Phe Met
65                  70                  75                      80
Val Leu Thr Asp Val Asp Leu Arg Val Lys Gln Tyr Tyr Glu Val Pro
                85                  90                  95
Ile Thr Met Lys Ser Val Phe Asp Leu Ile Asp Thr Phe Gln Ser Arg
            100                 105                 110
Ile Lys Asp Met Glu Lys Gln Lys Lys Glu Gly Ile Val Cys Lys Glu
        115                 120                 125
Asp Lys Lys Gln Ser Leu Glu Asn Phe Leu Ser Arg Phe Arg Trp Arg
    130                 135                 140
Arg Arg Leu Leu Val Ile Ser Ala Pro Asn Asp Glu Asp Trp Ala Tyr
145                 150                 155                 160
Ser Gln Gln Leu Ser Ala Leu Ser Gly Gln Ala Cys Asn Phe Gly Leu
                165                 170                 175
Arg His Ile Thr Ile Leu Lys Leu Leu Gly Val Gly Glu Glu Val Gly
            180                 185                 190
Gly Val Leu Glu Leu Phe Pro Ile Asn Gly Ser Ser Val Val Glu Arg
        195                 200                 205
Glu Asp Val Pro Ala His Leu Val Lys Asp Ile Arg Asn Tyr Phe Gln
    210                 215                 220
Val Ser Pro Glu Tyr Phe Ser Met Leu Leu Val Gly Lys Asp Gly Asn
225                 230                 235                 240
Val Lys Ser Trp Tyr Pro Ser Pro Met Trp Ser Met Val Ile Val Tyr
                245                 250                 255
Asp Leu Ile Asp Ser Met Gln Leu Arg Arg Gln Glu Met Ala Ile Gln
            260                 265                 270
Gln Ser Leu Gly Met Arg Cys Pro Glu Asp Glu Tyr Ala Gly Tyr Gly
```

275 280 285

Tyr His Ser Tyr Xaa Gln Gly Tyr Gln Asp Gly Tyr Gln Asp Asp Tyr
290 295 300

Arg His His Glu Ser Tyr His Xaa Gly Tyr Pro Tyr
305 310 315

<210> 948
<211> 162
<212> PRT
<213> Homo sapiens

<400> 948
Ser Thr His Ala Ser Ala His Ala Ser Gly Lys Gln Cys Gln Asp Ser
1 5 10 15

Lys Asp Ser Asn His Leu Pro Lys Met Ser Leu Ser Ala Phe Thr Leu
20 25 30

Phe Leu Ala Leu Ile Gly Gly Thr Ser Gly Gln Tyr Tyr Asp Tyr Asp
35 40 45

Phe Pro Leu Ser Ile Tyr Gly Gln Ser Ser Pro Asn Cys Ala Pro Glu
50 55 60

Cys Asn Cys Pro Glu Ser Tyr Pro Ser Ala Met Tyr Cys Asp Glu Leu
65 70 75 80

Lys Leu Lys Ser Val Pro Met Val Pro Pro Gly Ile Lys Tyr Leu Tyr
85 90 95

Leu Arg Asn Asn Gln Ile Asp His Ile Asp Glu Lys Ala Phe Glu Asn
100 105 110

Val Thr Asp Leu Gln Trp Leu Ile Leu Asp His Asn Leu Leu Glu Asn
115 120 125

Ser Lys Ile Lys Gly Arg Val Phe Ser Lys Leu Lys Gln Leu Lys Lys
130 135 140

Leu His Ile Asn His Asn Asn Leu Thr Glu Ser Val Gly Pro Leu Pro
145 150 155 160

Lys Ser

<210> 949
<211> 185
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (114)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 949
```
Leu Gly Phe Asn Tyr Tyr Tyr Lys Tyr Ser Asn Glu Gly Asp Ser His
 1               5                  10                  15

Leu Gly Gly Gly Ser Arg Glu Gly Ser Phe Lys Glu Thr Ile Thr Leu
            20                  25                  30

Lys Trp Cys Thr Pro Arg Thr Asn Asn Ile Glu Leu His Tyr Cys Thr
        35                  40                  45

Gly Ala Tyr Arg Ile Ser Pro Val Asp Val Asn Ser Arg Pro Ser Ser
    50                  55                  60

Cys Leu Thr Asn Phe Leu Leu Asn Gly Arg Ser Val Leu Leu Glu Gln
65                  70                  75                  80

Pro Arg Lys Ser Gly Ser Lys Val Ile Ser His Met Leu Ser Ser His
                85                  90                  95

Gly Gly Glu Ile Phe Leu His Val Leu Ser Ser Ser Arg Ser Ile Leu
            100                 105                 110

Glu Xaa Pro Pro Ser Ile Ser Glu Gly Cys Gly Gly Arg Val Thr Asp
        115                 120                 125

Tyr Arg Ile Thr Asp Phe Gly Glu Phe Met Arg Glu Asn Arg Leu Thr
    130                 135                 140

Pro Phe Leu Asp Pro Arg Tyr Lys Ile Asp Gly Ser Leu Glu Val Pro
145                 150                 155                 160

Leu Glu Arg Ala Lys Asp Gln Leu Glu Lys His Thr Arg Tyr Trp Pro
                165                 170                 175

Met Asp His Phe Thr Asn His His Phe
            180                 185
```

<210> 950
<211> 169

<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (161)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 950
Pro Arg Arg Pro His Arg Ser Cys Asp Met Pro Ala Ser Gly Glu Pro
1   5   10   15

Leu Gly Cys Thr Pro Leu Leu Pro Asn Asp Ser Gly His Pro Ser Glu
            20   25   30

Leu Gly Gly Thr Arg Arg Ala Gly Asn Gly Ala Leu Gly Gly Pro Lys
        35   40   45

Ala His Arg Lys Leu Gln Thr His Pro Ser Leu Ala Ser Gln Gly Ser
    50   55   60

Lys Lys Ser Lys Ser Ser Ser Lys Ser Thr Thr Ser Gln Ile Pro Leu
65   70   75   80

Gln Ala Gln Glu Asp Cys Cys Val His Cys Ile Leu Ser Cys Leu Phe
                85   90   95

Cys Glu Phe Leu Thr Leu Cys Asn Ile Val Leu Asp Cys Ala Thr Cys
            100   105   110

Gly Ser Cys Ser Ser Glu Asp Ser Cys Leu Cys Cys Cys Cys Cys Gly
        115   120   125

Ser Gly Glu Cys Ala Asp Cys Asp Leu Pro Cys Asp Leu Asp Cys Gly
    130   135   140

Ile Leu Asp Ala Cys Cys Glu Ser Ala Asp Cys Leu Glu Ile Cys Met
145   150   155   160

Xaa Cys Cys Gly Leu Cys Phe Ser Ser
                165

<210> 951
<211> 288
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (161)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (234)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 951
Met Ser Asp Glu Thr Gly Arg Val Pro Glu Arg Asp Thr Lys Arg Met
1   5   10   15

Gln Val Cys Leu Leu Ser Ala Met Pro Leu Pro Val Ala Leu Gln Thr
            20   25   30

Arg Leu Ala Lys Arg Gly Ile Leu Lys His Leu Glu Pro Glu Pro Glu
        35   40   45

Glu Glu Ile Ile Ala Glu Asp Tyr Asp Asp Asp Pro Val Asp Tyr Glu
    50   55   60

Ala Thr Arg Leu Glu Gly Leu Pro Pro Ser Trp Tyr Lys Val Phe Asp
65   70   75   80

Pro Ser Cys Gly Leu Pro Tyr Tyr Trp Asn Ala Asp Thr Asp Leu Val
                85   90   95

Ser Trp Leu Ser Pro His Asp Pro Asn Ser Val Val Thr Lys Ser Ala
            100   105   110

Lys Lys Leu Arg Ser Ser Asn Ala Asp Ala Glu Glu Lys Leu Asp Arg
        115   120   125

Ser His Asp Lys Ser Asp Arg Gly His Asp Lys Ser Asp Arg Ser His
    130   135   140

Glu Lys Leu Asp Arg Gly His Asp Lys Ser Asp Arg Gly His Asp Lys
145   150   155   160

Xaa Asp Arg Asp Arg Glu Arg Gly Tyr Asp Lys Val Asp Arg Glu Arg
                165   170   175

Glu Arg Asp Arg Glu Arg Asp Arg Asp Arg Gly Tyr Asp Lys Ala Asp
            180   185   190

Arg Glu Glu Gly Lys Glu Arg Arg His His Arg Arg Glu Glu Leu Ala
        195   200   205

Pro Tyr Pro Lys Ser Lys Lys Ala Val Ser Arg Lys Asp Glu Glu Leu
    210   215   220

Asp Pro Met Asp Pro Ser Ser Tyr Ser Xaa Arg Pro Arg Gly Thr Trp
225 230 235 240

Ser Thr Gly Leu Pro Lys Arg Asn Glu Ala Lys Thr Gly Ala Asp Thr
245 250 255

Thr Ala Ala Gly Pro Leu Phe Gln Gln Arg Pro Tyr Pro Ser Pro Gly
260 265 270

Ala Val Leu Arg Ala Asn Ala Glu Ala Ser Arg Thr Lys Gln Gln Asp
275 280 285

<210> 952
<211> 323
<212> PRT
<213> Homo sapiens

<400> 952
Val Gly Gly Val Leu Pro Gly Trp Lys Leu Arg Pro Arg Ser Asp Gly
1 5 10 15

Gly Leu Ser Glu Asp Gly Pro Gly Arg Asp His Gly Gly Gly Ser Arg
20 25 30

Gly Gly Arg Gly Gly Ala Ala Gly Gly Arg Gly Gly Cys Gly Pro Gln
35 40 45

Gly Ala Val Gly Gly Gly Met Ala Arg Ala Ser Ser Gly Asn Gly Ser
50 55 60

Glu Glu Ala Trp Gly Ala Leu Arg Ala Pro Gln Gln Gln Leu Arg Glu
65 70 75 80

Leu Cys Pro Gly Val Asn Asn Gln Pro Tyr Leu Cys Glu Ser Gly His
85 90 95

Cys Cys Gly Glu Thr Gly Cys Cys Thr Tyr Tyr Tyr Glu Leu Trp Trp
100 105 110

Phe Trp Leu Leu Trp Thr Val Leu Ile Leu Phe Ser Cys Cys Cys Ala
115 120 125

Phe Arg His Arg Arg Ala Lys Leu Arg Leu Gln Gln Gln Gln Arg Gln
130 135 140

Arg Glu Ile Asn Leu Leu Ala Tyr His Gly Ala Cys His Gly Ala Gly

145 150 155 160

Pro Phe Pro Thr Gly Ser Leu Leu Asp Leu Arg Phe Leu Ser Thr Phe
165 170 175

Lys Pro Pro Ala Tyr Glu Asp Val Val His Arg Pro Gly Thr Pro Pro
180 185 190

Pro Pro Tyr Thr Val Ala Pro Gly Arg Pro Leu Thr Ala Ser Ser Glu
195 200 205

Gln Thr Cys Cys Ser Ser Ser Ser Ser Cys Pro Ala His Phe Glu Gly
210 215 220

Thr Asn Val Glu Gly Val Ser Ser His Gln Ser Ala Pro Pro His Gln
225 230 235 240

Glu Gly Glu Pro Gly Ala Gly Val Thr Pro Ala Ser Thr Pro Pro Ser
245 250 255

Cys Arg Tyr Arg Arg Leu Thr Gly Asp Ser Gly Ile Glu Leu Cys Pro
260 265 270

Cys Pro Ala Ser Gly Glu Gly Glu Pro Val Lys Glu Val Arg Val Ser
275 280 285

Ala Thr Leu Pro Asp Leu Glu Asp Tyr Ser Pro Cys Ala Leu Pro Pro
290 295 300

Glu Ser Val Pro Gln Ile Phe Pro Met Gly Leu Ser Ser Ser Glu Gly
305 310 315 320

Asp Ile Pro

<210> 953
<211> 433
<212> PRT
<213> Homo sapiens

<400> 953
Ala Lys Met Ser Val Asn Val Asn Arg Ser Val Ser Asp Gln Phe Tyr
1 5 10 15

Arg Tyr Lys Met Pro Arg Leu Ile Ala Lys Val Glu Gly Lys Gly Asn
20 25 30

Gly Ile Lys Thr Val Ile Val Asn Met Val Asp Val Ala Lys Ala Leu
35 40 45

Asn Arg Pro Pro Thr Tyr Pro Thr Lys Tyr Phe Gly Cys Glu Leu Gly
50 55 60

Ala Gln Thr Gln Phe Asp Val Lys Asn Asp Arg Tyr Ile Val Asn Gly
65 70 75 80

Ser His Glu Ala Asn Lys Leu Gln Asp Met Leu Asp Gly Phe Ile Lys
85 90 95

Lys Phe Val Leu Cys Pro Glu Cys Glu Asn Pro Glu Thr Asp Leu His
100 105 110

Val Asn Pro Lys Lys Gln Thr Ile Gly Asn Ser Cys Lys Ala Cys Gly
115 120 125

Tyr Arg Gly Met Leu Asp Thr His His Lys Leu Cys Thr Phe Ile Leu
130 135 140

Lys Asn Pro Pro Glu Asn Ser Asp Ser Gly Thr Gly Lys Lys Glu Lys
145 150 155 160

Glu Lys Lys Asn Arg Lys Gly Lys Asp Lys Glu Asn Gly Ser Val Ser
165 170 175

Ser Ser Glu Thr Pro Pro Pro Pro Pro Pro Pro Asn Glu Ile Asn Pro
180 185 190

Pro Pro His Thr Met Glu Glu Glu Glu Asp Asp Asp Trp Gly Glu Asp
195 200 205

Thr Thr Glu Glu Ala Gln Arg Arg Arg Met Asp Glu Ile Ser Asp His
210 215 220

Ala Lys Val Leu Thr Leu Ser Asp Asp Leu Glu Arg Thr Ile Glu Glu
225 230 235 240

Arg Val Asn Ile Leu Phe Asp Phe Val Lys Lys Lys Lys Glu Glu Gly
245 250 255

Val Ile Asp Ser Ser Asp Lys Glu Ile Val Ala Glu Ala Glu Arg Leu
260 265 270

Asp Val Lys Ala Met Gly Pro Leu Val Leu Thr Glu Val Leu Phe Asn
275 280 285

Glu Lys Ile Arg Glu Gln Ile Lys Lys Tyr Arg Arg His Phe Leu Arg
290 295 300

Phe Cys His Asn Asn Lys Lys Ala Gln Arg Tyr Leu Leu His Gly Leu
305 310 315 320

Glu Cys Val Val Ala Met His Gln Ala Gln Leu Ile Ser Lys Ile Pro
325 330 335

His Ile Leu Lys Glu Met Tyr Asp Ala Asp Leu Leu Glu Glu Glu Val
340 345 350

Ile Ile Ser Trp Ser Glu Lys Ala Ser Lys Lys Tyr Val Ser Lys Glu
355 360 365

Leu Ala Lys Glu Ile Arg Val Lys Ala Glu Pro Phe Ile Lys Trp Leu
370 375 380

Lys Glu Ala Glu Glu Glu Ser Ser Gly Gly Glu Glu Glu Asp Glu Asp
385 390 395 400

Glu Asn Ile Glu Val Val Tyr Ser Lys Ala Ala Ser Val Pro Lys Val
405 410 415

Glu Thr Val Lys Ser Asp Asn Lys Asp Asp Asp Ile Asp Ile Asp Ala
420 425 430

Ile

<210> 954
<211> 428
<212> PRT
<213> Homo sapiens

<400> 954
Gly Tyr Gln Ile Gly Met Ala Leu Ala Ser Gly Pro Ala Arg Arg Ala
1 5 10 15

Leu Ala Gly Ser Gly Gln Leu Gly Leu Gly Gly Phe Gly Ala Pro Arg
20 25 30

Arg Gly Ala Tyr Glu Trp Gly Val Arg Ser Thr Arg Lys Ser Glu Pro
35 40 45

Pro Pro Leu Asp Arg Val Tyr Glu Ile Pro Gly Leu Glu Pro Ile Thr
50 55 60

Phe Ala Gly Lys Met His Phe Val Pro Trp Leu Ala Arg Pro Ile Phe
65 70 75 80

Pro Pro Trp Asp Arg Gly Tyr Lys Asp Pro Arg Phe Tyr Arg Ser Pro
85 90 95

Pro Leu His Glu His Pro Leu Tyr Lys Asp Gln Ala Cys Tyr Ile Phe
100 105 110

His His Arg Cys Arg Leu Leu Glu Gly Val Lys Gln Ala Leu Trp Leu
115 120 125

Thr Lys Thr Lys Leu Ile Glu Gly Leu Pro Glu Lys Val Leu Ser Leu
130 135 140

Val Asp Asp Pro Arg Asn His Ile Glu Asn Gln Asp Glu Cys Val Leu
145 150 155 160

Asn Val Ile Ser His Ala Arg Leu Trp Gln Thr Thr Glu Glu Ile Pro
165 170 175

Lys Arg Glu Thr Tyr Cys Pro Val Ile Val Asp Asn Leu Ile Gln Leu
180 185 190

Cys Lys Ser Gln Ile Leu Lys His Pro Ser Leu Ala Arg Arg Ile Cys
195 200 205

Val Gln Asn Ser Thr Phe Ser Ala Thr Trp Asn Arg Glu Ser Leu Leu
210 215 220

Leu Gln Val Arg Gly Ser Gly Gly Ala Arg Leu Ser Thr Lys Asp Pro
225 230 235 240

Leu Pro Thr Ile Ala Ser Arg Glu Glu Ile Glu Ala Thr Lys Asn His
245 250 255

Val Leu Glu Thr Phe Tyr Pro Ile Ser Pro Ile Ile Asp Leu His Glu
260 265 270

Cys Asn Ile Tyr Asp Val Lys Asn Asp Thr Gly Phe Gln Glu Gly Tyr
275 280 285

Pro Tyr Pro Tyr Pro His Thr Leu Tyr Leu Leu Asp Lys Ala Asn Leu
290 295 300

Arg Pro His Arg Leu Gln Pro Asp Gln Leu Arg Ala Lys Met Ile Leu
305 310 315 320

Phe Ala Phe Gly Ser Ala Leu Ala Gln Ala Arg Leu Leu Tyr Gly Asn
325 330 335

Asp Ala Lys Val Leu Glu Gln Pro Val Val Val Gln Ser Val Gly Thr
340 345 350

Asp Gly Arg Val Phe His Phe Leu Val Phe Gln Leu Asn Thr Thr Asp
355 360 365

Leu Asp Ser Asn Glu Gly Val Lys Asn Leu Ala Trp Val Asp Ser Asp
370 375 380

Gln Leu Leu Tyr Gln His Phe Trp Cys Leu Pro Val Ile Lys Lys Arg
385 390 395 400

Val Val Val Glu Pro Val Gly Pro Val Gly Phe Lys Pro Glu Thr Phe
405 410 415

Arg Lys Phe Leu Ala Leu Tyr Leu His Gly Ala Ala
420 425

<210> 955
<211> 169
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (131)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (140)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (166)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 955
Asp Pro Arg Val Arg Pro Arg Val Arg Pro Arg Val Arg Glu Pro Gly
1 5 10 15

Asp Arg Met Leu Val Leu Val Leu Gly Asp Leu His Ile Pro His Arg
20 25 30

Cys Asn Ser Leu Pro Ala Lys Phe Lys Lys Leu Leu Val Pro Gly Lys
35 40 45

Ile Gln His Ile Leu Cys Thr Gly Asn Leu Cys Thr Lys Glu Ser Tyr
50 55 60

Asp Tyr Leu Lys Thr Leu Ala Gly Asp Val His Ile Val Arg Gly Asp
65 70 75 80

Phe Asp Glu Asn Leu Asn Tyr Pro Glu Gln Lys Val Val Thr Val Gly

85 90 95

Gln Phe Lys Ile Gly Leu Ile His Gly His Gln Val Ile Pro Trp Gly
100 105 110

Asp Met Ala Ser Leu Ala Leu Leu Gln Arg Gln Phe Asp Val Asp Ile
115 120 125

Leu Ile Xaa Gly His Thr His Lys Phe Glu Ala Xaa Glu His Glu Asn
130 135 140

Lys Phe Tyr Ile Asn Pro Gly Ser Ala Thr Gly Ala Tyr Asn Ala Leu
145 150 155 160

Glu Thr Asn Ile Ile Xaa Ser Leu Cys
165

<210> 956
<211> 39
<212> PRT
<213> Homo sapiens

<400> 956
Ser Pro Tyr Cys Gly Leu Gln Val Met Leu Phe Leu Leu His His Thr
1 5 10 15

Leu Trp Cys Leu Leu Pro Cys Ala Ser Ser Leu Arg Leu Ile Lys Lys
20 25 30

Val Ser Arg Leu Leu Gln Leu
35

<210> 957
<211> 219
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 957

```
Gln Gly His Cys Gly Cys Xaa Leu Xaa Ser Leu Leu Ala Asn Gly His
  1               5                  10                  15

Asp Leu Ala Ala Ala Met Ala Val Asp Lys Ser Asn Pro Thr Ser Lys
             20                  25                  30

His Lys Ser Gly Ala Val Ala Ser Leu Leu Ser Lys Ala Glu Arg Ala
         35                  40                  45

Thr Glu Leu Ala Ala Glu Gly Gln Leu Thr Leu Gln Gln Phe Ala Gln
     50                  55                  60

Ser Thr Glu Met Leu Lys Arg Val Val Gln Glu His Leu Pro Leu Met
 65                  70                  75                  80

Ser Glu Ala Gly Ala Gly Leu Pro Asp Met Glu Ala Val Ala Gly Ala
                 85                  90                  95

Glu Ala Leu Asn Gly Gln Ser Asp Phe Pro Tyr Leu Gly Ala Phe Pro
            100                 105                 110

Ile Asn Pro Gly Leu Phe Ile Met Thr Pro Ala Gly Val Phe Leu Ala
        115                 120                 125

Glu Ser Ala Leu His Met Ala Gly Leu Ala Glu Tyr Pro Met Gln Gly
    130                 135                 140

Glu Leu Ala Ser Ala Ile Ser Ser Gly Lys Lys Lys Arg Lys Arg Cys
145                 150                 155                 160

Gly Met Cys Ala Pro Cys Arg Arg Arg Ile Asn Cys Glu Gln Cys Ser
                165                 170                 175

Ser Cys Arg Asn Arg Lys Thr Gly His Gln Ile Cys Lys Phe Arg Lys
            180                 185                 190

Cys Glu Glu Leu Lys Lys Lys Pro Ser Ala Ala Leu Glu Lys Val Met
        195                 200                 205

Leu Pro Thr Gly Ala Ala Phe Arg Trp Phe Gln
    210                 215
```

<210> 958
<211> 259
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (21)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 958

```
Leu Pro Gln Asn Ala Val Leu Glu Ala Asp Phe Ala Lys Arg Gly Tyr
  1               5                  10                  15

Lys Leu Pro Lys Xaa Arg Lys Thr Gly Thr Thr Ile Ala Gly Val Val
             20                  25                  30

Tyr Lys Asp Gly Ile Val Leu Gly Ala Asp Thr Arg Ala Thr Glu Gly
         35                  40                  45

Met Val Val Ala Asp Lys Asn Cys Ser Lys Ile His Phe Ile Ser Pro
     50                  55                  60

Asn Ile Tyr Cys Cys Gly Ala Gly Thr Xaa Ala Asp Thr Asp Met Thr
 65                  70                  75                  80

Thr Gln Leu Ile Ser Ser Asn Leu Glu Leu His Ser Leu Ser Thr Gly
                 85                  90                  95

Arg Leu Pro Arg Val Val Thr Ala Asn Arg Met Leu Lys Gln Met Leu
            100                 105                 110

Phe Arg Tyr Gln Gly Tyr Ile Gly Ala Ala Leu Val Leu Gly Gly Val
        115                 120                 125

Asp Val Thr Gly Pro His Leu Tyr Ser Ile Tyr Pro His Gly Ser Thr
    130                 135                 140

Asp Lys Leu Pro Tyr Val Thr Met Gly Ser Gly Ser Leu Ala Ala Met
145                 150                 155                 160

Ala Val Phe Glu Asp Lys Phe Arg Pro Asp Met Glu Glu Glu Glu Ala
                165                 170                 175

Lys Asn Leu Val Ser Glu Ala Ile Ala Ala Gly Ile Phe Asn Asp Leu
            180                 185                 190

Gly Ser Gly Ser Asn Ile Asp Leu Cys Val Ile Ser Lys Asn Lys Leu
        195                 200                 205

Asp Phe Leu Arg Pro Tyr Thr Val Pro Asn Lys Lys Gly Thr Arg Leu
    210                 215                 220
```

Gly Arg Tyr Arg Cys Glu Lys Gly Thr Thr Ala Val Leu Thr Glu Lys
225 230 235 240

Ile Thr Pro Leu Glu Ile Glu Val Leu Glu Glu Thr Val Gln Thr Met
245 250 255

Asp Thr Ser

<210> 959
<211> 75
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (41)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (53)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 959
Phe Trp Ser Ala Ala Lys Phe Asp Phe Thr Ser His Thr Pro Phe Leu
1 5 10 15

Pro Leu Glu Met Gln Phe Arg Gln Arg Pro Cys Gly Glu Ser Cys Asn
20 25 30

Ile Lys Phe Xaa Phe Arg Arg Ser Xaa Pro Gln Thr Ser Glu Pro Leu
35 40 45

Ala Val Leu Pro Xaa Asn Lys Asn Glu Leu Glu Lys Lys Val Ala Gln
50 55 60

Leu Gln Arg Ser Lys Ser Ser Tyr Phe Pro Thr
65 70 75

<210> 960

<211> 128
<212> PRT
<213> Homo sapiens

<400> 960
Gln Ser Arg Gly Leu Arg Leu Leu Gly Pro Gly Asp Gly Ala Gly Met
1 5 10 15

Thr Pro Gly Val Val His Ala Ser Pro Pro Gln Ser Gln Arg Val Pro
20 25 30

Arg Gln Ala Pro Cys Glu Trp Ala Ile Arg Asn Ile Gly Gln Lys Pro
35 40 45

Lys Glu Pro Asn Cys His Asn Cys Gly Thr His Ile Gly Leu Arg Ser
50 55 60

Lys Thr Leu Arg Gly Thr Pro Asn Tyr Leu Pro Ile Arg Gln Asp Thr
65 70 75 80

His Pro Pro Ser Val Ile Phe Cys Leu Ala Gly Val Gly Val Pro Gly
85 90 95

Gly Thr Cys Arg Pro Ala Pro Cys Val Pro Arg Phe Ala Ala Leu Pro
100 105 110

Trp Ala Thr Asn His Pro Gly Pro Gly Cys Leu Ser Asp Leu Arg Ala
115 120 125

<210> 961
<211> 564
<212> PRT
<213> Homo sapiens

<400> 961
Lys Met Lys Ser Val Lys Ile Ala Phe Ala Val Thr Leu Glu Thr Val
1 5 10 15

Leu Ala Gly His Glu Asn Trp Val Asn Ala Val His Trp Gln Pro Val
20 25 30

Phe Tyr Lys Asp Gly Val Leu Gln Gln Pro Val Arg Leu Leu Ser Ala
35 40 45

Ser Met Asp Lys Thr Met Ile Leu Trp Ala Pro Asp Glu Glu Ser Gly
50 55 60

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Val Trp Leu Glu Gln Val Arg Val Gly Glu Val Gly Gly Asn Thr Leu
 65                 70                  75                  80

Gly Phe Tyr Asp Cys Gln Phe Asn Glu Asp Gly Ser Met Ile Ile Ala
                85                  90                  95

His Ala Phe His Gly Ala Leu His Leu Trp Lys Gln Asn Thr Val Asn
            100                 105                 110

Pro Arg Glu Trp Thr Pro Glu Ile Val Ile Ser Gly His Phe Asp Gly
        115                 120                 125

Val Gln Asp Leu Val Trp Asp Pro Glu Gly Glu Phe Ile Ile Thr Val
    130                 135                 140

Gly Thr Asp Gln Thr Thr Arg Leu Phe Ala Pro Trp Lys Arg Lys Asp
145                 150                 155                 160

Gln Ser Gln Val Thr Trp His Glu Ile Ala Arg Pro Gln Ile His Gly
                165                 170                 175

Tyr Asp Leu Lys Cys Leu Ala Met Ile Asn Arg Phe Gln Phe Val Ser
            180                 185                 190

Gly Ala Asp Glu Lys Val Leu Arg Val Phe Ser Ala Pro Arg Asn Phe
        195                 200                 205

Val Glu Asn Phe Cys Ala Ile Thr Gly Gln Ser Leu Asn His Val Leu
    210                 215                 220

Cys Asn Gln Asp Ser Asp Leu Pro Glu Gly Ala Thr Val Pro Ala Leu
225                 230                 235                 240

Gly Leu Ser Asn Lys Ala Val Phe Gln Gly Asp Ile Ala Ser Gln Pro
                245                 250                 255

Ser Asp Glu Glu Glu Leu Leu Thr Ser Thr Gly Phe Glu Tyr Gln Gln
            260                 265                 270

Val Ala Phe Gln Pro Ser Ile Leu Thr Glu Pro Pro Thr Glu Asp His
        275                 280                 285

Leu Leu Gln Asn Thr Leu Trp Pro Glu Val Gln Lys Leu Tyr Gly His
    290                 295                 300

Gly Tyr Glu Ile Phe Cys Val Thr Cys Asn Ser Ser Lys Thr Leu Leu
305                 310                 315                 320

Ala Ser Ala Cys Lys Ala Ala Lys Lys Glu His Ala Ala Ile Ile Leu
                325                 330                 335
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Trp Asn Thr Thr Ser Trp Lys Gln Val Gln Asn Leu Val Phe His Ser
            340                 345                 350

Leu Thr Val Thr Gln Met Ala Phe Ser Pro Asn Glu Lys Phe Leu Leu
        355                 360                 365

Ala Val Ser Arg Asp Arg Thr Trp Ser Leu Trp Lys Lys Gln Asp Thr
    370                 375                 380

Ile Ser Pro Glu Phe Glu Pro Val Phe Ser Leu Phe Ala Phe Thr Asn
385                 390                 395                 400

Lys Ile Thr Ser Val His Ser Arg Ile Ile Trp Ser Cys Asp Trp Ser
                405                 410                 415

Pro Asp Ser Lys Tyr Phe Phe Thr Gly Ser Arg Asp Lys Lys Val Val
            420                 425                 430

Val Trp Gly Glu Cys Asp Ser Thr Asp Asp Cys Ile Glu His Asn Ile
        435                 440                 445

Gly Pro Cys Ser Ser Val Leu Asp Val Gly Gly Ala Val Thr Ala Val
    450                 455                 460

Ser Val Cys Pro Val Leu His Pro Ser Gln Arg Tyr Val Val Ala Val
465                 470                 475                 480

Gly Leu Glu Cys Gly Lys Ile Cys Leu Tyr Thr Trp Lys Lys Thr Asp
                485                 490                 495

Gln Val Pro Glu Ile Asn Asp Trp Thr His Cys Val Glu Thr Ser Gln
            500                 505                 510

Ser Gln Ser His Thr Leu Ala Ile Arg Lys Leu Cys Trp Lys Asn Cys
        515                 520                 525

Ser Gly Lys Thr Glu Gln Lys Glu Ala Glu Gly Ala Glu Trp Leu His
    530                 535                 540

Phe Ala Ser Cys Gly Glu Asp His Thr Val Lys Ile His Arg Val Asn
545                 550                 555                 560

Lys Cys Ala Leu
```

<210> 962
<211> 43
<212> PRT

<213> Homo sapiens

<400> 962
Phe Lys Tyr Val Lys Cys Gly Ser Phe Thr Pro His His Ser Glu His
1 5 10 15

Thr Gly Glu Met Cys Phe Phe Gly Lys Leu Lys Gly Ala Ser Ser Leu
20 25 30

Ile Gln Arg Asn Ile Ser His Val Cys Ser Phe
35 40

<210> 963
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (131)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 963
Glu Ser Arg Val Asp Pro Arg Val Arg Glu Arg Ser Ala Arg Thr Ala
1 5 10 15

Gly Ala Thr Val Gly Pro Ala Ala Val Met Ser Val Leu Arg Pro Leu
20 25 30

Asp Lys Leu Pro Gly Leu Asn Thr Ala Thr Ile Leu Leu Val Gly Thr
35 40 45

Glu Asp Ala Leu Leu Gln Gln Leu Ala Asp Ser Met Leu Lys Glu Asp
50 55 60

Cys Ala Ser Glu Leu Lys Val His Leu Ala Lys Ser Leu Pro Leu Pro
65 70 75 80

Ser Ser Val Asn Arg Pro Arg Ile Asp Leu Ile Val Phe Val Val Asn
85 90 95

Leu His Ser Lys Tyr Ser Leu Gln Asn Thr Glu Glu Ser Leu Arg His
100 105 110

Val Asp Ala Ser Phe Phe Leu Gly Lys Val Cys Phe Leu Ala Thr Gly
115 120 125

Gly Gly Xaa Leu
130

<210> 964
<211> 175
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 964
His Glu Arg Ser Cys Cys Asp Ala Arg Ser Glu Ala Xaa Gln Gly Arg
1 5 10 15

Gly Arg Val Gly Ala Gly Ala Gly Ala Ala Trp Ser Ser Cys Gly Val
20 25 30

Ser Gly Pro Gly Arg Gly Met Gly Val Leu Ala Ala Ala Ala Arg Cys
35 40 45

Leu Val Arg Gly Ala Asp Arg Met Ser Lys Trp Thr Ser Lys Arg Gly
50 55 60

Pro Arg Ser Phe Arg Gly Arg Xaa Gly Arg Gly Ala Lys Gly Ile Gly
65 70 75 80

Phe Leu Thr Ser Gly Trp Arg Phe Val Gln Ile Lys Glu Met Val Pro
85 90 95

Glu Phe Val Val Pro Asp Leu Thr Gly Phe Lys Leu Lys Pro Tyr Val
100 105 110

Ser Tyr Leu Ala Pro Glu Ser Glu Glu Thr Pro Leu Thr Ala Ala Gln
115 120 125

Leu Phe Ser Glu Ala Val Ala Pro Ala Ile Glu Lys Asp Phe Lys Asp
130 135 140

Gly Thr Phe Asp Pro Asp Asn Leu Glu Lys Tyr Gly Phe Glu Pro Thr
145 150 155 160

Gln Glu Gly Lys Leu Phe Gln Leu Tyr Pro Arg Asn Phe Leu Arg
165 170 175

<210> 965
<211> 363
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (356)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 965
```
Leu Leu Arg Arg Leu Arg Thr Ala Val Pro Gly Ser Leu Glu Ala Gln
  1               5                  10                  15

Lys Arg Lys Pro Ser Pro Gly Pro Gly Ser Leu Asp Leu Val Ser Leu
             20                  25                  30

Gly Ser Gly Asn Ser Gly Ser Gln Arg Thr Val Leu Ile Met Asp Lys
         35                  40                  45

Gln Asn Ser Gln Met Asn Ala Ser His Pro Glu Thr Asn Leu Pro Val
     50                  55                  60

Gly Tyr Pro Pro Gln Tyr Pro Pro Thr Ala Phe Gln Gly Pro Pro Gly
 65                  70                  75                  80

Tyr Ser Gly Tyr Pro Gly Pro Gln Val Ser Tyr Pro Pro Pro Pro Ala
                 85                  90                  95

Gly His Ser Gly Pro Gly Pro Ala Gly Phe Pro Val Pro Asn Gln Pro
            100                 105                 110

Val Tyr Asn Gln Pro Val Tyr Asn Gln Pro Val Gly Ala Ala Gly Val
        115                 120                 125

Pro Trp Met Pro Ala Pro Gln Pro Pro Leu Asn Cys Pro Pro Gly Leu
    130                 135                 140

Glu Tyr Leu Ser Gln Ile Asp Gln Ile Leu Ile His Gln Gln Ile Glu
145                 150                 155                 160

Leu Leu Glu Val Leu Thr Gly Phe Glu Thr Asn Asn Lys Tyr Glu Ile
                165                 170                 175

Lys Asn Ser Phe Gly Gln Arg Val Tyr Phe Ala Ala Glu Asp Thr Asp
            180                 185                 190

Cys Cys Thr Arg Asn Cys Cys Gly Pro Ser Arg Pro Phe Thr Leu Arg
```

195 200 205

Ile Ile Asp Asn Met Gly Gln Glu Val Ile Thr Leu Glu Arg Pro Leu
210 215 220

Arg Cys Ser Ser Cys Cys Cys Pro Cys Cys Leu Gln Glu Ile Glu Ile
225 230 235 240

Gln Ala Pro Pro Gly Val Pro Ile Gly Tyr Val Ile Gln Thr Trp His
245 250 255

Pro Cys Leu Pro Lys Phe Thr Ile Gln Asn Glu Lys Arg Glu Asp Val
260 265 270

Leu Lys Ile Ser Gly Pro Cys Val Val Cys Ser Cys Cys Gly Asp Val
275 280 285

Asp Phe Glu Ile Lys Ser Leu Asp Glu Gln Cys Val Val Gly Lys Ile
290 295 300

Ser Lys His Trp Thr Gly Ile Leu Arg Glu Ala Phe Thr Asp Ala Asp
305 310 315 320

Asn Phe Gly Ile Gln Phe Pro Leu Asp Leu Asp Val Lys Met Lys Ala
325 330 335

Val Met Ile Gly Ala Cys Phe Leu Ile Asp Phe Met Phe Phe Glu Ser
340 345 350

Thr Gly Ser Xaa Glu Gln Lys Ser Gly Val Trp
355 360

<210> 966
<211> 131
<212> PRT
<213> Homo sapiens

<400> 966
Ala Glu Val His Thr Arg Lys Gln Gly Pro Glu Ala Glu Pro Ala Ala
1 5 10 15

Met Ser Gly Glu Pro Gly Gln Thr Ser Val Ala Pro Pro Pro Glu Glu
20 25 30

Val Glu Pro Gly Ser Gly Val Arg Ile Val Val Glu Tyr Cys Glu Pro
35 40 45

Cys Gly Phe Glu Ala Thr Tyr Leu Glu Leu Ala Ser Ala Val Lys Glu
50 55 60

Gln Tyr Pro Gly Ile Glu Ile Glu Ser Arg Leu Gly Gly Thr Gly Ala
65 70 75 80

Phe Glu Ile Glu Ile Asn Gly Gln Leu Val Phe Ser Lys Leu Glu Asn
85 90 95

Gly Gly Phe Pro Tyr Glu Lys Asp Leu Ile Glu Ala Ile Arg Arg Ala
100 105 110

Ser Asn Gly Glu Thr Leu Glu Lys Ile Thr Asn Ser Arg Pro Pro Cys
115 120 125

Val Ile Leu
130

<210> 967
<211> 344
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (68)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (306)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 967
Pro Thr Pro Ala Ser His Ser Pro Ser Pro Ser Leu Pro Ala Leu Pro
1 5 10 15

Pro Ser Pro Pro His Arg Pro Asp Ser Pro Leu Phe Asn Ser Arg Cys
20 25 30

Ser Ser Pro Leu Gln Leu Asn Leu Leu Gln Leu Glu Glu Leu Pro Arg
35 40 45

Ala Glu Gly Ala Ala Val Ala Gly Gly Pro Gly Ser Ser Ala Gly Pro
50 55 60

Pro Pro Pro Xaa Ala Glu Ala Ala Glu Pro Glu Ala Arg Leu Ala Glu
65 70 75 80

Val Thr Glu Ser Ser Asn Gln Asp Ala Leu Ser Gly Ser Ser Asp Leu
85 90 95

Leu Glu Leu Leu Leu Gln Glu Asp Ser Arg Ser Gly Thr Gly Ser Ala
100 105 110

Ala Ser Gly Ser Leu Gly Ser Gly Leu Gly Ser Gly Ser Gly Ser Gly
115 120 125

Ser His Glu Gly Gly Ser Thr Ser Ala Ser Ile Thr Arg Ser Ser Gln
130 135 140

Ser Ser His Thr Ser Lys Tyr Phe Gly Ser Ile Asp Ser Ser Glu Ala
145 150 155 160

Glu Ala Gly Ala Ala Arg Gly Gly Ala Glu Pro Gly Asp Gln Val Ile
165 170 175

Lys Tyr Val Leu Gln Asp Pro Ile Trp Leu Leu Met Ala Asn Ala Asp
180 185 190

Gln Arg Val Met Met Thr Tyr Gln Val Pro Ser Arg Asp Met Thr Ser
195 200 205

Val Leu Lys Gln Asp Arg Glu Arg Leu Arg Ala Met Gln Lys Gln Gln
210 215 220

Pro Arg Phe Ser Glu Asp Gln Arg Arg Glu Leu Gly Ala Val His Ser
225 230 235 240

Trp Val Arg Lys Gly Gln Leu Pro Arg Ala Leu Asp Val Met Ala Cys
245 250 255

Val Asp Cys Gly Ser Ser Thr Gln Asp Pro Gly His Pro Asp Asp Pro
260 265 270

Leu Phe Ser Glu Leu Asp Gly Leu Gly Leu Glu Pro Met Glu Glu Gly
275 280 285

Gly Gly Glu Gln Gly Ser Ser Gly Gly Gly Ser Gly Glu Gly Glu Gly
290 295 300

Cys Xaa Glu Ala Gln Gly Gly Ala Lys Ala Ser Ser Ser Gln Asp Leu
305 310 315 320

Ala Met Glu Glu Glu Glu Glu Gly Arg Ser Ser Ser Ser Pro Ala Leu
325 330 335

Pro Thr Ala Gly Asn Cys Thr Ser
340

<210> 968
<211> 67
<212> PRT
<213> Homo sapiens

<400> 968
Arg Cys Ser Ser Phe Phe Leu Ser Leu Leu Val Lys Ile Thr Asn Ile
1 5 10 15

Trp Glu Gly Phe Lys Asp Ala Cys Tyr Gly Ala Asn Val Leu Ser Leu
20 25 30

Leu Asn Ser Arg Ser Glu Leu Leu Thr Cys Ile Gln Asn Ile Asn Ala
35 40 45

Gln Asn Leu Tyr Met Ser Pro Ile Arg Lys Ile His Trp His Ala Thr
50 55 60

Gly Asp Ser
65

<210> 969
<211> 325
<212> PRT
<213> Homo sapiens

<400> 969
Leu Asn Leu Arg Ser Pro His Ile Cys Phe Arg Ser Ser Lys Pro Ser
1 5 10 15

Trp Ala Asp Gln Val Glu Glu Glu Gly Glu Asp Asp Lys Cys Val Thr
20 25 30

Ser Glu Leu Leu Lys Gly Ile Pro Leu Ala Thr Gly Asp Thr Ser Pro
35 40 45

Glu Pro Glu Leu Leu Pro Gly Ala Pro Leu Pro Pro Pro Lys Glu Val
50 55 60

Ile Asn Gly Asn Ile Lys Thr Val Thr Glu Tyr Lys Ile Asp Glu Asp
65 70 75 80

Gly Lys Lys Phe Lys Ile Val Arg Thr Phe Arg Ile Glu Thr Arg Lys
85 90 95

Ala Ser Lys Ala Val Ala Arg Arg Lys Asn Trp Lys Lys Phe Gly Asn
100 105 110

Ser Glu Phe Asp Pro Pro Gly Pro Asn Val Ala Thr Thr Thr Val Ser

115 120 125

Asp Asp Val Ser Met Thr Phe Ile Thr Ser Lys Glu Asp Leu Asn Cys
130 135 140

Gln Glu Glu Glu Asp Pro Met Asn Lys Leu Lys Gly Gln Lys Ile Val
145 150 155 160

Ser Cys Arg Ile Cys Lys Gly Asp His Trp Thr Thr Arg Cys Pro Tyr
165 170 175

Lys Asp Thr Leu Gly Pro Met Gln Lys Glu Leu Ala Glu Gln Leu Gly
180 185 190

Leu Ser Thr Gly Glu Lys Glu Lys Leu Pro Gly Glu Leu Glu Pro Val
195 200 205

Gln Ala Thr Gln Asn Lys Thr Gly Lys Tyr Val Pro Pro Ser Leu Arg
210 215 220

Asp Gly Ala Ser Arg Arg Gly Glu Ser Met Gln Pro Asn Arg Arg Ala
225 230 235 240

Asp Asp Asn Ala Thr Ile Arg Val Thr Asn Leu Ser Glu Asp Thr Arg
245 250 255

Glu Thr Asp Leu Gln Glu Leu Phe Arg Pro Phe Gly Ser Ile Ser Arg
260 265 270

Ile Tyr Leu Ala Lys Asp Lys Thr Thr Gly Gln Ser Lys Gly Phe Ala
275 280 285

Phe Ile Ser Phe His Arg Arg Glu Asp Ala Ala Arg Ala Ile Ala Gly
290 295 300

Val Ser Gly Phe Gly Tyr Asp His Leu Ile Leu Asn Val Glu Trp Ala
305 310 315 320

Lys Pro Ser Thr Asn
325

<210> 970
<211> 357
<212> PRT
<213> Homo sapiens

<400> 970
Val Arg Val Lys Met Ala Ala Ala Glu Ala Ala Asn Cys Ile Met Glu
1 5 10 15

Val Ser Cys Gly Gln Ala Glu Ser Ser Glu Lys Pro Asn Ala Glu Asp
20 25 30

Met Thr Ser Lys Asp Tyr Tyr Phe Asp Ser Tyr Ala His Phe Gly Ile
35 40 45

His Glu Glu Met Leu Lys Asp Glu Val Arg Thr Leu Thr Tyr Arg Asn
50 55 60

Ser Met Phe His Asn Arg His Leu Phe Lys Asp Lys Val Val Leu Asp
65 70 75 80

Val Gly Ser Gly Thr Gly Ile Leu Cys Met Phe Ala Ala Lys Ala Gly
85 90 95

Ala Arg Lys Val Ile Gly Ile Glu Cys Ser Ser Ile Ser Asp Tyr Ala
100 105 110

Val Lys Ile Val Lys Ala Asn Lys Leu Asp His Val Val Thr Ile Ile
115 120 125

Lys Gly Lys Val Glu Glu Val Glu Leu Pro Val Glu Lys Val Asp Ile
130 135 140

Ile Ile Ser Glu Trp Met Gly Tyr Cys Leu Phe Tyr Glu Ser Met Leu
145 150 155 160

Asn Thr Val Leu Tyr Ala Arg Asp Lys Trp Leu Ala Pro Asp Gly Leu
165 170 175

Ile Phe Pro Asp Arg Ala Thr Leu Tyr Val Thr Ala Ile Glu Asp Arg
180 185 190

Gln Tyr Lys Asp Tyr Lys Ile His Trp Trp Glu Asn Val Tyr Gly Phe
195 200 205

Asp Met Ser Cys Ile Lys Asp Val Ala Ile Lys Glu Pro Leu Val Asp
210 215 220

Val Val Asp Pro Lys Gln Leu Val Thr Asn Ala Cys Leu Ile Lys Glu
225 230 235 240

Val Asp Ile Tyr Thr Val Lys Val Glu Asp Leu Thr Phe Thr Ser Pro
245 250 255

Phe Cys Leu Gln Val Lys Arg Asn Asp Tyr Val His Ala Leu Val Ala
260 265 270

Tyr Phe Asn Ile Glu Phe Thr Arg Cys His Lys Arg Thr Gly Phe Ser
275 280 285

Thr Ser Pro Glu Ser Pro Tyr Thr His Trp Lys Gln Thr Val Phe Tyr
    290   295   300

Met Glu Asp Tyr Leu Thr Val Lys Thr Gly Glu Glu Ile Phe Gly Thr
305   310   315   320

Ile Gly Met Arg Pro Asn Ala Lys Asn Asn Arg Asp Leu Asp Phe Thr
                325   330   335

Ile Asp Leu Asp Phe Lys Gly Gln Leu Cys Glu Leu Ser Cys Ser Thr
            340   345   350

Asp Tyr Arg Met Arg
        355

<210> 971
<211> 176
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (176)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 971
Gly Val Pro Arg Arg Ala Tyr Gln Ala Xaa Xaa Leu Arg Arg Val Asp
  1   5   10   15

Asp Phe Lys Lys Ala Phe Ser Lys Glu Lys Met Glu Lys Thr Lys Val
            20   25   30

Arg Thr Arg Glu Asn Leu Glu Lys Thr Arg Leu Lys Thr Lys Glu Asn
        35   40   45

Leu Glu Lys Thr Arg His Thr Leu Glu Lys Arg Met Asn Lys Leu Gly
    50   55   60

Thr Arg Leu Val Pro Ala Glu Arg Arg Glu Lys Leu Lys Thr Ser Arg
65 70 75 80

Asp Lys Leu Arg Lys Ser Phe Thr Pro Asp His Val Val Tyr Ala Arg
85 90 95

Ser Lys Thr Ala Val Tyr Lys Val Pro Pro Phe Thr Phe His Val Lys
100 105 110

Lys Ile Arg Glu Gly Gln Val Glu Val Leu Lys Ala Thr Glu Met Val
115 120 125

Glu Val Gly Ala Asp Asp Asp Glu Gly Gly Ala Glu Arg Gly Glu Ala
130 135 140

Gly Asp Leu Arg Arg Gly Ser Ser Pro Asp Val His Ala Leu Leu Glu
145 150 155 160

Ile Thr Glu Glu Ser Asp Ala Val Leu Val Asp Lys Ser Asp Ser Xaa
165 170 175

<210> 972
<211> 159
<212> PRT
<213> Homo sapiens

<400> 972
Gly Lys Ala Arg Arg Arg Ala Ala Lys Leu Gln Ser Ser Gln Glu Pro
1 5 10 15

Glu Ala Pro Pro Pro Arg Asp Val Ala Leu Leu Gln Gly Arg Ala Asn
20 25 30

Asp Leu Val Lys Tyr Leu Leu Ala Lys Asp Gln Thr Lys Ile Pro Ile
35 40 45

Lys Arg Ser Asp Met Leu Lys Asp Ile Ile Lys Glu Tyr Thr Asp Val
50 55 60

Tyr Pro Glu Ile Ile Glu Arg Ala Gly Tyr Ser Leu Glu Lys Val Phe
65 70 75 80

Gly Ile Gln Leu Lys Glu Ile Asp Lys Asn Asp His Leu Tyr Ile Leu
85 90 95

Leu Ser Thr Leu Glu Pro Thr Asp Ala Gly Ile Leu Gly Thr Thr Lys

100 105 110

Asp Ser Pro Lys Leu Gly Leu Leu Met Val Leu Leu Ser Ile Ile Phe
115 120 125

Met Asn Gly Asn Arg Ser Ser Glu Ala Val Ile Trp Glu Val Leu Arg
130 135 140

Lys Leu Gly Leu Arg Leu Gly Tyr Ile Ile His Ser Leu Gly Thr
145 150 155

<210> 973
<211> 233
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 973
Arg Ala Xaa Lys Ala Ala Pro Arg Arg Ala Leu Ala Arg Leu Val Leu
1 5 10 15

Ala Trp Cys Arg Trp Leu Val Ser Ala Thr Cys Val Gly Thr Ala Asp
20 25 30

Arg Lys Met Ser Ser Gly Asn Ala Lys Ile Gly His Pro Ala Pro Asn
35 40 45

Phe Lys Ala Thr Ala Val Met Pro Asp Gly Gln Phe Lys Asp Ile Ser
50 55 60

Leu Ser Asp Tyr Lys Gly Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu
65 70 75 80

Asp Phe Thr Phe Val Cys Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg
85 90 95

Ala Glu Glu Phe Lys Lys Leu Asn Cys Gln Val Ile Gly Ala Ser Val
100 105 110

Asp Ser His Phe Cys His Leu Ala Trp Val Asn Thr Pro Lys Lys Gln
115 120 125

Gly Gly Leu Gly Pro Met Asn Ile Pro Leu Val Ser Asp Pro Lys Arg
130 135 140

Thr Ile Ala Gln Asp Tyr Gly Val Leu Lys Ala Asp Glu Gly Ile Ser
145 150 155 160

Phe Arg Gly Leu Phe Ile Ile Asp Asp Lys Gly Ile Leu Arg Gln Ile
165 170 175

Thr Val Asn Asp Leu Pro Val Gly Arg Ser Val Asp Glu Thr Leu Arg
180 185 190

Leu Val Gln Ala Phe Gln Phe Thr Asp Lys His Gly Glu Val Cys Pro
195 200 205

Ala Gly Trp Lys Pro Gly Ser Asp Thr Ile Lys Pro Asp Val Gln Lys
210 215 220

Ser Lys Glu Tyr Phe Ser Lys Gln Lys
225 230

<210> 974
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (37)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 974
Ser Trp Asp Arg Arg Leu Met Gln Asp Asp Asn Arg Gly Leu Gly Gln
1 5 10 15

Gly Leu Lys Asp Asn Lys Arg Thr Cys Asn Arg Phe Arg Leu Leu Leu
20 25 30

Glu Arg Arg Thr Xaa Gly Ser Glu Val Gln Asp Ser His Ser Thr Ser
35 40 45

Tyr Pro Ser Leu Leu Ser His Leu Thr Ser Met Tyr Leu Asn Ala Pro
50 55 60

Ala Leu Ala Leu Pro Val Ala Arg Met Gln Leu Pro Gly Pro Gly Leu
65 70 75 80

Arg Ser Phe His Pro Leu Ala Ser Ser Leu Pro Cys Asp Phe His Leu
85 90 95

Leu Asn Leu Arg Thr Leu Gln Ala Glu Glu Asp Thr Leu Pro Ser Ala
100 105 110

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Glu Thr Ala Leu Ile Leu His Arg Lys Val Leu Thr Ala Ala Trp Arg
        115                 120                 125

Gln Glu Leu Gly Leu Gln Leu His His Lys Pro Arg Gln Gly Ser Pro
    130                 135                 140

Gly Gln Pro Phe Pro Trp Pro Gly Cys Gly Ile Pro Ser Ala Asn Leu
145                 150                 155                 160

Leu Asp Val Thr Val Pro Ser Gly Leu Pro Val Gln Gln His
                165                 170



<210> 975
<211> 380
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (134)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 975
Arg Pro Glu Val Arg His Ser Arg Glu Ala Pro Glu Ser Arg Arg Trp
  1               5                  10                  15

Ala Val Trp Arg Ser Leu Glu Ser Leu Pro Arg His Gln Leu Leu Cys
            20                  25                  30

Leu Pro Val Gly Ala Pro Pro Ala Pro Ala Met Leu Ser Ala Leu Ala
        35                  40                  45

Arg Pro Ala Ser Ala Ala Leu Arg Arg Ser Phe Ser Thr Ser Ala Gln
    50                  55                  60

Asn Asn Ala Lys Val Ala Val Leu Gly Ala Ser Gly Gly Ile Gly Gln
 65                  70                  75                  80

Pro Leu Ser Leu Leu Leu Lys Asn Ser Pro Leu Val Ser Arg Leu Thr
                 85                  90                  95

Leu Tyr Asp Ile Ala His Thr Pro Gly Val Ala Ala Asp Leu Ser His
            100                 105                 110

Ile Glu Thr Lys Ala Ala Val Lys Gly Tyr Leu Gly Pro Glu Gln Leu
        115                 120                 125

Pro Asp Cys Leu Lys Xaa Cys Asp Val Val Val Ile Pro Ala Gly Val
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130 135 140

Pro Arg Lys Pro Gly Met Thr Arg Asp Asp Leu Phe Asn Thr Asn Ala
145 150 155 160

Thr Ile Val Ala Thr Leu Thr Ala Ala Cys Ala Gln His Cys Pro Glu
165 170 175

Ala Met Ile Cys Val Ile Ala Asn Pro Val Asn Ser Thr Ile Pro Ile
180 185 190

Thr Ala Glu Val Phe Lys Lys His Gly Val Tyr Asn Pro Asn Lys Ile
195 200 205

Phe Gly Val Thr Thr Leu Asp Ile Val Arg Ala Asn Thr Phe Val Ala
210 215 220

Glu Leu Lys Gly Leu Asp Pro Ala Arg Val Asn Val Pro Val Ile Gly
225 230 235 240

Gly His Ala Gly Lys Thr Ile Ile Pro Leu Ile Ser Gln Cys Thr Pro
245 250 255

Lys Val Asp Phe Pro Gln Asp Gln Leu Thr Ala Leu Thr Gly Arg Ile
260 265 270

Gln Glu Ala Gly Thr Glu Val Val Lys Ala Lys Ala Gly Ala Gly Ser
275 280 285

Ala Thr Leu Ser Met Ala Tyr Ala Gly Ala Arg Phe Val Phe Ser Leu
290 295 300

Val Asp Ala Met Asn Gly Lys Glu Gly Val Val Glu Cys Ser Phe Val
305 310 315 320

Lys Ser Gln Glu Thr Glu Cys Thr Tyr Phe Ser Thr Pro Leu Leu Leu
325 330 335

Gly Lys Lys Gly Ile Glu Lys Asn Leu Gly Ile Gly Lys Val Ser Ser
340 345 350

Phe Glu Glu Lys Met Ile Ser Asp Ala Ile Pro Glu Leu Lys Ala Ser
355 360 365

Ile Lys Lys Gly Glu Asp Phe Val Lys Thr Leu Lys
370 375 380

<210> 976
<211> 269

<212> PRT
<213> Homo sapiens

<400> 976

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Ala Ala Leu Ser Gln Ile Thr Ile Ala Thr Pro Pro Ala Val Lys Gln
  1               5                  10                  15

Thr Ile Ser Asn Ile Ser Gly Phe Asn Glu Thr Cys Leu Arg Trp Arg
             20                  25                  30

Ser Ile Lys Thr Ala Asp Met Glu Glu Met Tyr Leu Phe His Ile Trp
         35                  40                  45

Gly Gln Arg Trp Tyr Gln Lys Glu Phe Ala Gln Glu Met Thr Phe Asn
     50                  55                  60

Ile Ser Ser Ser Ser Arg Asp Pro Glu Val Cys Leu Asp Leu Arg Pro
 65                  70                  75                  80

Gly Thr Asn Tyr Asn Val Ser Leu Arg Ala Leu Ser Ser Glu Leu Pro
                 85                  90                  95

Val Val Ile Ser Leu Thr Thr Gln Ile Thr Glu Pro Pro Leu Pro Glu
            100                 105                 110

Val Glu Phe Phe Thr Val His Arg Gly Pro Leu Pro Arg Leu Arg Leu
        115                 120                 125

Arg Lys Ala Lys Glu Lys Asn Gly Pro Ile Ser Ser Tyr Gln Val Leu
    130                 135                 140

Val Leu Pro Leu Ala Leu Gln Ser Thr Phe Ser Cys Asp Ser Glu Gly
145                 150                 155                 160

Ala Ser Ser Phe Phe Ser Asn Ala Ser Asp Ala Asp Gly Tyr Val Ala
                165                 170                 175

Ala Glu Leu Leu Ala Lys Asp Val Pro Asp Asp Ala Met Glu Ile Pro
            180                 185                 190

Ile Gly Asp Arg Leu Tyr Tyr Gly Glu Tyr Tyr Asn Ala Pro Leu Lys
        195                 200                 205

Arg Gly Ser Asp Tyr Cys Ile Ile Leu Arg Ile Thr Ser Glu Trp Asn
    210                 215                 220

Lys Val Arg Arg His Ser Cys Ala Val Trp Ala Gln Val Lys Asp Ser
225                 230                 235                 240

Ser Leu Met Leu Leu Gln Met Ala Gly Val Gly Leu Gly Ser Leu Ala
                245                 250                 255
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Val Val Ile Ile Leu Thr Phe Leu Ser Phe Ser Ala Val
            260                 265



<210> 977
<211> 477
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (471)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (473)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 977
Leu Phe Ser Pro Gln Val Glu Leu Thr Lys Ala Met Val Met Glu Lys
  1               5                  10                  15

Pro Ser Pro Leu Leu Val Gly Arg Glu Phe Val Arg Gln Tyr Tyr Thr
             20                  25                  30

Leu Leu Asn Gln Ala Pro Asp Met Leu His Arg Phe Tyr Gly Lys Asn
         35                  40                  45

Ser Ser Tyr Val His Gly Gly Leu Asp Ser Asn Gly Lys Pro Ala Asp
     50                  55                  60

Ala Val Tyr Gly Gln Lys Glu Ile His Arg Lys Val Met Ser Gln Asn
 65                  70                  75                  80

Phe Thr Asn Cys His Thr Lys Ile Arg His Val Asp Ala His Ala Thr
                 85                  90                  95

Leu Asn Asp Gly Val Val Val Gln Val Met Gly Leu Leu Ser Asn Asn
            100                 105                 110

Asn Gln Ala Leu Arg Arg Phe Met Gln Thr Phe Val Leu Ala Pro Glu
        115                 120                 125

Gly Ser Val Ala Asn Lys Phe Tyr Val His Asn Asp Ile Phe Arg Tyr
    130                 135                 140

Gln Asp Glu Val Phe Gly Gly Phe Val Thr Glu Pro Gln Glu Glu Ser
145                 150                 155                 160
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Glu Glu Glu Val Glu Glu Pro Glu Glu Arg Gln Gln Thr Pro Glu Val
165 170 175

Val Pro Asp Asp Ser Gly Thr Phe Tyr Asp Gln Ala Val Val Ser Asn
180 185 190

Asp Met Glu Glu His Leu Glu Glu Pro Val Ala Glu Pro Glu Pro Asp
195 200 205

Pro Glu Pro Glu Pro Glu Gln Glu Pro Val Ser Glu Ile Gln Glu Glu
210 215 220

Lys Pro Glu Pro Val Leu Glu Glu Thr Ala Pro Glu Asp Ala Gln Lys
225 230 235 240

Ser Ser Ser Pro Ala Pro Ala Asp Ile Ala Gln Thr Val Gln Glu Asp
245 250 255

Leu Arg Thr Phe Ser Trp Ala Ser Val Thr Ser Lys Asn Leu Pro Pro
260 265 270

Ser Gly Ala Val Pro Val Thr Gly Ile Pro Pro His Val Val Lys Val
275 280 285

Pro Ala Ser Gln Pro Arg Pro Glu Ser Lys Pro Glu Ser Gln Ile Pro
290 295 300

Pro Gln Arg Pro Gln Arg Asp Gln Arg Val Arg Glu Gln Arg Ile Asn
305 310 315 320

Ile Pro Pro Gln Arg Gly Pro Arg Pro Ile Arg Glu Ala Gly Glu Gln
325 330 335

Gly Asp Ile Glu Pro Arg Arg Met Val Arg His Pro Asp Ser His Gln
340 345 350

Leu Phe Ile Gly Asn Leu Pro His Glu Val Asp Lys Ser Glu Leu Lys
355 360 365

Asp Phe Phe Gln Ser Tyr Gly Asn Val Val Glu Leu Arg Ile Asn Ser
370 375 380

Gly Gly Lys Leu Pro Asn Phe Gly Phe Val Val Phe Asp Asp Ser Glu
385 390 395 400

Pro Val Gln Lys Val Leu Ser Asn Arg Pro Ile Met Phe Arg Gly Glu
405 410 415

Val Arg Leu Asn Val Glu Glu Lys Lys Thr Arg Ala Ala Arg Glu Gly
420 425 430

Asp Arg Arg Asp Asn Arg Leu Arg Gly Pro Gly Gly Pro Arg Gly Gly
435 440 445

Leu Gly Gly Gly Met Arg Gly Pro Pro Arg Gly Gly Met Val Gln Lys
450 455 460

Pro Gly Phe Gly Val Gly Xaa Gly Xaa Ala Pro Arg Gln
465 470 475

<210> 978
<211> 339
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (128)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (326)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (336)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (339)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 978
Pro Val Ala Ala Val Ser Gly Arg Ala Val Gly Gly Ser Arg Gly Gly
1 5 10 15

Gly Arg Gly Gly Met Ala Ala Ala Ala Ala Gly Ala Gly Ser Gly Pro
20 25 30

Trp Ala Ala Gln Glu Lys Gln Phe Pro Pro Ala Leu Leu Ser Phe Phe
35 40 45

Ile Tyr Asn Pro Arg Phe Gly Pro Arg Glu Gly Gln Glu Glu Asn Lys
50 55 60

Ile Leu Phe Tyr His Pro Asn Glu Val Glu Lys Asn Glu Lys Ile Arg

65 70 75 80

Asn Val Gly Leu Cys Glu Ala Ile Val Gln Phe Thr Arg Thr Phe Ser
85 90 95

Pro Ser Lys Pro Ala Lys Ser Leu His Thr Gln Lys Asn Arg Gln Phe
100 105 110

Phe Asn Glu Pro Glu Glu Asn Phe Trp Met Val Met Val Val Arg Xaa
115 120 125

Pro Ile Ile Glu Lys Gln Ser Lys Asp Gly Lys Pro Val Ile Glu Tyr
130 135 140

Gln Glu Glu Glu Leu Leu Asp Lys Val Tyr Ser Ser Val Leu Arg Gln
145 150 155 160

Cys Tyr Ser Met Tyr Lys Leu Phe Asn Gly Thr Phe Leu Lys Ala Met
165 170 175

Glu Asp Gly Gly Val Lys Leu Leu Lys Glu Arg Leu Glu Lys Phe Phe
180 185 190

His Arg Tyr Leu Gln Thr Leu His Leu Gln Ser Cys Asp Leu Leu Asp
195 200 205

Ile Phe Gly Gly Ile Ser Phe Phe Pro Leu Asp Lys Met Thr Tyr Leu
210 215 220

Lys Ile Gln Ser Phe Ile Asn Arg Met Glu Glu Ser Leu Asn Ile Val
225 230 235 240

Lys Tyr Thr Ala Phe Leu Tyr Asn Asp Gln Leu Ile Trp Ser Gly Leu
245 250 255

Glu Gln Asp Asp Met Arg Ile Leu Tyr Lys Tyr Leu Thr Thr Ser Leu
260 265 270

Phe Pro Arg His Ile Glu Pro Glu Leu Ala Gly Arg Asp Ser Pro Ile
275 280 285

Arg Ala Glu Met Pro Gly Asn Leu Gln His Tyr Gly Arg Phe Leu Thr
290 295 300

Gly Pro Leu Asn Leu Asn Asp Pro Asp Ala Lys Cys Arg Phe Pro Lys
305 310 315 320

Ile Phe Val Asn Thr Xaa Asp Thr Tyr Glu Glu Leu His Leu Ile Xaa
325 330 335

Tyr Lys Xaa

<210> 979
<211> 283
<212> PRT
<213> Homo sapiens

<400> 979
His Arg Glu Arg Arg Val Gly Leu Arg Cys Ala Arg Arg Thr Ser Glu
1 5 10 15

Ala Ala Gly Ser Gly Ala Gly Pro Pro Gly Pro Leu Gln Gly Arg Ser
20 25 30

Gly Ser Ser Trp Ala Pro Arg Pro Gly Arg Arg Thr Glu Glu Arg Arg
35 40 45

Lys Gly Ala Gly Gly Thr Arg Pro Arg Pro Ala Ala Ala Met Asn Ser
50 55 60

Asn Val Glu Asn Leu Pro Pro His Ile Ile Arg Leu Val Tyr Lys Glu
65 70 75 80

Val Thr Thr Leu Thr Ala Asp Pro Pro Asp Gly Ile Lys Val Phe Pro
85 90 95

Asn Glu Glu Asp Leu Thr Asp Leu Gln Val Thr Ile Glu Gly Pro Glu
100 105 110

Gly Thr Pro Tyr Ala Gly Gly Leu Phe Arg Met Lys Leu Leu Leu Gly
115 120 125

Lys Asp Phe Pro Ala Ser Pro Pro Lys Gly Tyr Phe Leu Thr Lys Ile
130 135 140

Phe His Pro Asn Val Gly Ala Asn Gly Glu Ile Cys Val Asn Val Leu
145 150 155 160

Lys Arg Asp Trp Thr Ala Glu Leu Gly Ile Arg His Val Leu Leu Thr
165 170 175

Ile Lys Cys Leu Leu Ile His Pro Asn Pro Glu Ser Ala Leu Asn Glu
180 185 190

Glu Ala Gly Arg Leu Leu Leu Glu Asn Tyr Glu Glu Tyr Ala Ala Arg
195 200 205

Ala Arg Leu Leu Thr Glu Ile His Gly Gly Ala Gly Gly Pro Ser Gly
210 215 220

Arg Ala Glu Ala Gly Arg Ala Leu Ala Ser Gly Thr Glu Ala Ser Ser
225 230 235 240

Thr Asp Pro Gly Ala Pro Gly Gly Pro Gly Gly Ala Glu Gly Pro Met
245 250 255

Ala Lys Lys His Ala Gly Glu Arg Asp Lys Lys Leu Ala Ala Lys Lys
260 265 270

Lys Thr Asp Lys Lys Arg Ala Leu Arg Arg Leu
275 280

<210> 980
<211> 353
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (333)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (346)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 980
Arg Lys Gln Cys Gln Asp Ser Lys Asp Ser Asn His Leu Pro Lys Met
1 5 10 15

Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr Ser
20 25 30

Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln Ser
35 40 45

Ser Pro Asn Cys Ala Pro Glu Cys Asn Cys Pro Glu Ser Tyr Pro Ser
50 55 60

Ala Met Tyr Cys Asp Glu Leu Lys Leu Lys Ser Val Pro Met Val Pro
65 70 75 80

Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His Ile
85 90 95

Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile Leu
100 105 110

Asp His Asn Leu Leu Glu Asn Ser Lys Ile Lys Gly Arg Val Phe Ser
115 120 125

Lys Leu Lys Gln Leu Lys Lys Leu His Ile Asn His Asn Asn Leu Thr
130 135 140

Glu Ser Val Gly Pro Leu Pro Lys Ser Leu Glu Asp Leu Gln Leu Thr
145 150 155 160

His Asn Lys Ile Thr Lys Leu Gly Ser Phe Glu Gly Leu Val Asn Leu
165 170 175

Thr Phe Ile His Leu Gln His Asn Arg Leu Lys Glu Asp Ala Val Ser
180 185 190

Ala Ala Phe Lys Gly Leu Lys Ser Leu Glu Tyr Leu Asp Leu Ser Phe
195 200 205

Asn Gln Ile Ala Arg Leu Pro Ser Gly Leu Pro Val Ser Leu Leu Thr
210 215 220

Leu Tyr Leu Asp Asn Asn Lys Ile Ser Asn Ile Pro Asp Glu Tyr Phe
225 230 235 240

Lys Arg Phe Asn Ala Leu Gln Tyr Leu Arg Leu Ser His Asn Glu Leu
245 250 255

Ala Asp Ser Gly Ile Pro Gly Asn Ser Phe Asn Val Ser Ser Leu Val
260 265 270

Glu Leu Asp Leu Ser Tyr Asn Lys Leu Lys Asn Ile Pro Thr Val Asn
275 280 285

Glu Asn Leu Glu Asn Tyr Tyr Leu Glu Val Asn Gln Leu Glu Lys Phe
290 295 300

Asp Ile Lys Ser Phe Cys Lys Ile Leu Gly Pro Leu Ser Tyr Ser Lys
305 310 315 320

Ile Lys His Leu Arg Leu Asp Gly Asn Arg Ile Ser Xaa Thr Ser Leu
325 330 335

Pro Pro Asp Met Tyr Glu Cys Leu Arg Xaa Ala Asn Glu Val Thr Leu
340 345 350

Asn

<210> 981
<211> 343
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (343)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 981
Asn Leu Thr Lys Asn Met Thr Ala Leu Ser Ser Glu Asn Cys Ser Phe
1   5   10   15

Gln Tyr Gln Leu Arg Gln Thr Asn Gln Pro Leu Asp Val Asn Tyr Leu
            20   25   30

Leu Phe Leu Ile Ile Leu Gly Lys Ile Leu Leu Asn Ile Leu Thr Leu
        35   40   45

Gly Met Arg Arg Lys Asn Thr Cys Gln Asn Phe Met Glu Tyr Phe Cys
    50   55   60

Ile Ser Leu Ala Phe Val Asp Leu Leu Leu Leu Val Asn Ile Ser Ile
65   70   75   80

Ile Leu Tyr Phe Arg Asp Phe Val Leu Leu Ser Ile Arg Phe Thr Lys
                85   90   95

Tyr His Ile Cys Leu Phe Thr Gln Ile Ile Ser Phe Thr Tyr Gly Phe
            100   105   110

Leu His Tyr Pro Val Phe Leu Thr Ala Cys Ile Asp Tyr Cys Leu Asn
        115   120   125

Phe Ser Lys Thr Thr Lys Leu Ser Phe Lys Cys Gln Lys Leu Phe Tyr
    130   135   140

Phe Phe Thr Val Ile Leu Ile Trp Ile Ser Val Leu Ala Tyr Val Leu
145   150   155   160

Gly Asp Pro Ala Ile Tyr Gln Ser Leu Lys Ala Gln Asn Ala Tyr Ser
                165   170   175

Arg His Cys Pro Phe Tyr Val Ser Ile Gln Ser Tyr Trp Leu Ser Phe
            180   185   190

Phe Met Val Met Ile Leu Phe Val Ala Phe Ile Thr Cys Trp Glu Glu
        195   200   205

Val Thr Thr Leu Val Gln Ala Ile Arg Ile Thr Ser Tyr Met Asn Glu

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    210                 215                 220

Thr Ile Leu Tyr Phe Pro Phe Ser Ser His Ser Ser Tyr Thr Val Arg
225                 230                 235                 240

Ser Lys Lys Ile Phe Leu Ser Lys Leu Ile Val Cys Phe Leu Ser Thr
                245                 250                 255

Trp Leu Pro Phe Val Leu Leu Gln Val Ile Ile Val Leu Leu Lys Val
            260                 265                 270

Gln Ile Pro Ala Tyr Ile Glu Met Asn Ile Pro Trp Leu Tyr Phe Val
        275                 280                 285

Asn Ser Phe Leu Ile Ala Thr Val Tyr Trp Phe Asn Cys His Lys Leu
    290                 295                 300

Asn Leu Lys Asp Ile Gly Leu Pro Leu Asp Pro Phe Val Asn Trp Lys
305                 310                 315                 320

Cys Cys Phe Ile Pro Leu Thr Ile Pro Asn Leu Glu Gln Ile Glu Lys
                325                 330                 335

Pro Ile Ser Ile Met Ile Xaa
            340



<210> 982
<211> 142
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (111)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (114)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (121)
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (122)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (126)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (127)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (132)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 982
Gly Leu Pro Pro Ser Thr Phe Leu His Ser Ala Val Ser Thr Leu Pro
1 5 10 15

His Arg Pro Ser Pro Pro Ser Leu Leu Pro Ala Pro Cys Lys Pro Leu
20 25 30

Arg Leu Gly Leu Ala Thr Val Pro Ala Gly Ser Pro Gly Leu Gly Val
35 40 45

Gly Asp Ser Leu Gln Ala Arg Ser Pro Glu Thr Ser Glu Gly His Pro
50 55 60

Leu Arg Val Ala Arg Pro Pro Val Ala Asn Leu Ser Ala Ala Ser Ala
65 70 75 80

Thr Ser Pro Ala Gly Pro Trp Phe Arg Trp Pro Pro Arg Cys Leu Ala
85 90 95

Glu Thr Arg His Gly Pro Ser Ala Gly Pro His Xaa Phe Pro Xaa Pro
100 105 110

Gly Xaa Trp His Cys Ser Arg Gln Xaa Xaa Gly His Gln Xaa Xaa Asn
115 120 125

Arg Thr Gln Xaa Pro Ala Gln Thr Ala Ala Gly Met Gly Ala
130 135 140

<210> 983
<211> 193
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (135)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (139)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 983
Val Asn Phe Lys Ala Phe Glu Met Gly Lys Asp Tyr Tyr Cys Ile Leu
1   5   10   15

Gly Ile Glu Lys Gly Ala Ser Asp Glu Asp Ile Lys Lys Ala Tyr Arg
            20   25   30

Lys Gln Ala Leu Lys Phe His Pro Asp Lys Asn Lys Ser Pro Gln Ala
        35   40   45

Glu Glu Lys Phe Lys Glu Val Ala Glu Ala Tyr Glu Val Leu Ser Asp
    50   55   60

Pro Lys Lys Arg Glu Ile Tyr Xaa Gln Phe Gly Glu Glu Gly Leu Lys
65   70   75   80

Gly Gly Ala Gly Gly Thr Asp Gly Gln Gly Gly Thr Phe Arg Tyr Thr
                85   90   95

Phe His Gly Asp Pro His Ala Thr Phe Ala Ala Phe Phe Gly Gly Ser
            100   105   110

Asn Pro Phe Glu Ile Phe Phe Gly Arg Arg Met Gly Gly Gly Arg Asp
        115   120   125

Ser Glu Glu Met Glu Ile Xaa Gly Asp Pro Xaa Ser Ala Phe Gly Phe
    130   135   140

Ser Met Asn Gly Tyr Pro Arg Asp Arg Asn Ser Val Gly Pro Ser Arg
145   150   155   160

Leu Lys Gln Asp Pro Pro Val Ile His Glu Leu Arg Val Ser Leu Glu
165 170 175

Glu Ile Tyr Ser Gly Cys Thr Lys Arg Asp Glu Arg Phe Leu Glu Lys
180 185 190

Gly

<210> 984
<211> 402
<212> PRT
<213> Homo sapiens

<400> 984
Lys Ser Tyr Glu Met Glu Leu Glu Glu Gly Lys Ala Gly Ser Gly Leu
1 5 10 15

Arg Gln Tyr Tyr Leu Ser Lys Ile Glu Glu Leu Gln Leu Ile Val Asn
20 25 30

Asp Lys Ser Gln Asn Leu Arg Arg Leu Gln Ala Gln Arg Asn Glu Leu
35 40 45

Asn Ala Lys Val Arg Leu Leu Arg Glu Glu Leu Gln Leu Leu Gln Glu
50 55 60

Gln Gly Ser Tyr Val Gly Glu Val Val Arg Ala Met Asp Lys Lys Lys
65 70 75 80

Val Leu Val Lys Val His Pro Glu Gly Lys Phe Val Val Asp Val Asp
85 90 95

Lys Asn Ile Asp Ile Asn Asp Val Thr Pro Asn Cys Arg Val Ala Leu
100 105 110

Arg Asn Asp Ser Tyr Thr Leu His Lys Ile Leu Pro Asn Lys Val Asp
115 120 125

Pro Leu Val Ser Leu Met Met Val Glu Lys Val Pro Asp Ser Thr Tyr
130 135 140

Glu Met Ile Gly Gly Leu Asp Lys Gln Ile Lys Glu Ile Lys Glu Val
145 150 155 160

Ile Glu Leu Pro Val Lys His Pro Glu Leu Phe Glu Ala Leu Gly Ile
165 170 175

```
Ala Gln Pro Lys Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys
            180                 185                 190

Thr Leu Leu Ala Arg Ala Val Ala His His Thr Asp Cys Thr Phe Ile
        195                 200                 205

Arg Val Ser Gly Ser Glu Leu Val Gln Lys Phe Ile Gly Glu Gly Ala
    210                 215                 220

Arg Met Val Arg Glu Leu Phe Val Met Ala Arg Glu His Ala Pro Ser
225                 230                 235                 240

Ile Ile Phe Met Asp Glu Ile Asp Ser Ile Gly Ser Ser Arg Leu Glu
                245                 250                 255

Gly Gly Ser Gly Gly Asp Ser Glu Val Gln Arg Thr Met Leu Glu Leu
            260                 265                 270

Leu Asn Gln Leu Asp Gly Phe Glu Ala Thr Lys Asn Ile Lys Val Ile
        275                 280                 285

Met Ala Thr Asn Arg Ile Asp Ile Leu Asp Ser Ala Leu Leu Arg Pro
    290                 295                 300

Gly Arg Ile Asp Arg Lys Ile Glu Phe Pro Pro Pro Asn Glu Glu Ala
305                 310                 315                 320

Arg Leu Asp Ile Leu Lys Ile His Ser Arg Lys Met Asn Leu Thr Arg
                325                 330                 335

Gly Ile Asn Leu Arg Lys Ile Ala Glu Leu Met Pro Gly Ala Ser Gly
            340                 345                 350

Ala Glu Val Lys Gly Val Cys Thr Glu Ala Gly Met Tyr Ala Leu Arg
        355                 360                 365

Glu Arg Arg Val His Val Thr Gln Glu Asp Phe Glu Met Ala Val Ala
    370                 375                 380

Lys Val Met Gln Lys Asp Ser Glu Lys Asn Met Ser Ile Lys Lys Leu
385                 390                 395                 400

Trp Lys
```

<210> 985
<211> 347
<212> PRT
<213> Homo sapiens

<400> 985

Arg Arg Arg Arg Trp His Pro Gly Pro Gly Gly Pro Arg Arg Thr Ala
1   5   10   15

Gly Lys Gly Pro Arg Lys Val Ala Ser Ala Ser Ala Ala Ala Ser Thr
            20   25   30

Leu Ser Glu Pro Pro Arg Arg Thr Gln Glu Ser Arg Thr Arg Thr Arg
        35   40   45

Ala Leu Gly Leu Pro Thr Leu Pro Met Glu Lys Leu Ala Ala Ser Thr
    50   55   60

Glu Pro Gln Gly Pro Arg Pro Val Leu Gly Arg Glu Ser Val Gln Val
65   70   75   80

Pro Asp Asp Gln Asp Phe Arg Ser Phe Arg Ser Glu Cys Glu Ala Glu
                85   90   95

Val Gly Trp Asn Leu Thr Tyr Ser Arg Ala Gly Val Ser Val Trp Val
            100   105   110

Gln Ala Val Glu Met Asp Arg Thr Leu His Lys Ile Lys Cys Arg Met
        115   120   125

Glu Cys Cys Asp Val Pro Ala Glu Thr Leu Tyr Asp Val Leu His Asp
    130   135   140

Ile Glu Tyr Arg Lys Lys Trp Asp Ser Asn Val Ile Glu Thr Phe Asp
145   150   155   160

Ile Ala Arg Leu Thr Val Asn Ala Asp Val Gly Tyr Tyr Ser Trp Arg
                165   170   175

Cys Pro Lys Pro Leu Lys Asn Arg Asp Val Ile Thr Leu Arg Ser Trp
            180   185   190

Leu Pro Met Gly Ala Asp Tyr Ile Ile Met Asn Tyr Ser Val Lys His
        195   200   205

Pro Lys Tyr Pro Pro Arg Lys Asp Leu Val Arg Ala Val Ser Ile Gln
    210   215   220

Thr Gly Tyr Leu Ile Gln Ser Thr Gly Pro Lys Ser Cys Val Ile Thr
225   230   235   240

Tyr Leu Ala Gln Val Asp Pro Lys Gly Ser Leu Pro Lys Trp Val Val
                245   250   255

Asn Lys Ser Ser Gln Phe Leu Ala Pro Lys Ala Met Lys Lys Met Tyr

```
            260                 265                 270

Lys Ala Cys Leu Lys Tyr Pro Glu Trp Lys Gln Lys His Leu Pro His
        275                 280                 285

Phe Lys Pro Trp Leu His Pro Glu Gln Ser Pro Leu Pro Ser Leu Ala
    290                 295                 300

Leu Ser Glu Leu Ser Val Gln His Ala Asp Ser Leu Glu Asn Ile Asp
305                 310                 315                 320

Glu Ser Ala Val Ala Glu Ser Arg Glu Glu Arg Met Gly Gly Ala Gly
                325                 330                 335

Gly Glu Gly Ser Asp Asp Asp Thr Ser Leu Thr
            340                 345



<210> 986
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 986
Ala Ser Ile Cys Ala Asp Ala Lys Leu Trp Thr Met Tyr Ala Arg Pro
  1               5                  10                  15

Ser Asn Arg Gln Arg Cys Leu Gly Ser Lys His Thr Glu Arg Thr Trp
             20                  25                  30

Thr Ala Trp Xaa Arg Ser Leu Ile Arg Pro Phe Ser Met His Ile Leu
         35                  40                  45

Pro Lys Gln Ser Gln Ile Pro Leu Lys Gly Ala Asp Ser Ile Ser Ser
     50                  55                  60

Ser Val Gln Thr Leu Arg Ala Glu Arg Ser Gly Ser Gly Ser His Val
 65                  70                  75                  80

Thr Ala Gln Asn Asn Leu Arg Asn Pro Leu Cys Pro Glu Gly Ser Leu
                 85                  90                  95

Thr Ser Pro Ser Gly Ser Glu Gln Ser Leu
            100                 105
```

<210> 987
<211> 172
<212> PRT
<213> Homo sapiens

<400> 987
Thr Pro Arg Gly Ala Val Lys Pro Ser Ala Asn Lys Tyr Pro Ile Phe
1 5 10 15

Phe Phe Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe
20 25 30

Pro Tyr Lys Glu Tyr Lys Asp Lys Phe Gly Lys Ser Asn Lys Arg Lys
35 40 45

Gly Phe Asn Glu Gly Leu Trp Glu Ile Glu Asn Asn Pro Gly Val Lys
50 55 60

Phe Thr Gly Tyr Gln Ala Ile Gln Gln Gln Ser Ser Ser Glu Thr Glu
65 70 75 80

Gly Glu Gly Gly Asn Thr Ala Asp Ala Ser Ser Glu Glu Glu Gly Asp
85 90 95

Arg Val Glu Glu Asp Gly Lys Gly Lys Arg Lys Asn Glu Lys Ala Gly
100 105 110

Ser Lys Arg Lys Lys Ser Tyr Thr Ser Lys Lys Ser Ser Lys Gln Ser
115 120 125

Arg Lys Ser Pro Gly Asp Glu Asp Asp Lys Asp Cys Lys Glu Glu Glu
130 135 140

Asn Lys Ser Ser Ser Glu Gly Gly Asp Ala Gly Asn Asp Thr Arg Asn
145 150 155 160

Thr Thr Ser Asp Leu Gln Lys Thr Ser Glu Gly Thr
165 170

<210> 988
<211> 238
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (101)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (146)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 988
```
Ala Lys Gln Asp Pro Val Pro Glu Gln Glu Met Ser Pro Ser Ile Ser
 1               5                  10                  15

Asp Pro Cys Leu Gly Gln Ala Leu Met Gly Gly Pro Ser Phe Lys Ala
            20                  25                  30

Val Val Gly Thr Ala Pro Pro Asn Ala Ser Leu Ser Phe Leu Pro Ile
        35                  40                  45

His Gln Tyr Thr Ala Gly Pro Phe Leu Val Phe Val Gln Gln Glu Thr
    50                  55                  60

His Phe Trp Trp Asp Met Pro Ser Ser Ala Thr Gly Pro Leu Thr Pro
65                  70                  75                  80

Cys Ile Ser Val Leu Pro Val Ser Ala Gly Thr Asp Ser Lys Gly Lys
                85                  90                  95

Pro Ser Val Trp Xaa Ile Gly Gly Trp Glu Gln Arg Gly Glu Asn Ala
            100                 105                 110

Val Leu Ser Phe Cys Leu Gly Ile Pro His Thr Thr Trp Val Leu Pro
        115                 120                 125

Gly Lys Pro Val Leu Ser Lys Thr Met Asp Leu Ala Ser Pro Thr Gly
    130                 135                 140

Leu Xaa Ser Gln His Leu Arg Glu Gly Gly Trp Lys Arg Leu Cys Pro
145                 150                 155                 160

His Phe Glu Leu Gln Ala Gly Ser Ala Ala Leu Lys Pro Ser Ser Asp
                165                 170                 175

Phe Leu Thr Gln Asp Pro Ala Pro Gly Arg Arg Arg Val Gly Ala Gly
            180                 185                 190

Leu Val Gly Gln Lys Glu Ala Ser Ala Gly Leu Glu Asp Pro Ser Ser
        195                 200                 205

Thr Ser His Ser Val Ser Ser Ser Trp Glu Asn Leu Cys Gln Ala Arg
    210                 215                 220

Ala Val Ile Gly Pro His Glu Val Ser Glu Ala Pro Ser Trp
```

225 230 235

<210> 989
<211> 74
<212> PRT
<213> Homo sapiens

<400> 989
Ser Leu Ile Lys Ala Leu Tyr Ile Leu Tyr Gly Phe Arg His His His
1 5 10 15

Thr Lys Lys Leu Thr Pro Ser Ile Pro Val Phe Val Gly Gln Ala Ser
20 25 30

Phe Phe Ser Pro Cys Ser Val Ser His Thr Val Cys Leu Gln Lys Leu
35 40 45

Leu Ile Gly Ala Lys Tyr Asn Cys Gln Tyr Asn Leu Lys Thr Thr Met
50 55 60

Cys Pro Arg Arg Pro Thr Cys Leu Phe Pro
65 70

<210> 990
<211> 295
<212> PRT
<213> Homo sapiens

<400> 990
Ala Pro Ala Arg Pro Gly Ser Leu Pro Ser Thr Arg Ser Ala Pro Leu
1 5 10 15

Val Pro Ser Ser Arg Arg Arg Pro Ala Glu Ser Pro Leu Arg Ser Arg
20 25 30

Arg Cys Arg Gly Asp Met Val Leu Cys Val Gln Gly Pro Arg Pro Leu
35 40 45

Leu Ala Val Glu Arg Thr Gly Gln Arg Pro Leu Trp Ala Pro Ser Leu
50 55 60

Glu Leu Pro Lys Pro Val Met Gln Pro Leu Pro Ala Gly Ala Phe Leu
65 70 75 80

Glu Glu Val Ala Glu Gly Thr Pro Ala Gln Thr Glu Ser Glu Pro Lys
85 90 95

Val Leu Asp Pro Glu Glu Asp Leu Leu Cys Ile Ala Lys Thr Phe Ser
100 105 110

Tyr Leu Arg Glu Ser Gly Trp Tyr Trp Gly Ser Ile Thr Ala Ser Glu
115 120 125

Ala Arg Gln His Leu Gln Lys Met Pro Glu Gly Thr Phe Leu Val Arg
130 135 140

Asp Ser Thr His Pro Ser Tyr Leu Phe Thr Leu Ser Val Lys Thr Thr
145 150 155 160

Arg Gly Pro Thr Asn Val Arg Ile Glu Tyr Ala Asp Ser Ser Phe Arg
165 170 175

Leu Asp Ser Asn Cys Leu Ser Arg Pro Arg Ile Leu Ala Phe Pro Asp
180 185 190

Val Val Ser Leu Val Gln His Tyr Val Ala Ser Cys Thr Ala Asp Thr
195 200 205

Arg Ser Asp Ser Pro Asp Pro Ala Pro Thr Pro Ala Leu Pro Met Pro
210 215 220

Lys Glu Asp Ala Pro Ser Asp Pro Ala Leu Pro Ala Pro Pro Pro Ala
225 230 235 240

Thr Ala Val His Leu Lys Leu Val Gln Pro Phe Val Arg Arg Ser Ser
245 250 255

Ala Arg Ser Leu Gln His Leu Cys Arg Leu Val Ile Asn Arg Leu Val
260 265 270

Ala Asp Val Asp Cys Leu Pro Leu Pro Arg Arg Met Ala Asp Tyr Leu
275 280 285

Arg Gln Tyr Pro Phe Gln Leu
290 295

<210> 991
<211> 58
<212> PRT
<213> Homo sapiens

<400> 991
Leu His Lys Val Ser Ile Leu Leu Tyr Ser Ala Val Leu Val Ser Phe
1 5 10 15

Ser Cys Ile Gly Phe His Cys Ile Tyr Ser Leu Phe Met Leu Asn Leu

20 25 30

Ala Lys Asp Glu His Cys Pro Pro Leu Lys Cys Leu Cys His Phe Glu
35 40 45

Phe Cys Ala Asn Phe Val Ala Arg Met Arg
50 55

<210> 992
<211> 203
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 992
Ala His Ala Ser Pro Thr Arg Xaa Glu Ala Arg Val Val Val Val Arg
1 5 10 15

Cys Leu Pro Ala Cys Val Arg Asp Leu Pro Asp Ser Val Ala Ala Met
20 25 30

Ala Ser Asp Glu Gly Lys Leu Phe Val Gly Gly Leu Ser Phe Asp Thr
35 40 45

Asn Glu Gln Ser Leu Glu Gln Val Phe Ser Lys Tyr Gly Gln Ile Ser
50 55 60

Glu Val Val Val Val Lys Asp Arg Glu Thr Gln Arg Ser Arg Gly Phe
65 70 75 80

Gly Phe Val Thr Phe Glu Asn Ile Asp Asp Ala Lys Asp Ala Met Met
85 90 95

Ala Met Asn Gly Lys Ser Val Asp Gly Arg Gln Ile Arg Val Asp Gln
100 105 110

Ala Gly Lys Ser Ser Asp Asn Arg Ser Arg Gly Tyr Arg Gly Gly Ser
115 120 125

Ala Gly Gly Arg Gly Phe Phe Arg Gly Gly Arg Gly Arg Gly Arg Gly
130 135 140

Phe Ser Arg Gly Gly Gly Asp Arg Gly Tyr Gly Gly Asn Arg Phe Glu
145 150 155 160

Ser Arg Ser Gly Gly Tyr Gly Gly Ser Arg Asp Tyr Tyr Ser Ser Arg
165 170 175

Ser Gln Ser Gly Gly Tyr Ser Asp Arg Ser Ser Gly Gly Ser Tyr Arg
180 185 190

Asp Ser Tyr Asp Ser Tyr Ala Thr His Asn Glu
195 200

<210> 993
<211> 252
<212> PRT
<213> Homo sapiens

<400> 993
Gly Gly Leu Ala Trp Arg Ala Leu Arg Thr Ser Gly Thr Leu Leu Arg
1 5 10 15

Val Glu Arg Leu Leu Leu Glu Asp Tyr Cys Pro Glu Glu Lys Met Phe
20 25 30

Gly Phe His Lys Pro Lys Met Tyr Arg Ser Ile Glu Gly Cys Cys Ile
35 40 45

Cys Arg Ala Lys Ser Ser Ser Ser Arg Phe Thr Asp Ser Lys Arg Tyr
50 55 60

Glu Lys Asp Phe Gln Ser Cys Phe Gly Leu His Glu Thr Arg Ser Gly
65 70 75 80

Asp Ile Cys Asn Ala Cys Val Leu Leu Val Lys Arg Trp Lys Lys Leu
85 90 95

Pro Ala Gly Ser Lys Lys Asn Trp Asn His Val Val Asp Ala Arg Ala
100 105 110

Gly Pro Ser Leu Lys Thr Thr Leu Lys Pro Lys Lys Val Lys Thr Leu
115 120 125

Ser Gly Asn Arg Ile Lys Ser Asn Gln Ile Ser Lys Leu Gln Lys Glu
130 135 140

Phe Lys Arg His Asn Ser Asp Ala His Ser Thr Thr Ser Ser Ala Ser
145 150 155 160

Pro Ala Gln Ser Pro Cys Tyr Ser Asn Gln Ser Asp Asp Gly Ser Asp
165 170 175

Thr Glu Met Ala Ser Gly Ser Asn Arg Thr Pro Val Phe Ser Phe Leu

```
            180                 185                 190

Asp Leu Thr Tyr Trp Lys Arg Gln Lys Ile Cys Cys Gly Ile Ile Tyr
        195                 200                 205

Lys Gly Arg Phe Gly Glu Val Leu Ile Asp Thr His Leu Phe Lys Pro
    210                 215                 220

Cys Cys Ser Asn Lys Lys Ala Ala Ala Glu Lys Pro Glu Glu Gln Gly
225                 230                 235                 240

Gln Ser Leu Cys Pro Ser Pro Leu Arg Ser Gly Asp
                245                 250



<210> 994
<211> 170
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 994
Arg Thr Arg Gly Xaa Asp Thr Gln Pro Thr Val Cys Thr Asp Ala Pro
  1               5                  10                  15

Ser Leu Leu Pro Leu Ser Arg Leu His Leu Arg Gly Ser Trp Asp Arg
            20                  25                  30

Arg Ser Val Ala Asn Met Gln Leu Phe Val Arg Ala Gln Glu Leu His
        35                  40                  45

Thr Phe Glu Val Thr Gly Gln Glu Thr Val Ala Gln Ile Lys Ala His
    50                  55                  60

Val Ala Ser Leu Glu Gly Ile Ala Pro Glu Asp Gln Val Val Leu Leu
65                  70                  75                  80

Ala Gly Ala Pro Leu Glu Asp Glu Ala Thr Leu Gly Gln Cys Gly Val
                85                  90                  95

Glu Ala Leu Thr Thr Leu Glu Val Ala Gly Arg Met Leu Gly Gly Lys
            100                 105                 110

Val His Gly Ser Leu Ala Arg Ala Gly Lys Val Arg Gly Gln Thr Pro
        115                 120                 125
```

Lys Val Ala Lys Gln Glu Lys Lys Lys Lys Lys Thr Gly Arg Ala Lys
130 135 140

Arg Arg Met Gln Tyr Asn Arg Arg Phe Val Asn Val Val Pro Thr Phe
145 150 155 160

Gly Lys Lys Lys Gly Pro Asn Ala Asn Ser
165 170

<210> 995
<211> 156
<212> PRT
<213> Homo sapiens

<400> 995
Gly Ser Gly Thr His Pro Ala Arg Ala Ala Pro Ala Pro His Ala Arg
1 5 10 15

Ala Ser Phe Ser Arg Pro Leu Ala Pro Arg Arg Ser His Leu Ser Ser
20 25 30

Leu Ala His Ala Arg Pro Ala Arg Glu Pro Arg Arg Arg Leu Gly Pro
35 40 45

Ala Glu Ala Pro Pro Arg His Val Phe Ala Ser Arg Arg Lys Leu Glu
50 55 60

Thr Lys Ala Gly His Pro Pro Ala Val Lys Ala Gly Gly Met Arg Ile
65 70 75 80

Val Gln Lys His Pro His Thr Gly Asp Thr Lys Glu Glu Lys Asp Lys
85 90 95

Asp Asp Gln Glu Trp Glu Ser Pro Ser Pro Pro Lys Pro Thr Val Phe
100 105 110

Ile Ser Gly Val Ile Ala Arg Gly Asp Lys Asp Phe Pro Pro Ala Ala
115 120 125

Ala Gln Val Ala His Gln Lys Pro His Ala Ser Met Asp Lys His Pro
130 135 140

Ser Pro Arg Thr Gln His Ile Gln Gln Pro Arg Lys
145 150 155

<210> 996
<211> 217

<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 996
Asn Ser Ala Glu Gln Glu Gly Ser Gln Trp Ser Leu Pro Val Leu His
1   5   10   15

Ser Val Pro Asp Pro Ala Cys Leu Thr Leu Xaa Arg Val Ser Lys Gly
            20   25   30

Leu Ala Ala Val Arg Ser Ser Val Pro Arg Ala Gly Gly Val Ser Arg
        35   40   45

Arg Leu Ala Ala Val Arg Ser Thr Val Leu Cys Arg Ala Val Gly Cys
    50   55   60

Ile Leu Ala Glu Leu Leu Ala His Arg Pro Leu Leu Pro Gly Thr Ser
65   70   75   80

Glu Ile His Gln Ile Asp Leu Ile Val Gln Leu Leu Gly Thr Pro Ser
                85   90   95

Glu Asn Ile Trp Pro Gly Phe Ser Lys Leu Pro Leu Val Gly Gln Tyr
            100   105   110

Ser Leu Arg Lys Gln Pro Tyr Asn Asn Leu Lys His Lys Phe Pro Trp
        115   120   125

Leu Ser Glu Ala Gly Leu Arg Cys Cys Thr Ser Cys Ser Cys Thr Thr
    130   135   140

Leu Arg Lys Gly Arg Arg Pro Gly Thr Ala Trp Arg Ala Pro Ile Ser
145   150   155   160

Arg Arg Ser Pro Tyr Pro Val Ser Arg Ser Ser Cys Arg Pro Phe Pro
                165   170   175

Thr Thr Ala Thr Ser Gly Pro Pro Gln Pro Pro Pro Arg Ala Arg Ala
            180   185   190

Ser Ala Val Asn Pro Asp Gly Gly Pro Gly Thr Arg Leu Tyr Ser His
        195   200   205

Thr Arg Ser Ser Asp Gln Trp Cys Leu
    210   215

<210> 997
<211> 466
<212> PRT
<213> Homo sapiens

<400> 997
Val Ser Pro Arg Ala Gly Gly Ala Gly Asn Asn Arg Gly Arg Ala His
1   5   10   15

Arg Ala Ser Ser Cys Ser Leu Pro Ala Pro Pro Ala Thr Leu Asp Pro
            20   25   30

Arg Ile Pro Pro Ala Arg Leu Pro Ala Met Ala Asp Lys Glu Ala Ala
        35   40   45

Phe Asp Asp Ala Val Glu Glu Arg Val Ile Asn Glu Glu Tyr Lys Ile
    50   55   60

Trp Lys Lys Asn Thr Pro Phe Leu Tyr Asp Leu Val Met Thr His Ala
65   70   75   80

Leu Glu Trp Pro Ser Leu Thr Ala Gln Trp Leu Pro Asp Val Thr Arg
                85   90   95

Pro Glu Gly Lys Asp Phe Ser Ile His Arg Leu Val Leu Gly Thr His
            100   105   110

Thr Ser Asp Glu Gln Asn His Leu Val Ile Ala Ser Val Gln Leu Pro
        115   120   125

Asn Asp Asp Ala Gln Phe Asp Ala Ser His Tyr Asp Ser Glu Lys Gly
    130   135   140

Glu Phe Gly Gly Phe Gly Ser Val Ser Gly Lys Ile Glu Ile Glu Ile
145   150   155   160

Lys Ile Asn His Glu Gly Glu Val Asn Arg Ala Arg Tyr Met Pro Gln
                165   170   175

Asn Pro Cys Ile Ile Ala Thr Lys Thr Pro Ser Ser Asp Val Leu Val
            180   185   190

Phe Asp Tyr Thr Lys His Pro Ser Lys Pro Asp Pro Ser Gly Glu Cys
        195   200   205

Asn Pro Asp Leu Arg Leu Arg Gly His Gln Lys Glu Gly Tyr Gly Leu
    210   215   220

Ser Trp Asn Pro Asn Leu Ser Gly His Leu Leu Ser Ala Ser Asp Asp

225 230 235 240

His Thr Ile Cys Leu Trp Asp Ile Ser Ala Val Pro Lys Glu Gly Lys
245 250 255

Val Val Asp Ala Lys Thr Ile Phe Thr Gly His Thr Ala Val Val Glu
260 265 270

Asp Val Ser Trp His Leu Leu His Glu Ser Leu Phe Gly Ser Val Ala
275 280 285

Asp Asp Gln Lys Leu Met Ile Trp Asp Thr Arg Ser Asn Asn Thr Ser
290 295 300

Lys Pro Ser His Ser Val Asp Ala His Thr Ala Glu Val Asn Cys Leu
305 310 315 320

Ser Phe Asn Pro Tyr Ser Glu Phe Ile Leu Ala Thr Gly Ser Ala Asp
325 330 335

Lys Thr Val Ala Leu Trp Asp Leu Arg Asn Leu Lys Leu Lys Leu His
340 345 350

Ser Phe Glu Ser His Lys Asp Glu Ile Phe Gln Val Gln Trp Ser Pro
355 360 365

His Asn Glu Thr Ile Leu Ala Ser Ser Gly Thr Asp Arg Arg Leu Asn
370 375 380

Val Trp Asp Leu Ser Lys Ile Gly Glu Glu Gln Ser Pro Glu Asp Ala
385 390 395 400

Glu Asp Gly Pro Pro Glu Leu Leu Phe Ile His Gly Gly His Thr Ala
405 410 415

Lys Ile Ser Asp Phe Ser Trp Asn Pro Asn Glu Pro Trp Val Ile Cys
420 425 430

Ser Val Ser Glu Asp Asn Ile Met Gln Val Trp Gln Met Ala Glu Asn
435 440 445

Ile Tyr Asn Asp Glu Asp Pro Glu Gly Ser Val Asp Pro Glu Gly Gln
450 455 460

Gly Ser
465

<210> 998
<211> 165

<212> PRT
<213> Homo sapiens

<400> 998
Thr Arg Pro Pro Thr Arg Arg Pro Thr Arg Pro Pro Lys Ala Lys Lys
1 5 10 15

Glu Ala Pro Ala Pro Pro Lys Ala Glu Ala Lys Ala Lys Ala Leu Lys
20 25 30

Ala Lys Lys Ala Val Leu Lys Gly Val His Ser His Lys Lys Lys Lys
35 40 45

Ile Arg Thr Ser Pro Thr Phe Arg Arg Pro Lys Thr Leu Arg Leu Arg
50 55 60

Arg Gln Pro Lys Tyr Pro Arg Lys Ser Ala Pro Arg Arg Asn Lys Leu
65 70 75 80

Asp His Tyr Ala Ile Ile Lys Phe Pro Leu Thr Thr Glu Ser Ala Met
85 90 95

Lys Lys Ile Glu Asp Asn Asn Thr Leu Val Phe Ile Val Asp Val Lys
100 105 110

Ala Asn Lys His Gln Ile Lys Gln Ala Val Lys Lys Leu Tyr Asp Ile
115 120 125

Asp Val Ala Lys Val Asn Thr Leu Ile Arg Pro Asp Gly Glu Lys Lys
130 135 140

Ala Tyr Val Arg Leu Ala Pro Asp Tyr Asp Ala Leu Asp Val Ala Asn
145 150 155 160

Lys Ile Gly Ile Ile
165

<210> 999
<211> 194
<212> PRT
<213> Homo sapiens

<400> 999
Pro Glu Asn Ser Thr Ser Ser Phe Leu Leu Trp Gly Cys Pro Pro Ser
1 5 10 15

Val Val Cys Phe Thr Val Gly Ser Pro Ala Arg Arg Pro Gln Cys Phe
20 25 30

Leu Arg Ala Glu Met Ala Asn Ser Gly Leu Gln Leu Leu Gly Phe Ser
35 40 45

Met Ala Leu Leu Gly Trp Val Gly Leu Val Ala Cys Thr Ala Ile Pro
50 55 60

Gln Trp Gln Met Ser Ser Tyr Ala Gly Asp Asn Ile Ile Thr Ala Gln
65 70 75 80

Ala Met Tyr Lys Gly Leu Trp Met Asp Cys Val Thr Gln Ser Thr Gly
85 90 95

Met Met Ser Cys Lys Met Tyr Asp Ser Val Leu Ala Leu Ser Ala Ala
100 105 110

Leu Gln Ala Thr Arg Ala Leu Met Val Val Ser Leu Val Leu Gly Phe
115 120 125

Leu Ala Met Phe Val Ala Thr Met Gly Met Lys Cys Thr Arg Cys Gly
130 135 140

Gly Asp Asp Lys Val Lys Lys Ala Arg Ile Ala Met Gly Gly Gly Ile
145 150 155 160

Ile Phe Ile Val Ala Gly Leu Ala Ala Leu Val Ala Cys Ser Trp Tyr
165 170 175

Gly His Gln Ile Val Thr Asp Phe Tyr Asn Pro Leu Ile Pro Thr Asn
180 185 190

Ile Lys

<210> 1000
<211> 362
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (25)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1000
Arg Gln Gln Arg Thr Arg Lys Lys Lys Pro Ala Gly Ala Ala Leu Gly
1 5 10 15

Ala Leu Gly Pro Arg Ala Gln Leu Xaa Ala Ala Ala Gln Thr Asn Ser
20 25 30

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Asn Ala Ala Gly Lys Gln Leu Arg Lys Glu Ser Gln Lys Asp Arg Lys
        35                  40                  45

Asn Pro Leu Pro Pro Ser Val Gly Val Val Asp Lys Lys Glu Glu Thr
    50                  55                  60

Gln Pro Pro Val Ala Leu Lys Lys Glu Gly Ile Arg Arg Val Gly Arg
65                  70                  75                  80

Arg Pro Asp Gln Gln Leu Gln Gly Glu Gly Lys Ile Ile Asp Arg Arg
                85                  90                  95

Pro Glu Arg Arg Pro Pro Arg Glu Arg Arg Phe Glu Lys Pro Leu Glu
            100                 105                 110

Glu Lys Gly Glu Gly Gly Glu Phe Ser Val Asp Arg Pro Ile Ile Asp
        115                 120                 125

Arg Pro Ile Arg Gly Arg Gly Gly Leu Gly Arg Gly Arg Gly Gly Arg
    130                 135                 140

Gly Arg Gly Met Gly Arg Gly Asp Gly Phe Asp Ser Arg Gly Lys Arg
145                 150                 155                 160

Glu Phe Asp Arg His Ser Gly Ser Asp Arg Ser Ser Phe Ser His Tyr
                165                 170                 175

Ser Gly Leu Lys His Glu Asp Lys Arg Gly Gly Ser Gly Ser His Asn
            180                 185                 190

Trp Gly Thr Val Lys Asp Glu Leu Thr Asp Leu Asp Gln Ser Asn Val
        195                 200                 205

Thr Glu Glu Thr Pro Glu Gly Glu Glu His His Pro Val Ala Asp Thr
    210                 215                 220

Glu Asn Lys Glu Asn Glu Val Glu Glu Val Lys Glu Glu Gly Pro Lys
225                 230                 235                 240

Glu Met Thr Leu Asp Glu Trp Lys Ala Ile Gln Asn Lys Asp Arg Ala
                245                 250                 255

Lys Val Glu Phe Asn Ile Arg Lys Pro Asn Glu Gly Ala Asp Gly Gln
            260                 265                 270

Trp Lys Lys Gly Phe Val Leu His Lys Ser Lys Ser Glu Glu Ala His
        275                 280                 285

Ala Glu Asp Ser Val Met Asp His His Phe Arg Lys Pro Ala Asn Asp
    290                 295                 300
```

Ile Thr Ser Gln Leu Glu Ile Asn Phe Gly Asp Leu Gly Arg Pro Gly
305 310 315 320

Arg Gly Gly Arg Gly Gly Arg Gly Gly Arg Gly Arg Gly Gly Arg Pro
325 330 335

Asn Arg Gly Ser Arg Thr Asp Lys Ser Ser Ala Ser Ala Pro Asp Val
340 345 350

Asp Asp Pro Glu Ala Phe Pro Ala Leu Ala
355 360

<210> 1001
<211> 207
<212> PRT
<213> Homo sapiens

<400> 1001
Leu Met Ser Val Val Arg Gly Phe Ser Glu Ala Ala Ala Gln Tyr Asn
1 5 10 15

Pro Glu Pro Pro Pro Pro Arg Thr His Tyr Ser Asn Ile Glu Ala Asn
20 25 30

Glu Ser Glu Glu Val Arg Gln Phe Arg Arg Leu Phe Ala Gln Leu Ala
35 40 45

Gly Asp Asp Met Glu Val Ser Ala Thr Glu Leu Met Asn Ile Leu Asn
50 55 60

Lys Val Val Thr Arg His Pro Asp Leu Lys Thr Asp Gly Phe Gly Ile
65 70 75 80

Asp Thr Cys Arg Ser Met Val Ala Val Met Asp Ser Asp Thr Thr Gly
85 90 95

Lys Leu Gly Phe Glu Glu Phe Lys Tyr Leu Trp Asn Asn Ile Lys Arg
100 105 110

Trp Gln Ala Ile Tyr Lys Gln Phe Asp Thr Asp Arg Ser Gly Thr Ile
115 120 125

Cys Ser Ser Glu Leu Pro Gly Ala Phe Glu Ala Ala Gly Phe His Leu
130 135 140

Asn Glu His Leu Tyr Asn Met Ile Ile Arg Arg Tyr Ser Asp Glu Ser
145 150 155 160

Gly Asn Met Asp Phe Asp Asn Phe Ile Ser Cys Leu Val Arg Leu Asp
                165   170   175

Ala Met Phe Arg Ala Phe Lys Ser Leu Asp Lys Asp Gly Thr Gly Gln
            180   185   190

Ile Gln Val Asn Ile Gln Glu Trp Leu Gln Leu Thr Met Tyr Ser
        195   200   205

<210> 1002
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (12)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1002
Ile Phe Cys Asp Thr Arg Ser His Gln Val Ala Xaa Gly Trp Phe Arg
  1   5   10   15

Ile Pro Gly Leu Lys
             20

<210> 1003
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1003

Met Pro Gln Leu Gly Leu Ser Cys Ile Pro Val Glu Gly Pro Xaa Pro
1 5 10 15

Cys Leu Xaa Glu Val Arg Leu Cys Cys Val Asn Gly Gln Ala Leu Pro
20 25 30

Gln Pro Thr Pro Gly Lys Val His Leu Phe Ser Gly Leu Tyr Lys Val
35 40 45

Ser Trp Gly Pro Val Ala Ser Leu Pro Val Arg Ser Asp Phe Ser Leu
50 55 60

Ser Ser Ser Pro Val Gly Glu Thr Lys Pro Asp Trp Gly Ala Gln Gly
65 70 75 80

Glu His Gly Lys Gly Arg Leu Pro Cys Leu Ser Leu Ala Val Arg Val
85 90 95

Arg Val Thr His Thr Lys Xaa Glu Cys Gly Gln Gln Val
100 105

<210> 1004
<211> 542
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (252)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (519)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1004
Lys Asp Pro Glu Glu Tyr Cys Cys Thr Pro Ala Ala Arg Gly Arg Gly
1 5 10 15

Lys Ser Ala Ala Leu Gly Leu Ala Ile Ala Gly Ala Val Ala Phe Gly
20 25 30

Tyr Ser Asn Ile Phe Val Thr Ser Pro Ser Pro Asp Asn Leu His Thr
35 40 45

Leu Phe Glu Phe Val Phe Lys Gly Phe Asp Ala Leu Gln Tyr Gln Glu
50 55 60

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His Leu Asp Tyr Glu Ile Ile Gln Ser Leu Asn Pro Glu Phe Asn Lys
 65                  70                  75                  80

Ala Val Ile Arg Val Asn Val Phe Arg Glu His Arg Gln Thr Ile Gln
                 85                  90                  95

Tyr Ile His Pro Ala Asp Ala Val Lys Leu Gly Gln Ala Glu Leu Val
            100                 105                 110

Val Ile Asp Glu Ala Ala Ala Ile Pro Leu Pro Leu Val Lys Ser Leu
        115                 120                 125

Leu Gly Pro Tyr Leu Val Phe Met Ala Ser Thr Ile Asn Gly Tyr Glu
    130                 135                 140

Gly Thr Gly Arg Ser Leu Ser Leu Lys Leu Ile Gln Gln Leu Arg Gln
145                 150                 155                 160

Gln Ser Ala Gln Ser Gln Val Ser Thr Thr Ala Glu Asn Lys Thr Thr
                165                 170                 175

Thr Thr Ala Arg Leu Ala Ser Ala Arg Thr Leu His Glu Val Ser Leu
            180                 185                 190

Gln Glu Ser Ile Arg Tyr Ala Pro Gly Asp Ala Val Glu Lys Trp Leu
        195                 200                 205

Asn Asp Leu Leu Cys Leu Asp Cys Leu Asn Ile Thr Arg Ile Val Ser
    210                 215                 220

Gly Cys Pro Leu Pro Glu Ala Cys Glu Leu Tyr Tyr Val Asn Arg Asp
225                 230                 235                 240

Thr Leu Phe Cys Tyr His Lys Ala Ser Glu Val Xaa Leu Gln Arg Leu
                245                 250                 255

Met Ala Leu Tyr Val Ala Ser His Tyr Lys Asn Ser Pro Asn Asp Leu
            260                 265                 270

Gln Met Leu Ser Asp Ala Pro Ala His His Leu Phe Cys Leu Leu Pro
        275                 280                 285

Pro Val Pro Pro Thr Gln Asn Ala Leu Pro Glu Val Leu Ala Val Ile
    290                 295                 300

Gln Val Cys Leu Glu Gly Glu Ile Ser Arg Gln Ser Ile Leu Asn Ser
305                 310                 315                 320

Leu Ser Arg Gly Lys Lys Ala Ser Gly Asp Leu Ile Pro Trp Thr Val
                325                 330                 335
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Ser Glu Gln Phe Gln Asp Pro Asp Phe Gly Gly Leu Ser Gly Gly Arg
340 345 350

Val Val Arg Ile Ala Val His Pro Asp Tyr Gln Gly Met Gly Tyr Gly
355 360 365

Ser Arg Ala Leu Gln Leu Leu Gln Met Tyr Tyr Glu Gly Arg Phe Pro
370 375 380

Cys Leu Glu Glu Lys Val Leu Glu Thr Pro Gln Glu Ile His Thr Val
385 390 395 400

Ser Ser Glu Ala Val Ser Leu Leu Glu Glu Val Ile Thr Pro Arg Lys
405 410 415

Asp Leu Pro Pro Leu Leu Leu Lys Leu Asn Glu Arg Pro Ala Glu Arg
420 425 430

Leu Asp Tyr Leu Gly Val Ser Tyr Gly Leu Thr Pro Arg Leu Leu Lys
435 440 445

Phe Trp Lys Arg Ala Gly Phe Val Pro Val Tyr Leu Arg Gln Thr Pro
450 455 460

Asn Asp Leu Thr Gly Glu His Ser Cys Ile Met Leu Lys Thr Leu Thr
465 470 475 480

Asp Glu Asp Glu Ala Asp Gln Gly Gly Trp Leu Ala Ala Phe Trp Lys
485 490 495

Asp Phe Arg Arg Arg Phe Leu Ala Leu Leu Ser Tyr Gln Phe Ser Thr
500 505 510

Phe Ser Pro Ser Leu Ala Xaa Asn Ile Ile Gln Asn Arg Asn Met Gly
515 520 525

Lys Pro Ala Gln Pro Ala Leu Ser Arg Glu Glu Leu Glu Ala
530 535 540

<210> 1005
<211> 202
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (77)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1005
Asp Ala Ala Asp Thr Ile Glu Thr Asp Thr Ala Thr Ala Asp Thr Thr
1 5 10 15

Val Ala Asn Asn Val Pro Pro Ala Ala Thr Ser Leu Ile Asp Leu Trp
20 25 30

Pro Gly Asn Gly Glu Gly Ala Ser Thr Leu Gln Gly Glu Pro Arg Ala
35 40 45

Pro Thr Pro Pro Ser Gly Thr Glu Val Thr Leu Ala Glu Val Pro Leu
50 55 60

Leu Asp Glu Val Ala Pro Glu Pro Leu Leu Pro Ala Xaa Glu Gly Cys
65 70 75 80

Ala Thr Leu Leu Asn Phe Asp Glu Leu Pro Glu Pro Pro Ala Thr Phe
85 90 95

Cys Asp Pro Glu Glu Val Glu Gly Glu Pro Leu Ala Ala Pro Gln Thr
100 105 110

Pro Thr Leu Pro Ser Ala Leu Glu Glu Leu Glu Gln Glu Gln Glu Pro
115 120 125

Glu Pro His Leu Leu Thr Asn Gly Glu Thr Thr Gln Lys Glu Gly Thr
130 135 140

Gln Ala Ser Glu Gly Tyr Phe Ser Gln Ser Gln Glu Glu Glu Phe Ala
145 150 155 160

Gln Ser Glu Glu Leu Cys Ala Lys Ala Pro Pro Pro Val Phe Tyr Asn
165 170 175

Lys Pro Pro Glu Ile Asp Ile Thr Cys Trp Asp Ala Asp Pro Val Pro
180 185 190

Glu Glu Glu Glu Gly Phe Glu Gly Gly Asp
195 200

<210> 1006
<211> 561
<212> PRT
<213> Homo sapiens

<400> 1006
Ser Ala Met Arg Lys Phe Ala Tyr Cys Lys Val Val Leu Ala Thr Ser
1 5 10 15

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Leu Ile Trp Val Leu Leu Asp Met Phe Leu Leu Leu Tyr Phe Ser Glu
            20                  25                  30

Cys Asn Lys Cys Asp Glu Lys Lys Glu Arg Gly Leu Pro Ala Gly Asp
        35                  40                  45

Val Leu Glu Pro Val Gln Lys Pro His Glu Gly Pro Gly Glu Met Gly
    50                  55                  60

Lys Pro Val Val Ile Pro Lys Glu Asp Gln Glu Lys Met Lys Glu Met
65                  70                  75                  80

Phe Lys Ile Asn Gln Phe Asn Leu Met Ala Ser Glu Met Ile Ala Leu
                85                  90                  95

Asn Arg Ser Leu Pro Asp Val Arg Leu Glu Gly Cys Lys Thr Lys Val
            100                 105                 110

Tyr Pro Asp Asn Leu Pro Thr Thr Ser Val Val Ile Val Phe His Asn
        115                 120                 125

Glu Ala Trp Ser Thr Leu Leu Arg Thr Val His Ser Val Ile Asn Arg
    130                 135                 140

Ser Pro Arg His Met Ile Glu Glu Ile Val Leu Val Asp Asp Ala Ser
145                 150                 155                 160

Glu Arg Asp Phe Leu Lys Arg Pro Leu Glu Ser Tyr Val Lys Lys Leu
                165                 170                 175

Lys Val Pro Val His Val Ile Arg Met Glu Gln Arg Ser Gly Leu Ile
            180                 185                 190

Arg Ala Arg Leu Lys Gly Ala Ala Val Ser Lys Gly Gln Val Ile Thr
        195                 200                 205

Phe Leu Asp Ala His Cys Glu Cys Thr Val Gly Trp Leu Glu Pro Leu
    210                 215                 220

Leu Ala Arg Ile Lys His Asp Arg Arg Thr Val Val Cys Pro Ile Ile
225                 230                 235                 240

Asp Val Ile Ser Asp Asp Thr Phe Glu Tyr Met Ala Gly Ser Asp Met
                245                 250                 255

Thr Tyr Gly Gly Phe Asn Trp Lys Leu Asn Phe Arg Trp Tyr Pro Val
            260                 265                 270

Pro Gln Arg Glu Met Asp Arg Arg Lys Gly Asp Arg Thr Leu Pro Val
        275                 280                 285
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Arg Thr Pro Thr Met Ala Gly Gly Leu Phe Ser Ile Asp Arg Asp Tyr
    290                 295                 300

Phe Gln Glu Ile Gly Thr Tyr Asp Ala Gly Met Asp Ile Trp Gly Gly
305                 310                 315                 320

Glu Asn Leu Glu Ile Ser Phe Arg Ile Trp Gln Cys Gly Gly Thr Leu
                325                 330                 335

Glu Ile Val Thr Cys Ser His Val Gly His Val Phe Arg Lys Ala Thr
            340                 345                 350

Pro Tyr Thr Phe Pro Gly Gly Thr Gly Gln Ile Ile Asn Lys Asn Asn
        355                 360                 365

Arg Arg Leu Ala Glu Val Trp Met Asp Glu Phe Lys Asn Phe Phe Tyr
    370                 375                 380

Ile Ile Ser Pro Gly Val Thr Lys Val Asp Tyr Gly Asp Ile Ser Ser
385                 390                 395                 400

Arg Val Gly Leu Arg His Lys Leu Gln Cys Lys Pro Phe Ser Trp Tyr
                405                 410                 415

Leu Glu Asn Ile Tyr Pro Asp Ser Gln Ile Pro Arg His Tyr Phe Ser
            420                 425                 430

Leu Gly Glu Ile Arg Asn Val Glu Thr Asn Gln Cys Leu Asp Asn Met
        435                 440                 445

Ala Arg Lys Glu Asn Glu Lys Val Gly Ile Phe Asn Cys His Gly Met
    450                 455                 460

Gly Gly Asn Gln Val Phe Ser Tyr Thr Ala Asn Lys Glu Ile Arg Thr
465                 470                 475                 480

Asp Asp Leu Cys Leu Asp Val Ser Lys Leu Asn Gly Pro Val Thr Met
                485                 490                 495

Leu Lys Cys His His Leu Lys Gly Asn Gln Leu Trp Glu Tyr Asp Pro
            500                 505                 510

Val Lys Leu Thr Leu Gln His Val Asn Ser Asn Gln Cys Leu Asp Lys
        515                 520                 525

Ala Thr Glu Glu Asp Ser Gln Val Pro Ser Ile Arg Asp Cys Asn Gly
    530                 535                 540

Ser Arg Ser Gln Gln Trp Leu Leu Arg Asn Val Thr Leu Pro Glu Ile
545                 550                 555                 560
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Phe

<210> 1007
<211> 189
<212> PRT
<213> Homo sapiens

<400> 1007
Phe Ile Pro Ile Gly Glu Asn Ser Ala Thr Gly Glu Asn Arg Leu Ala
1 5 10 15

Ser Ala Leu Trp Ile Gly Asp Arg Ser Tyr Pro Gly Leu Ser Glu Gly
20 25 30

Asn Ser Arg Pro Pro Ile Pro Gly Pro Pro Tyr Val Ala Ser Pro Asp
35 40 45

Leu Trp Ser His Trp Glu Asp Ser Ala Leu Pro Pro Pro Ser Leu Arg
50 55 60

Pro Val Gln Pro Thr Trp Glu Gly Ser Ser Glu Ala Gly Leu Asp Trp
65 70 75 80

Ala Gly Ala Ser Phe Ser Pro Gly Thr Pro Met Trp Ala Ala Leu Asp
85 90 95

Glu Gln Met Leu Gln Glu Gly Ile Gln Ala Ser Leu Leu Asp Gly Pro
100 105 110

Ala Gln Glu Pro Gln Ser Ala Pro Trp Leu Ser Lys Ser Ser Val Ser
115 120 125

Ser Leu Arg Leu Gln Gln Leu Glu Arg Met Gly Phe Pro Thr Glu Gln
130 135 140

Ala Val Val Ala Leu Ala Ala Thr Gly Arg Val Glu Gly Ala Val Ser
145 150 155 160

Leu Leu Val Gly Gly Gln Val Gly Thr Glu Thr Leu Val Thr His Gly
165 170 175

Lys Gly Gly Pro Ala His Ser Glu Gly Pro Gly Pro Pro
180 185

<210> 1008
<211> 300

<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (39)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1008
Arg Gln Lys Ser Ser Xaa Leu Trp Pro His Pro Leu Xaa Arg His Arg
1   5   10   15

Ala Gly Pro Gly Leu Ala Gly Asn Gly Gly Ile Leu Pro Asn Leu Gly
            20   25   30

Asp Gly Gly Gly Gly Trp Xaa Trp Trp Glu Gly Asn His Val Leu Leu
        35   40   45

Asn Leu Phe Leu Val Pro Pro Ile Pro Arg Pro Thr Arg His His Thr
    50   55   60

Ala Asp Asn Thr His Pro Leu Ala Gln Ala Ser Ile His Met Cys Cys
65   70   75   80

Thr Phe Ser Ser Arg His Ala Asp Asn Pro Thr Arg Pro His His His
                85   90   95

Met Pro Lys Cys Thr His Thr Glu Pro His Arg Pro Ser Gly Pro Ala
            100   105   110

Gly Ser Ser Leu Gly Phe Pro Leu Ala His Phe Gln Gly Pro Gly Ala
        115   120   125

Ala Thr Lys Cys Glu Ser Ser Val Ala Ala Pro Ser Phe Ser Pro Ser
    130   135   140

Thr Ser Ile Gly Pro Ile Gly Lys His Arg Gly Leu Thr Leu Phe His
145   150   155   160

Ile Pro Cys Pro Ala Leu Lys Trp Thr Ile Thr Phe Trp Asp Arg Leu
                165   170   175

Lys Phe Leu Lys Ser Leu His His Ser Val Pro Ser Lys Gly Ser Pro
180 185 190

Cys Gln Trp Gly Phe Glu Arg Glu Phe Leu Glu Pro Thr Phe Lys Phe
195 200 205

Cys Leu Ile Trp Arg Glu Thr Lys Ile Gly Arg Gly Lys Arg Thr Pro
210 215 220

Asp Val Leu Leu Leu Pro Glu Ile Leu Glu Thr Asp Ser Leu Asp Trp
225 230 235 240

Lys Met Asp Lys Ser Ala Leu Thr Trp Arg Val Gly Thr Arg Trp Gly
245 250 255

Pro Ala Leu Pro Thr Ala Ala Val Ala Ser Ser Leu Ala Gly Phe Ala
260 265 270

Gly Arg Gln Gln Glu Gly Glu Gly Gly Ser Thr Ala Arg Gly Thr Gly
275 280 285

Gly Ala Ala Gly Leu Gln Glu Leu Phe Phe His Cys
290 295 300

<210> 1009
<211> 344
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (38)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1009
Arg Pro Pro Cys Pro His Ser Arg Ser Xaa Trp Arg Ile Leu Ser Leu
1 5 10 15

Thr Pro Asn Pro Asp Pro Leu Pro Asn Met Ser Val Phe Phe Phe Ile
20 25 30

Phe Leu Asn Ile Phe Xaa Leu Ala Phe Ser Ser Pro Gly Ser Gln Pro
35 40 45

Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg Gly Phe Met
50 55 60

Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys Arg Phe Cys
65 70 75 80

Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe Pro Glu Glu
85 90 95

Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe Ser Ser Trp Pro
100 105 110

Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu Gln Val Gln Arg
115 120 125

Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp Val Ser Glu Leu
130 135 140

Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln Val Arg Trp Leu
145 150 155 160

Arg Pro Val His Arg Gln Leu Gly Glu Ala Asn Glu Glu Phe Ala Leu
165 170 175

Arg Val Gln Gln Leu Val Ala Lys Glu Leu Gly Gln Thr Gly Thr Arg
180 185 190

Leu Thr Pro Ala Asp Lys Ala Glu His Met Lys Arg Gln Arg His Pro
195 200 205

Arg Leu Arg Pro Gln Ser Ala Gln Ser Ser Phe Pro Pro Ser Pro Gly
210 215 220

Pro Ser Pro Asp Val Gln Leu Ala Thr Leu Ala Gln Arg Val Lys Glu
225 230 235 240

Val Leu Pro His Val Pro Leu Gly Val Ile Gln Arg Asp Leu Ala Lys
245 250 255

Thr Gly Cys Val Asp Leu Thr Ile Thr Asn Leu Leu Glu Gly Ala Val
260 265 270

Ala Phe Met Pro Glu Asp Ile Thr Lys Gly Thr Gln Ser Leu Pro Thr
275 280 285

Ala Ser Ala Ser Lys Phe Pro Ser Ser Gly Pro Val Thr Pro Gln Pro
290 295 300

Thr Ala Leu Thr Phe Ala Lys Ser Ser Trp Ala Arg Gln Glu Ser Leu
305 310 315 320

Gln Glu Arg Lys Gln Ala Leu Tyr Glu Tyr Ala Arg Arg Arg Phe Thr
325 330 335

Glu Arg Arg Ala Gln Glu Ala Asp
340

<210> 1010
<211> 233
<212> PRT
<213> Homo sapiens

<400> 1010
Pro His Cys Glu Pro Asn Pro Gly Ala Gly Ala Met Val Leu Leu His
1 5 10 15

Val Leu Phe Glu His Ala Val Gly Tyr Ala Leu Leu Ala Leu Lys Glu
20 25 30

Val Glu Glu Ile Ser Leu Leu Gln Pro Gln Val Glu Glu Ser Val Leu
35 40 45

Asn Leu Gly Lys Phe His Ser Ile Val Arg Leu Val Ala Phe Cys Pro
50 55 60

Phe Ala Ser Ser Gln Val Ala Leu Glu Asn Ala Asn Ala Val Ser Glu
65 70 75 80

Gly Val Val His Glu Asp Leu Arg Leu Leu Leu Glu Thr His Leu Pro
85 90 95

Ser Lys Lys Lys Lys Val Leu Leu Gly Val Gly Asp Pro Lys Ile Gly
100 105 110

Ala Ala Ile Gln Glu Glu Leu Gly Tyr Asn Cys Gln Thr Gly Gly Val
115 120 125

Ile Ala Glu Ile Leu Arg Gly Val Arg Leu His Phe His Asn Leu Val
130 135 140

Lys Gly Leu Thr Asp Leu Ser Ala Cys Lys Ala Gln Leu Gly Leu Gly
145 150 155 160

His Ser Tyr Ser Arg Ala Lys Val Lys Phe Asn Val Asn Arg Val Asp
165 170 175

Asn Met Ile Ile Gln Ser Ile Ser Leu Leu Asp Gln Leu Asp Lys Asp
180 185 190

Ile Asn Thr Phe Ser Met Arg Val Arg Glu Trp Tyr Gly Tyr His Phe
195 200 205

Pro Glu Leu Val Lys Ile Ile Asn Asp Asn Ala Thr Tyr Cys Arg Leu
210 215 220

Ala Gln Phe Ile Gly Asn Arg Arg Asn
225 230

<210> 1011
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1011
Gly Thr Ser Xaa Phe Ser Phe Pro Leu Gly Arg Glu Glu Ala Met Ala
1 5 10 15

Ala Met Ala Ser Leu Gly Ala Leu Ala Leu Leu Leu Leu Ser Ser Leu
20 25 30

Ser Arg Cys Ser Ala Glu Ala Cys Leu Glu Pro Gln Ile Thr Pro Ser
35 40 45

Tyr Tyr Thr Thr Ser Asp Ala Val Ile Ser Thr Glu Thr Val Phe Ile
50 55 60

Val Glu Ile Ser Leu Thr Cys Lys Asn Arg Val Gln Asn Met Ala Leu
65 70 75 80

Tyr Ala Asp Val Gly Gly Lys Gln Phe Pro Val Thr Arg Gly Gln Asp
85 90 95

Val Gly Arg Tyr Gln Val Ser Trp Ser Leu Asp His Lys Ser Ala His
100 105 110

Ala Gly Thr Tyr Glu Val Arg Phe Phe Asp Glu Glu Ser Tyr Ser Leu
115 120 125

Leu Arg Lys Ala Gln Arg Asn Asn Glu Asp Ile Ser Ile Ile Pro Pro
130 135 140

Leu Phe Thr Val Ser Val Asp His Arg Gly Thr Trp Asn Gly Pro Trp
145 150 155 160

Val Ser Thr Glu Val Leu Ala Ala Ala Ile Gly Leu Val Ile Tyr Tyr
165 170 175

Leu Ala Phe Ser Ala Lys Ser His Ile Gln Ala
180 185

<210> 1012
<211> 708
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (18)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (153)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (229)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (433)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1012
Ala Leu Arg Pro Ile Ser Ser Val Arg Ala Gly Asp Arg Cys Gln Arg
1 5 10 15

Ser Xaa Ala Ala Asp Met Ala Ala Ser Thr Ala Ala Gly Lys Gln Arg
20 25 30

Ile Pro Lys Val Ala Lys Val Lys Asn Lys Ala Pro Ala Glu Val Gln
35 40 45

Ile Thr Ala Glu Gln Leu Leu Arg Glu Ala Lys Glu Arg Glu Leu Glu
50 55 60

Leu Leu Pro Pro Pro Pro Gln Gln Lys Ile Thr Asp Glu Glu Glu Leu
65 70 75 80

Asn Asp Tyr Lys Leu Arg Lys Arg Lys Thr Phe Glu Asp Asn Ile Arg

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                85                  90                  95

Lys Asn Arg Thr Val Ile Ser Asn Trp Ile Lys Tyr Ala Gln Trp Glu
            100                 105                 110

Glu Ser Leu Lys Glu Ile Gln Arg Ala Arg Ser Ile Tyr Glu Arg Ala
        115                 120                 125

Leu Asp Val Asp Tyr Arg Asn Ile Thr Leu Trp Leu Lys Tyr Ala Glu
    130                 135                 140

Met Glu Met Lys Asn Arg Gln Val Xaa His Ala Arg Asn Ile Trp Asp
145                 150                 155                 160

Arg Ala Ile Thr Thr Leu Pro Arg Val Asn Gln Phe Trp Tyr Lys Tyr
                165                 170                 175

Thr Tyr Met Glu Glu Met Leu Gly Asn Val Ala Gly Ala Arg Gln Val
            180                 185                 190

Phe Glu Arg Trp Met Glu Trp Gln Pro Glu Glu Gln Ala Trp His Ser
        195                 200                 205

Tyr Ile Asn Phe Glu Leu Arg Tyr Lys Glu Val Asp Arg Ala Arg Thr
    210                 215                 220

Ile Tyr Glu Arg Xaa Val Leu Val His Pro Asp Val Lys Asn Trp Ile
225                 230                 235                 240

Lys Tyr Ala Arg Phe Glu Glu Lys His Ala Tyr Phe Ala His Ala Arg
                245                 250                 255

Lys Val Tyr Glu Arg Ala Val Glu Phe Phe Gly Asp Glu His Met Asp
            260                 265                 270

Glu His Leu Tyr Val Ala Phe Ala Lys Phe Glu Glu Asn Gln Lys Glu
        275                 280                 285

Phe Glu Arg Val Arg Val Ile Tyr Lys Tyr Ala Leu Asp Arg Ile Ser
    290                 295                 300

Lys Gln Asp Ala Gln Glu Leu Phe Lys Asn Tyr Thr Ile Phe Glu Lys
305                 310                 315                 320

Lys Phe Gly Asp Arg Arg Gly Ile Glu Asp Ile Ile Val Ser Lys Arg
                325                 330                 335

Arg Phe Gln Tyr Glu Glu Glu Val Lys Ala Asn Pro His Asn Tyr Asp
            340                 345                 350

Ala Trp Phe Asp Tyr Leu Arg Leu Val Glu Ser Asp Ala Glu Ala Glu
```

355 360 365

Ala Val Arg Glu Val Tyr Glu Arg Ala Ile Ala Asn Val Pro Pro Ile
370 375 380

Gln Glu Lys Arg His Trp Lys Arg Tyr Ile Tyr Leu Trp Ile Asn Tyr
385 390 395 400

Ala Leu Tyr Glu Glu Leu Glu Ala Lys Asp Pro Glu Arg Thr Arg Gln
405 410 415

Val Tyr Gln Ala Ser Leu Glu Leu Ile Pro His Lys Lys Phe Thr Phe
420 425 430

Xaa Lys Met Trp Ile Leu Tyr Ala Gln Phe Glu Ile Arg Gln Lys Asn
435 440 445

Leu Ser Leu Ala Arg Arg Ala Leu Gly Thr Ser Ile Gly Lys Cys Pro
450 455 460

Lys Asn Lys Leu Phe Lys Val Tyr Ile Glu Leu Glu Leu Gln Leu Arg
465 470 475 480

Glu Phe Asp Arg Cys Arg Lys Leu Tyr Glu Lys Phe Leu Glu Phe Gly
485 490 495

Pro Glu Asn Cys Thr Ser Trp Ile Lys Phe Ala Glu Leu Glu Thr Ile
500 505 510

Leu Gly Asp Ile Asp Arg Ala Arg Ala Ile Tyr Glu Leu Ala Ile Ser
515 520 525

Gln Pro Arg Leu Asp Met Pro Glu Val Leu Trp Lys Ser Tyr Ile Asp
530 535 540

Phe Glu Ile Glu Gln Glu Glu Thr Glu Arg Thr Arg Asn Leu Tyr Arg
545 550 555 560

Arg Leu Leu Gln Arg Thr Gln His Val Lys Val Trp Ile Ser Phe Ala
565 570 575

Gln Phe Glu Leu Ser Ser Gly Lys Glu Gly Ser Leu Thr Lys Cys Arg
580 585 590

Gln Ile Tyr Glu Glu Ala Asn Lys Thr Met Arg Asn Cys Glu Glu Lys
595 600 605

Glu Glu Arg Leu Met Leu Leu Glu Ser Trp Arg Ser Phe Glu Glu Glu
610 615 620

Phe Gly Thr Ala Ser Asp Lys Glu Arg Val Asp Lys Leu Met Pro Glu

625 630 635 640

Lys Val Lys Lys Arg Arg Lys Val Gln Thr Asp Asp Gly Ser Asp Ala
645 650 655

Gly Trp Glu Glu Tyr Phe Asp Tyr Ile Phe Pro Glu Asp Ala Ala Asn
660 665 670

Gln Pro Asn Leu Lys Leu Leu Ala Met Ala Lys Leu Trp Lys Lys Gln
675 680 685

Gln Gln Glu Lys Glu Asp Ala Glu His His Pro Asp Glu Asp Val Asp
690 695 700

Glu Ser Glu Ser
705

<210> 1013
<211> 183
<212> PRT
<213> Homo sapiens

<400> 1013
Leu Pro Pro Gln Val Ala Asp Thr Met Leu Pro Pro Met Ala Leu Pro
1 5 10 15

Ser Val Ser Trp Met Leu Leu Ser Cys Leu Met Leu Leu Ser Gln Val
20 25 30

Gln Gly Glu Glu Pro Gln Arg Glu Leu Pro Ser Ala Arg Ile Arg Cys
35 40 45

Pro Lys Gly Ser Lys Ala Tyr Gly Ser His Cys Tyr Ala Leu Phe Leu
50 55 60

Ser Pro Lys Ser Trp Thr Asp Ala Asp Leu Ala Cys Gln Lys Arg Pro
65 70 75 80

Ser Gly Asn Leu Val Ser Val Leu Ser Gly Ala Glu Gly Ser Phe Val
85 90 95

Ser Ser Leu Val Lys Ser Ile Gly Asn Ser Tyr Ser Tyr Val Trp Ile
100 105 110

Gly Leu His Asp Pro Thr Gln Gly Thr Glu Pro Asn Gly Glu Gly Trp
115 120 125

Glu Trp Ser Ser Ser Asp Val Met Asn Tyr Phe Ala Trp Glu Arg Asn
130 135 140

Pro Ser Thr Ile Ser Ser Pro Gly His Cys Ala Ser Leu Ser Arg Ser
145 150 155 160

Thr Ala Phe Leu Arg Trp Lys Asp Tyr Asn Cys Asn Val Arg Leu Pro
165 170 175

Tyr Val Cys Lys Phe Thr Asp
180

<210> 1014
<211> 213
<212> PRT
<213> Homo sapiens

<400> 1014
Val Thr Asp Gly Gly Ser Ala Arg Lys Pro Lys Met Ala Val Pro Ala
1 5 10 15

Ala Leu Ile Leu Arg Glu Ser Pro Ser Met Lys Lys Ala Val Ser Leu
20 25 30

Ile Asn Ala Ile Asp Thr Gly Arg Phe Pro Arg Leu Leu Thr Arg Ile
35 40 45

Leu Gln Lys Leu His Leu Lys Ala Glu Ser Ser Phe Ser Glu Glu Glu
50 55 60

Glu Glu Lys Leu Gln Ala Ala Phe Ser Leu Glu Lys Gln Asp Leu His
65 70 75 80

Leu Val Leu Glu Thr Ile Ser Phe Ile Leu Glu Gln Ala Val Tyr His
85 90 95

Asn Val Lys Pro Ala Ala Leu Gln Gln Gln Leu Glu Asn Ile His Leu
100 105 110

Arg Gln Asp Lys Ala Glu Ala Phe Val Asn Thr Trp Ser Ser Met Gly
115 120 125

Gln Glu Thr Val Glu Lys Phe Arg Gln Arg Ile Leu Ala Pro Cys Lys
130 135 140

Leu Glu Thr Val Gly Trp Gln Leu Asn Leu Gln Met Ala His Ser Ala
145 150 155 160

Gln Ala Lys Leu Lys Ser Pro Gln Ala Val Leu Gln Leu Gly Val Asn
165 170 175

Asn Glu Asp Ser Lys Ser Leu Glu Lys Val Leu Val Glu Phe Ser His
180 185 190

Lys Glu Leu Phe Asp Phe Tyr Asn Lys Leu Glu Thr Ile Gln Ala Gln
195 200 205

Leu Asp Ser Leu Thr
210

<210> 1015
<211> 544
<212> PRT
<213> Homo sapiens

<400> 1015
Ala Pro Gly Thr Met Asn Gly Glu Ala Ile Cys Ser Ala Leu Pro Thr
1 5 10 15

Ile Pro Tyr His Lys Leu Ala Asp Leu Arg Tyr Leu Ser Arg Gly Ala
20 25 30

Ser Gly Thr Val Ser Ser Ala Arg His Ala Asp Trp Arg Val Gln Val
35 40 45

Ala Val Lys His Leu His Ile His Thr Pro Leu Leu Asp Ser Glu Arg
50 55 60

Lys Asp Val Leu Arg Glu Ala Glu Ile Leu His Lys Ala Arg Phe Ser
65 70 75 80

Tyr Ile Leu Pro Ile Leu Gly Ile Cys Asn Glu Pro Glu Phe Leu Gly
85 90 95

Ile Val Thr Glu Tyr Met Pro Asn Gly Ser Leu Asn Glu Leu Leu His
100 105 110

Arg Lys Thr Glu Tyr Pro Asp Val Ala Trp Pro Leu Arg Phe Arg Ile
115 120 125

Leu His Glu Ile Ala Leu Gly Val Asn Tyr Leu His Asn Met Thr Pro
130 135 140

Pro Leu Leu His His Asp Leu Lys Thr Gln Asn Ile Leu Leu Asp Asn
145 150 155 160

Glu Phe His Val Lys Ile Ala Asp Phe Gly Leu Ser Lys Trp Arg Met
165 170 175

Met Ser Leu Ser Gln Ser Arg Ser Ser Lys Ser Ala Pro Glu Gly Gly

```
            180                 185                 190

Thr Ile Ile Tyr Met Pro Pro Glu Asn Tyr Glu Pro Gly Gln Lys Ser
        195                 200                 205

Arg Ala Ser Ile Lys His Asp Ile Tyr Ser Tyr Ala Val Ile Thr Trp
    210                 215                 220

Glu Val Leu Ser Arg Lys Gln Pro Phe Glu Asp Val Thr Asn Pro Leu
225                 230                 235                 240

Gln Ile Met Tyr Ser Val Ser Gln Gly His Arg Pro Val Ile Asn Glu
                245                 250                 255

Glu Ser Leu Pro Tyr Asp Ile Pro His Arg Ala Arg Met Ile Ser Leu
            260                 265                 270

Ile Glu Ser Gly Trp Ala Gln Asn Pro Asp Glu Arg Pro Ser Phe Leu
        275                 280                 285

Lys Cys Leu Ile Glu Leu Glu Pro Val Leu Arg Thr Phe Glu Glu Ile
    290                 295                 300

Thr Phe Leu Glu Ala Val Ile Gln Leu Lys Lys Thr Lys Leu Gln Ser
305                 310                 315                 320

Val Ser Ser Ala Ile His Leu Cys Asp Lys Lys Lys Met Glu Leu Ser
                325                 330                 335

Leu Asn Ile Pro Val Asn His Gly Pro Gln Glu Glu Ser Cys Gly Ser
            340                 345                 350

Ser Gln Leu His Glu Asn Ser Gly Ser Pro Glu Thr Ser Arg Ser Leu
        355                 360                 365

Pro Ala Pro Gln Asp Asn Asp Phe Leu Ser Arg Lys Ala Gln Asp Cys
    370                 375                 380

Tyr Phe Met Lys Leu His His Cys Pro Gly Asn His Ser Trp Asp Ser
385                 390                 395                 400

Thr Ile Ser Gly Ser Gln Arg Ala Ala Phe Cys Asp His Lys Thr Thr
                405                 410                 415

Pro Cys Ser Ser Ala Ile Ile Asn Pro Leu Ser Thr Ala Gly Asn Ser
            420                 425                 430

Glu Arg Leu Gln Pro Gly Ile Ala Gln Gln Trp Ile Gln Ser Lys Arg
        435                 440                 445

Glu Asp Ile Val Asn Gln Met Thr Glu Ala Cys Leu Asn Gln Ser Leu
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450 455 460

Asp Ala Leu Leu Ser Arg Asp Leu Ile Met Lys Glu Asp Tyr Glu Leu
465 470 475 480

Val Ser Thr Lys Pro Thr Arg Thr Ser Lys Val Arg Gln Leu Leu Asp
485 490 495

Thr Thr Asp Ile Gln Gly Glu Glu Phe Ala Lys Val Ile Val Gln Lys
500 505 510

Leu Lys Asp Asn Lys Gln Met Gly Leu Gln Pro Tyr Pro Glu Ile Leu
515 520 525

Val Val Ser Arg Ser Pro Ser Leu Asn Leu Leu Gln Asn Lys Ser Met
530 535 540

<210> 1016
<211> 257
<212> PRT
<213> Homo sapiens

<400> 1016
His Pro Ser Ala Pro Arg Ala Gly Lys Ala His Leu Lys Arg Ala Ile
1 5 10 15

Leu Gly Gln Glu Glu Ala Leu Arg Leu His Ala Leu Cys Arg Val Leu
20 25 30

Arg Glu Val Asp Leu Leu Arg Ala Val Ile Ser Gln Thr Leu Gln Arg
35 40 45

Ser Leu Ala Lys Tyr Ala Glu Leu Asp Arg Glu Asp Asp Phe Cys Glu
50 55 60

Ala Ala Glu Ala Pro Asp Ile Gln Pro Lys Thr His Gln Lys Pro Glu
65 70 75 80

Ala Arg Met Pro Arg Leu Ser Gln Gly Lys Gly Pro Asp Ile Phe His
85 90 95

Arg Leu Gly Pro Leu Ser Val Phe Ser Ala Lys Asn Arg Trp Arg Leu
100 105 110

Val Gly Pro Val His Leu Thr Arg Gly Glu Gly Gly Phe Gly Leu Thr
115 120 125

Leu Arg Gly Asp Ser Pro Val Leu Ile Ala Ala Val Ile Pro Gly Ser
130 135 140

Gln Ala Ala Ala Ala Gly Leu Lys Glu Gly Asp Tyr Ile Val Ser Val
145 150 155 160

Asn Gly Gln Pro Cys Arg Trp Trp Arg His Ala Glu Val Val Thr Glu
165 170 175

Leu Lys Ala Ala Gly Glu Ala Gly Ala Ser Leu Gln Val Val Ser Leu
180 185 190

Leu Pro Ser Ser Arg Leu Pro Ser Leu Gly Asp Arg Arg Pro Val Leu
195 200 205

Leu Gly Pro Arg Gly Leu Leu Arg Ser Gln Arg Glu His Gly Cys Lys
210 215 220

Thr Pro Ala Ser Thr Trp Ala Ser Pro Arg Ala Leu Leu Asn Trp Ser
225 230 235 240

Arg Lys Ala Gln Gln Gly Lys Thr Gly Gly Cys Pro Ser Pro Val Pro
245 250 255

Gln

<210> 1017
<211> 248
<212> PRT
<213> Homo sapiens

<400> 1017
Ala Ser Asp Arg Arg Gly Tyr Ser Ser Arg Ile Val Gly Gly Asn Met
1 5 10 15

Ser Leu Leu Ser Gln Trp Pro Trp Gln Ala Ser Leu Gln Phe Gln Gly
20 25 30

Tyr His Leu Cys Gly Gly Ser Val Ile Thr Pro Leu Trp Ile Ile Thr
35 40 45

Ala Ala His Cys Val Tyr Asp Leu Tyr Leu Pro Lys Ser Trp Thr Ile
50 55 60

Gln Val Gly Leu Val Ser Leu Leu Asp Asn Pro Ala Pro Ser His Leu
65 70 75 80

Val Glu Lys Ile Val Tyr His Ser Lys Tyr Lys Pro Lys Arg Leu Gly
85 90 95

Asn Asp Ile Ala Leu Met Lys Leu Ala Gly Pro Leu Thr Phe Asn Glu
100 105 110

Met Ile Gln Pro Val Cys Leu Pro Asn Ser Glu Glu Asn Phe Pro Asp
115 120 125

Gly Lys Val Cys Trp Thr Ser Gly Trp Gly Ala Thr Glu Asp Gly Ala
130 135 140

Gly Asp Ala Ser Pro Val Leu Asn His Ala Ala Val Pro Leu Ile Ser
145 150 155 160

Asn Lys Ile Cys Asn His Arg Asp Val Tyr Gly Gly Ile Ile Ser Pro
165 170 175

Ser Met Leu Cys Ala Gly Tyr Leu Thr Gly Gly Val Asp Ser Cys Gln
180 185 190

Gly Asp Ser Gly Gly Pro Leu Val Cys Gln Glu Arg Arg Leu Trp Lys
195 200 205

Leu Val Gly Ala Thr Ser Phe Gly Ile Gly Cys Ala Glu Val Asn Lys
210 215 220

Pro Gly Val Tyr Thr Arg Val Thr Ser Phe Leu Asp Trp Ile His Glu
225 230 235 240

Gln Met Glu Arg Asp Leu Lys Thr
245

<210> 1018
<211> 224
<212> PRT
<213> Homo sapiens

<400> 1018
Gly Arg Val Ser Ala Pro Val Pro Gly Lys Met Val Leu Gly Gly Cys
1 5 10 15

Pro Val Ser Tyr Leu Leu Leu Cys Gly Gln Ala Ala Leu Leu Leu Gly
20 25 30

Asn Leu Leu Leu Leu His Cys Val Ser Arg Ser His Ser Gln Asn Ala
35 40 45

Thr Ala Glu Pro Glu Leu Thr Ser Ala Gly Ala Ala Gln Pro Glu Gly

50 55 60

Pro Gly Gly Ala Ala Ser Trp Glu Tyr Gly Asp Pro His Ser Pro Val
65 70 75 80

Ile Leu Cys Ser Tyr Leu Pro Asp Glu Phe Ile Glu Cys Glu Asp Pro
85 90 95

Val Asp His Val Gly Asn Ala Thr Ala Ser Gln Glu Leu Gly Tyr Gly
100 105 110

Cys Leu Lys Phe Gly Gly Gln Ala Tyr Ser Asp Val Glu His Thr Ser
115 120 125

Val Gln Cys His Ala Leu Asp Gly Ile Glu Cys Ala Ser Pro Arg Thr
130 135 140

Phe Leu Arg Glu Asn Lys Pro Cys Ile Lys Tyr Thr Gly His Tyr Phe
145 150 155 160

Ile Thr Thr Leu Leu Tyr Ser Phe Phe Leu Gly Cys Phe Gly Val Asp
165 170 175

Arg Phe Cys Leu Gly His Thr Gly Thr Ala Val Gly Lys Leu Leu Thr
180 185 190

Leu Gly Gly Leu Gly Ile Trp Trp Phe Val Asp Leu Ile Leu Leu Ile
195 200 205

Thr Gly Gly Leu Met Pro Ser Asp Gly Ser Asn Trp Cys Thr Val Tyr
210 215 220

<210> 1019
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1019
Asn Val Pro Val Cys His Leu Ser Thr Trp Lys Ile Leu Tyr Ile Trp
1 5 10 15

Lys Val Tyr Ala Ser Leu Asn Lys Tyr Met Leu Leu Asn Lys Pro Tyr
20 25 30

His Ser Leu Arg Asn Cys Ile Tyr Phe Ile Ile Cys Pro Phe Arg Asn
35 40 45

Gln Val Phe Cys Ile
50

<210> 1020
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1020
Phe Tyr Thr Asn Leu Ile Trp Leu Pro Phe Val Pro Leu Ile Ser Gln
1 5 10 15

Met Phe Lys Cys Ile Gly Phe Gly Phe Ser Met Tyr Lys Leu Pro Tyr
20 25 30

Leu Leu Met Ser Ile Phe Cys Leu Phe Asn Phe Val Tyr Leu Leu Phe
35 40 45

Cys Phe Trp Ile His Phe Leu Ile Arg Ser His Met Ile Asn Ile Ile
50 55 60

Ser Ile Val Ile Ile Pro
65 70

<210> 1021
<211> 337
<212> PRT
<213> Homo sapiens

<400> 1021
Arg Lys Arg Lys Gln Ala Ala Arg Ala Ala Glu Glu Pro Gly Ala Ala
1 5 10 15

Met Asp Val Arg Ala Leu Pro Trp Leu Pro Trp Leu Leu Trp Leu Leu
20 25 30

Cys Arg Gly Gly Gly Asp Ala Asp Ser Arg Ala Pro Phe Thr Pro Thr
35 40 45

Trp Pro Arg Ser Arg Glu Arg Glu Ala Ala Ala Phe Arg Glu Ser Leu
50 55 60

Asn Arg His Arg Tyr Leu Asn Ser Leu Phe Pro Ser Glu Asn Ser Thr
65 70 75 80

Ala Phe Tyr Gly Ile Asn Gln Phe Ser Tyr Leu Phe Pro Glu Glu Phe

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                85                  90                  95

Lys Ala Ile Tyr Leu Arg Ser Lys Pro Ser Lys Phe Pro Arg Tyr Ser
            100                 105                 110

Ala Glu Val His Met Ser Ile Pro Asn Val Ser Leu Pro Leu Arg Phe
        115                 120                 125

Asp Trp Arg Asp Lys Gln Val Val Thr Gln Val Arg Asn Gln Gln Met
    130                 135                 140

Cys Gly Gly Cys Trp Ala Phe Ser Val Val Gly Ala Val Glu Ser Ala
145                 150                 155                 160

Tyr Ala Ile Lys Gly Lys Pro Leu Glu Asp Leu Ser Val Gln Gln Val
                165                 170                 175

Ile Asp Cys Ser Tyr Asn Asn Tyr Gly Cys Asn Gly Gly Ser Thr Leu
            180                 185                 190

Asn Ala Leu Asn Trp Leu Asn Lys Met Gln Val Lys Leu Val Lys Asp
        195                 200                 205

Ser Glu Tyr Pro Phe Lys Ala Gln Asn Gly Leu Cys His Tyr Phe Ser
    210                 215                 220

Gly Ser His Ser Gly Phe Ser Ile Lys Gly Tyr Ser Ala Tyr Asp Phe
225                 230                 235                 240

Ser Asp Gln Glu Asp Glu Met Ala Lys Ala Leu Leu Thr Phe Gly Pro
                245                 250                 255

Leu Val Val Ile Val Asp Ala Val Ser Trp Gln Asp Tyr Leu Gly Gly
            260                 265                 270

Ile Ile Gln His His Cys Ser Ser Gly Glu Ala Asn His Ala Val Leu
        275                 280                 285

Ile Thr Gly Phe Asp Lys Thr Gly Ser Thr Pro Tyr Trp Ile Val Arg
    290                 295                 300

Asn Ser Trp Gly Ser Ser Trp Gly Val Asp Gly Tyr Ala His Val Lys
305                 310                 315                 320

Met Gly Ser Asn Val Cys Gly Ile Ala Asp Ser Val Ser Ser Ile Phe
                325                 330                 335

Val
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<210> 1022
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1022
Ala Ser Ala Glu Phe Glu Met Ala Gly Gly Lys Ala Gly Lys Asp Ser
1 5 10 15

Gly Lys Ala Lys Thr Lys Ala Val Ser Arg Ser Gln Arg Ala Gly Leu
20 25 30

Gln Phe Pro Val Gly Arg Ile His Arg His Leu Lys Ser Arg Thr Thr
35 40 45

Ser His Gly Arg Val Gly Ala Thr Ala Ala Val Tyr Ser Ala Ala Ile
50 55 60

Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu Ala Gly Asn Ala Ser
65 70 75 80

Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg His Leu Gln Leu Ala
85 90 95

Ile Arg Gly Asp Glu Glu Leu Asp Ser Leu Ile Lys Ala Thr Ile Ala
100 105 110

Gly Gly Gly Val Ile Pro His Ile His Lys Ser Leu Ile Gly Lys Lys
115 120 125

Gly Gln Gln Lys Thr Val
130

<210> 1023
<211> 226
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (33)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1023
Gly Leu Phe Gln Thr Cys Ile His Leu Leu Thr Leu Pro Val Leu Val
1 5 10 15

His Gly Glu Leu Phe Ala Pro Pro Arg Trp Leu Arg Arg Ala Ala Gly
20 25 30

Xaa Pro Trp Thr Leu Val Thr Ser Cys Xaa Ser Leu Arg Pro Ser Gly
35 40 45

Pro Cys Pro Arg Pro Gly Arg Ala Leu Leu Pro Ser Cys Ala Pro Ala
50 55 60

Ala Arg Xaa Pro Trp Gly Gly Val Val Trp Cys Trp Glu Gly Val Leu
65 70 75 80

Gln Gly Glu Glu Asp Leu Glu Gly Leu Gly Ala Ala Val Leu Asn Arg
85 90 95

Leu Thr Leu Arg Arg Pro Leu Ser Ala Ala Leu Leu Phe Ile Thr Val
100 105 110

Pro His Ser Gly Arg Arg Ser Pro Val Ala Gly Gln Val Pro Met Ala
115 120 125

Cys Ser Leu Glu Pro Asp Phe Arg Cys Phe Gly Ile Arg Ser Pro Gln
130 135 140

His Arg Gln Val His Pro Ile Ile Thr Leu Pro Val Pro Gly Trp Ala
145 150 155 160

Gly Asp Ser Gly Thr Val Met Pro Gly Ala Arg Thr Ala Ala Leu Pro
165 170 175

Leu His Thr Asp Gly Leu Gly Val Ala Leu Arg Pro His Pro Thr Leu
180 185 190

Ile Ser Gly Arg Gly Ser Pro Glu Trp Ser Leu Val Arg Ala Val Ala
195 200 205

Lys Pro Ala Val Ser Phe Leu His Lys Val Pro Pro Pro Leu Ser Val
210 215 220

Ser Gly
225

<210> 1024
<211> 760
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (330)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1024
Gln Gly Lys Lys Arg Ala Gly Asn Phe Ala Ile Met Glu Ile Gln Cys
1 5 10 15

Pro Ala Leu Arg Lys Thr Leu Pro Ile Leu Phe Gly Ser Leu Arg Arg
20 25 30

Cys Leu Cys Leu Ser Asp Lys Tyr Ser Gln Ala Cys His Pro Leu Gly
35 40 45

Ser Lys Val Arg Arg Cys Arg Lys Pro Gly Pro Arg Asp Arg Gln Leu
50 55 60

Thr Arg Val Asp Lys Ser Pro Glu Met Trp Cys Ile Val Leu Phe Ser
65 70 75 80

Leu Leu Ala Trp Val Tyr Ala Glu Pro Thr Met Tyr Gly Glu Ile Leu
85 90 95

Ser Pro Asn Tyr Pro Gln Ala Tyr Pro Ser Glu Val Glu Lys Ser Trp
100 105 110

Asp Ile Glu Val Pro Glu Gly Tyr Gly Ile His Leu Tyr Phe Thr His
115 120 125

Leu Asp Ile Glu Leu Ser Glu Asn Cys Ala Tyr Asp Ser Val Gln Ile
130 135 140

Ile Ser Gly Asp Thr Glu Glu Gly Arg Leu Cys Gly Gln Arg Ser Ser
145 150 155 160

Asn Asn Pro His Ser Pro Ile Val Glu Glu Phe Gln Val Pro Tyr Asn
165 170 175

Lys Leu Gln Val Ile Phe Lys Ser Asp Phe Ser Asn Glu Glu Arg Phe
180 185 190

Thr Gly Phe Ala Ala Tyr Tyr Val Ala Thr Asp Ile Asn Glu Cys Thr
195 200 205

Asp Phe Val Asp Val Pro Cys Ser His Phe Cys Asn Asn Phe Ile Gly
    210   215   220

Gly Tyr Phe Cys Ser Cys Pro Pro Glu Tyr Phe Leu His Asp Asp Met
225   230   235   240

Lys Asn Cys Gly Val Asn Cys Ser Gly Asp Val Phe Thr Ala Leu Ile
                245   250   255

Gly Glu Ile Ala Ser Pro Asn Tyr Pro Lys Pro Tyr Pro Glu Asn Ser
            260   265   270

Arg Cys Glu Tyr Gln Ile Arg Leu Glu Lys Gly Phe Gln Val Val Val
        275   280   285

Thr Leu Arg Arg Glu Asp Phe Asp Val Glu Ala Ala Asp Ser Ala Gly
    290   295   300

Asn Cys Leu Asp Ser Leu Val Phe Val Ala Gly Asp Arg Gln Phe Gly
305   310   315   320

Pro Tyr Cys Gly His Gly Phe Pro Gly Xaa Leu Asn Ile Glu Thr Lys
                325   330   335

Ser Asn Ala Leu Asp Ile Ile Phe Gln Thr Asp Leu Thr Gly Gln Lys
            340   345   350

Lys Gly Trp Lys Leu Arg Tyr His Gly Asp Pro Met Pro Cys Pro Lys
        355   360   365

Glu Asp Thr Pro Asn Ser Val Trp Glu Pro Ala Lys Ala Lys Tyr Val
    370   375   380

Phe Arg Asp Val Val Gln Ile Thr Cys Leu Asp Gly Phe Glu Val Val
385   390   395   400

Glu Gly Arg Val Gly Ala Thr Ser Phe Tyr Ser Thr Cys Gln Ser Asn
                405   410   415

Gly Lys Trp Ser Asn Ser Lys Leu Lys Cys Gln Pro Val Asp Cys Gly
            420   425   430

Ile Pro Glu Ser Ile Glu Asn Gly Lys Val Glu Asp Pro Glu Ser Thr
        435   440   445

Leu Phe Gly Ser Val Ile Arg Tyr Thr Cys Glu Glu Pro Tyr Tyr Tyr
    450   455   460

Met Glu Asn Gly Gly Gly Gly Glu Tyr His Cys Ala Gly Asn Gly Ser
465   470   475   480

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Trp Val Asn Glu Val Leu Gly Pro Glu Leu Pro Lys Cys Val Pro Val
                485                 490                 495

Cys Gly Val Pro Arg Glu Pro Phe Glu Glu Lys Gln Arg Ile Ile Gly
            500                 505                 510

Gly Ser Asp Ala Asp Ile Lys Asn Phe Pro Trp Gln Val Phe Phe Asp
        515                 520                 525

Asn Pro Trp Ala Gly Gly Ala Leu Ile Asn Glu Tyr Trp Val Leu Thr
    530                 535                 540

Ala Ala His Val Val Glu Gly Asn Arg Glu Pro Thr Met Tyr Val Gly
545                 550                 555                 560

Ser Thr Ser Val Gln Thr Ser Arg Leu Ala Lys Ser Lys Met Leu Thr
                565                 570                 575

Pro Glu His Val Phe Ile His Pro Gly Trp Lys Leu Leu Glu Val Pro
            580                 585                 590

Glu Gly Arg Thr Asn Phe Asp Asn Asp Ile Ala Leu Val Arg Leu Lys
        595                 600                 605

Asp Pro Val Lys Met Gly Pro Thr Val Ser Pro Ile Cys Leu Pro Gly
    610                 615                 620

Thr Ser Ser Asp Tyr Asn Leu Met Asp Gly Asp Leu Gly Leu Ile Ser
625                 630                 635                 640

Gly Trp Gly Arg Thr Glu Lys Arg Asp Arg Ala Val Arg Leu Lys Ala
                645                 650                 655

Ala Arg Leu Pro Val Ala Pro Leu Arg Lys Cys Lys Glu Val Lys Val
            660                 665                 670

Glu Lys Pro Thr Ala Asp Ala Glu Ala Tyr Val Phe Thr Pro Asn Met
        675                 680                 685

Ile Cys Ala Gly Gly Glu Lys Gly Met Asp Ser Cys Lys Gly Asp Ser
    690                 695                 700

Gly Gly Ala Phe Ala Val Gln Asp Pro Asn Asp Lys Thr Lys Phe Tyr
705                 710                 715                 720

Ala Ala Gly Leu Val Ser Trp Gly Pro Gln Cys Gly Thr Tyr Gly Leu
                725                 730                 735

Tyr Thr Arg Val Lys Asn Tyr Val Asp Trp Ile Met Lys Thr Met Gln
            740                 745                 750
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Glu Asn Ser Thr Pro Arg Glu Asp
        755                 760



<210> 1025
<211> 216
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (115)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (139)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1025
Gly Gly Gly Arg Leu Arg Arg Arg Arg Ser Gly Ser Pro Gly Trp Arg
  1               5                  10                  15

Ala Pro Arg Thr Gly Met Leu Leu Gly Leu Ala Ala Met Glu Leu Lys
            20                  25                  30

Val Trp Val Asp Gly Ile Gln Arg Val Val Cys Gly Val Ser Glu Gln
        35                  40                  45

Thr Thr Cys Gln Glu Val Val Ile Ala Leu Ala Gln Ala Ile Gly Gln
    50                  55                  60

Thr Gly Arg Phe Val Leu Val Gln Arg Leu Arg Glu Lys Glu Arg Gln
 65                  70                  75                  80

Leu Leu Pro Gln Glu Cys Pro Val Gly Ala Gln Ala Thr Cys Gly Gln
                85                  90                  95

Phe Ala Ser Asp Val Gln Phe Val Leu Arg Arg Thr Gly Pro Ser Leu
            100                 105                 110

Ala Gly Xaa Pro Ser Ser Asp Ser Cys Pro Pro Pro Glu Arg Cys Leu
        115                 120                 125

Ile Arg Ala Ser Leu Pro Val Lys Pro Arg Xaa Ala Leu Gly Cys Glu
    130                 135                 140

Pro Arg Lys Thr Leu Thr Pro Glu Pro Ala Pro Ser Leu Ser Arg Pro
145                 150                 155                 160
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Gly Pro Ala Ala Cys Glu His Pro His Gln Ala Ala Ala Gln Thr Cys
165 170 175

Gly Ala Trp Ser Ser Gly Cys Arg Gly Met Leu Arg Ser Trp Ala Met
180 185 190

Arg Pro Ser Gly Ser Lys Ser Cys Ala Gly Ser Arg Pro Gly Ser Glu
195 200 205

Arg Asp Arg His Ala Cys Arg His
210 215

<210> 1026
<211> 604
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (303)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (359)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1026
Gly Thr Ser Ser Asp Ile Leu Lys Gly Asn Phe Ser Ile Arg Thr Ala
1 5 10 15

Lys Met Gln Gln His Val Cys Glu Thr Ile Ile Arg Ile Phe Lys Arg
20 25 30

His Gly Ala Val Gln Leu Cys Thr Pro Leu Leu Leu Pro Arg Asn Arg
35 40 45

Gln Ile Tyr Glu His Asn Glu Ala Ala Leu Phe Met Asp His Ser Gly
50 55 60

Met Leu Val Met Leu Pro Phe Asp Leu Arg Ile Pro Phe Ala Arg Tyr
65 70 75 80

Val Ala Arg Asn Asn Ile Leu Asn Leu Lys Arg Tyr Cys Ile Glu Arg
85 90 95

Val Phe Arg Pro Arg Lys Leu Asp Arg Phe His Pro Lys Glu Leu Leu
100 105 110

Glu Cys Ala Phe Asp Ile Val Thr Ser Thr Thr Asn Ser Phe Leu Pro
115 120 125

Thr Ala Glu Ile Ile Tyr Thr Ile Tyr Glu Ile Ile Gln Glu Phe Pro
130 135 140

Ala Leu Gln Glu Arg Asn Tyr Ser Ile Tyr Leu Asn His Thr Met Leu
145 150 155 160

Leu Lys Ala Ile Leu Leu His Cys Gly Ile Pro Glu Asp Lys Leu Ser
165 170 175

Gln Val Tyr Ile Ile Leu Tyr Asp Ala Val Thr Glu Lys Leu Thr Arg
180 185 190

Arg Glu Val Glu Ala Lys Phe Cys Asn Leu Ser Leu Ser Ser Asn Ser
195 200 205

Leu Cys Arg Leu Tyr Lys Phe Ile Glu Gln Lys Gly Asp Leu Gln Asp
210 215 220

Leu Met Pro Thr Ile Asn Ser Leu Ile Lys Gln Lys Thr Gly Ile Ala
225 230 235 240

Gln Leu Val Lys Tyr Gly Leu Lys Asp Leu Glu Glu Val Val Gly Leu
245 250 255

Leu Lys Lys Leu Gly Ile Lys Leu Gln Val Leu Ile Asn Leu Gly Leu
260 265 270

Val Tyr Lys Val Gln Gln His Asn Gly Ile Ile Phe Gln Phe Val Ala
275 280 285

Phe Ile Lys Arg Arg Gln Arg Ala Val Pro Glu Ile Leu Ala Xaa Gly
290 295 300

Gly Arg Tyr Asp Leu Leu Ile Pro Gln Phe Arg Gly Pro Gln Ala Leu
305 310 315 320

Gly Pro Val Pro Thr Ala Ile Gly Val Ser Ile Ala Ile Asp Lys Ile
325 330 335

Ser Ala Ala Val Leu Asn Met Glu Glu Ser Val Thr Ile Ser Ser Cys
340 345 350

Asp Leu Leu Val Val Ser Xaa Gly Gln Met Ser Met Ser Arg Ala Ile
355 360 365

Asn Leu Thr Gln Lys Leu Trp Thr Ala Gly Ile Thr Ala Glu Ile Met
370 375 380

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Tyr Asp Trp Ser Gln Ser Gln Glu Glu Leu Gln Glu Tyr Cys Arg His
385                 390                 395                 400

His Glu Ile Thr Tyr Val Ala Leu Val Ser Asp Lys Glu Gly Ser His
                405                 410                 415

Val Lys Val Lys Ser Phe Glu Lys Glu Arg Gln Thr Glu Lys Arg Val
            420                 425                 430

Leu Glu Thr Glu Leu Val Asp His Val Leu Gln Lys Leu Arg Thr Lys
        435                 440                 445

Val Thr Asp Glu Arg Asn Gly Arg Glu Ala Ser Asp Asn Leu Ala Val
    450                 455                 460

Gln Asn Leu Lys Gly Ser Phe Ser Asn Ala Ser Gly Leu Phe Glu Ile
465                 470                 475                 480

His Gly Ala Thr Val Val Pro Ile Val Ser Val Leu Ala Pro Glu Lys
                485                 490                 495

Leu Ser Ala Ser Thr Arg Arg Arg Tyr Glu Thr Gln Val Gln Thr Arg
            500                 505                 510

Leu Gln Thr Ser Leu Ala Asn Leu His Gln Lys Ser Ser Glu Ile Glu
        515                 520                 525

Ile Leu Ala Val Asp Leu Pro Lys Glu Thr Ile Leu Gln Phe Leu Ser
    530                 535                 540

Leu Glu Trp Asp Ala Asp Glu Gln Ala Phe Asn Thr Thr Val Lys Gln
545                 550                 555                 560

Leu Leu Ser Arg Leu Pro Lys Gln Arg Tyr Leu Lys Leu Val Cys Asp
                565                 570                 575

Glu Ile Tyr Asn Ile Lys Val Glu Lys Lys Val Ser Val Leu Phe Leu
            580                 585                 590

Tyr Ser Tyr Arg Asp Asp Tyr Tyr Arg Ile Leu Phe
        595                 600
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<210> 1027
<211> 459
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1027
Thr Ser Cys Gly Ile Asn Thr Lys Phe Thr Ser Lys Glu Pro Ile Phe
1   5   10   15

Leu Thr Gln Leu Leu His Phe Ser Asn Leu Xaa Gln Glu Tyr Lys Ile
            20   25   30

Asn Ser Arg Leu Leu Gln Asn Ile Leu Asp Ala Gly Phe Gln Met Pro
        35   40   45

Thr Pro Ile Gln Met Gln Ala Ile Pro Val Met Leu His Gly Arg Glu
    50   55   60

Leu Leu Ala Ser Ala Pro Thr Gly Ser Gly Lys Thr Leu Ala Phe Ser
65   70   75   80

Ile Pro Ile Leu Met Gln Leu Lys Gln Pro Ala Asn Lys Gly Phe Arg
                85   90   95

Ala Leu Ile Ile Ser Pro Thr Arg Glu Leu Ala Ser Gln Ile His Arg
            100   105   110

Glu Leu Ile Lys Ile Ser Glu Gly Thr Gly Phe Arg Ile His Met Ile
        115   120   125

His Lys Ala Ala Val Ala Ala Lys Lys Phe Gly Pro Lys Ser Ser Lys
    130   135   140

Lys Phe Asp Ile Leu Val Thr Thr Pro Asn Arg Leu Ile Tyr Leu Leu
145   150   155   160

Lys Gln Asp Pro Pro Gly Ile Asp Leu Ala Ser Val Glu Trp Leu Val
                165   170   175

Val Asp Glu Ser Asp Lys Leu Phe Glu Asp Gly Lys Thr Gly Phe Arg
            180   185   190

Asp Gln Leu Ala Ser Ile Phe Leu Ala Cys Thr Ser His Lys Val Arg
        195   200   205

Arg Ala Met Phe Ser Ala Thr Phe Ala Tyr Asp Val Glu Gln Trp Cys
    210   215   220

Lys Leu Asn Leu Asp Asn Val Ile Ser Val Ser Ile Gly Ala Arg Asn
225   230   235   240

Ser Ala Val Glu Thr Val Glu Gln Glu Leu Leu Phe Val Gly Ser Glu

245 250 255

Thr Gly Lys Leu Leu Ala Val Arg Glu Leu Val Lys Lys Gly Phe Asn
260 265 270

Pro Pro Val Leu Val Phe Val Gln Ser Ile Glu Arg Ala Lys Glu Leu
275 280 285

Phe His Glu Leu Ile Tyr Glu Gly Ile Asn Val Asp Val Ile His Ala
290 295 300

Glu Arg Thr Gln Gln Gln Arg Asp Asn Thr Val His Ser Phe Arg Ala
305 310 315 320

Gly Lys Ile Trp Val Leu Ile Cys Thr Ala Leu Leu Ala Arg Gly Ile
325 330 335

Asp Phe Lys Gly Val Asn Leu Val Ile Asn Tyr Asp Phe Pro Thr Ser
340 345 350

Ser Val Glu Tyr Ile His Arg Ile Gly Arg Thr Gly Arg Ala Gly Asn
355 360 365

Lys Gly Lys Ala Ile Thr Phe Phe Thr Glu Asp Asp Lys Pro Leu Leu
370 375 380

Arg Ser Val Ala Asn Val Ile Gln Gln Ala Gly Cys Pro Val Pro Glu
385 390 395 400

Tyr Ile Lys Gly Phe Gln Lys Leu Leu Ser Lys Gln Lys Lys Lys Met
405 410 415

Ile Lys Lys Pro Leu Glu Arg Glu Ser Ile Ser Thr Thr Pro Lys Cys
420 425 430

Phe Leu Glu Lys Ala Lys Asp Lys Gln Lys Lys Val Thr Gly Gln Asn
435 440 445

Ser Lys Lys Lys Val Ala Leu Glu Asp Lys Ser
450 455

<210> 1028
<211> 68
<212> PRT
<213> Homo sapiens

<400> 1028
Gln Arg Gly Phe Tyr Ala Asn Ala Leu Thr Ser Ala Leu Gly Asn Glu
1 5 10 15

Arg Val Thr Ser Ala Ser Ser Leu Ala Ser Phe Leu Val Leu Glu Arg
20 25 30

Leu Thr Asn Val Cys His Ser His Lys Cys Phe Glu Leu Asp Leu Cys
35 40 45

Asp Leu Cys Phe Phe Ser Phe Ser Leu Glu Ser Glu Tyr His Cys Leu
50 55 60

Pro Pro Arg Ser
65

<210> 1029
<211> 215
<212> PRT
<213> Homo sapiens

<400> 1029
Tyr Pro Leu Thr Pro Ala Pro Ala Pro His Asp Pro Ser Pro Arg Ala
1 5 10 15

His Gly Arg Gly Asp Asp Val Thr Gln Ala Thr Ala Leu Thr Ser His
20 25 30

Ile Thr Val Val Met Ala Ser Arg Gly His Val Asp Val Thr Lys Arg
35 40 45

Tyr Ser Asp Gly Val Val Gln Met Gln His Val Ala His Arg His Gly
50 55 60

Glu Leu Gly Met Thr Ser His Arg Asp Ala Ala Thr Thr Ser Arg Ala
65 70 75 80

Met Ser Thr Ser His Ile Leu Met Ser His Arg Arg Gly Asp Gly Ile
85 90 95

Thr Gln Thr Val Met Met Ser His Thr Asp Thr Val Thr Thr His Thr
100 105 110

Met Thr Thr Thr Pro Ile Asp Met Ala Pro Thr Ser His Ala Arg Met
115 120 125

Pro Phe His Thr His Phe Leu Pro Asn Ser His Leu Val Ser Arg Ser
130 135 140

Pro Asp Pro Gly Thr Arg Ala Lys Val Pro Thr Gly Ser His Pro Leu
145 150 155 160

Pro His Ser Pro Gly Pro Gln His Leu Pro Ser Ser Ser Phe Leu Ala
165 170 175

Ser Gln Pro Leu Pro His Pro Gln Cys Leu Asp Pro Glu Val Arg Thr
180 185 190

Gly Ser His Ser Pro Pro Leu Leu Glu Arg Glu Cys Phe Gln Asp Pro
195 200 205

Leu Gly Ala Leu Ser Arg Gly
210 215

<210> 1030
<211> 297
<212> PRT
<213> Homo sapiens

<400> 1030
Lys Val Arg Leu Gln Val Pro Val Arg Asn Ser Arg Val Asp Pro Arg
1 5 10 15

Val Arg Pro Arg Val Arg Pro Arg Val Arg Trp Thr Ala Ala Met Arg
20 25 30

Leu Thr Val Leu Cys Ala Val Cys Leu Leu Pro Gly Ser Leu Ala Leu
35 40 45

Pro Leu Pro Gln Glu Ala Gly Gly Met Ser Glu Leu Gln Trp Glu Gln
50 55 60

Ala Gln Asp Tyr Leu Lys Arg Phe Tyr Leu Tyr Asp Ser Glu Thr Lys
65 70 75 80

Asn Ala Asn Ser Leu Glu Ala Lys Leu Lys Glu Met Gln Lys Phe Phe
85 90 95

Gly Leu Pro Ile Thr Gly Met Leu Asn Ser Arg Val Ile Glu Ile Met
100 105 110

Gln Lys Pro Arg Cys Gly Val Pro Asp Val Ala Glu Tyr Ser Leu Phe
115 120 125

Pro Asn Ser Pro Lys Trp Thr Ser Lys Val Val Thr Tyr Arg Ile Val
130 135 140

Ser Tyr Thr Arg Asp Leu Pro His Ile Thr Val Asp Arg Leu Val Ser
145 150 155 160

Lys Ala Leu Asn Met Trp Gly Lys Glu Ile Pro Leu His Phe Arg Lys

165 170 175

Val Val Trp Gly Thr Ala Asp Ile Met Ile Gly Phe Ala Arg Gly Ala
180 185 190

His Gly Asp Ser Tyr Pro Phe Asp Gly Pro Gly Asn Thr Leu Ala His
195 200 205

Ala Phe Ala Pro Gly Thr Gly Leu Gly Gly Asp Ala His Phe Asp Glu
210 215 220

Asp Glu Arg Trp Thr Asp Gly Ser Ser Leu Gly Ile Asn Phe Leu Tyr
225 230 235 240

Ala Ala Thr His Glu Leu Gly His Ser Leu Gly Met Gly His Ser Ser
245 250 255

Asp Pro Asn Ala Val Met Tyr Pro Thr Tyr Gly Asn Gly Asp Pro Gln
260 265 270

Asn Phe Lys Leu Ser Gln Asp Asp Ile Lys Gly Ile Gln Lys Leu Tyr
275 280 285

Gly Lys Arg Ser Asn Ser Arg Lys Lys
290 295

<210> 1031
<211> 571
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (44)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (81)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (484)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1031
Arg Val Arg Ser Lys Val Pro Arg Cys Val Asn Thr Gln Pro Gly Phe
1 5 10 15

His Cys Leu Pro Cys Pro Pro Arg Tyr Arg Gly Asn Gln Pro Val Gly
20 25 30

Val Gly Leu Glu Ala Ala Lys Thr Glu Lys Gln Xaa Cys Glu Pro Glu
35 40 45

Asn Pro Cys Lys Asp Lys Thr His Asn Cys His Lys His Ala Glu Cys
50 55 60

Ile Tyr Leu Gly His Phe Ser Asp Pro Met Tyr Lys Cys Glu Cys Gln
65 70 75 80

Xaa Gly Tyr Ala Gly Asp Gly Leu Ile Cys Gly Glu Asp Ser Asp Leu
85 90 95

Asp Gly Trp Pro Asn Leu Asn Leu Val Cys Ala Thr Asn Ala Thr Tyr
100 105 110

His Cys Ile Lys Asp Asn Cys Pro His Leu Pro Asn Ser Gly Gln Glu
115 120 125

Asp Phe Asp Lys Asp Gly Ile Gly Asp Ala Cys Asp Asp Asp Asp Asp
130 135 140

Asn Asp Gly Val Thr Asp Glu Lys Asp Asn Cys Gln Leu Leu Phe Asn
145 150 155 160

Pro Arg Gln Ala Asp Tyr Asp Lys Asp Glu Val Gly Asp Arg Cys Asp
165 170 175

Asn Cys Pro Tyr Val His Asn Pro Ala Gln Ile Asp Thr Asp Asn Asn
180 185 190

Gly Glu Gly Asp Ala Cys Ser Val Asp Ile Asp Gly Asp Asp Val Phe
195 200 205

Asn Glu Arg Asp Asn Cys Pro Tyr Val Tyr Asn Thr Asp Gln Arg Asp
210 215 220

Thr Asp Gly Asp Gly Val Gly Asp His Cys Asp Asn Cys Pro Leu Val
225 230 235 240

His Asn Pro Asp Gln Thr Asp Val Asp Asn Asp Leu Val Gly Asp Gln
245 250 255

Cys Asp Asn Asn Glu Asp Ile Asp Asp Asp Gly His Gln Asn Asn Gln
260 265 270

Asp Asn Cys Pro Tyr Ile Ser Asn Ala Asn Gln Ala Asp His Asp Arg
275 280 285

Asp Gly Gln Gly Asp Ala Cys Asp Pro Asp Asp Asp Asn Asp Gly Val
290 295 300

Pro Asp Asp Arg Asp Asn Cys Arg Leu Val Phe Asn Pro Asp Gln Glu
305 310 315 320

Asp Leu Asp Gly Asp Gly Arg Gly Asp Ile Cys Lys Asp Asp Phe Asp
325 330 335

Asn Asp Asn Ile Pro Asp Ile Asp Asp Val Cys Pro Glu Asn Asn Ala
340 345 350

Ile Ser Glu Thr Asp Phe Arg Asn Phe Gln Met Val Pro Leu Asp Pro
355 360 365

Lys Gly Thr Thr Gln Ile Asp Pro Asn Trp Val Ile Arg His Gln Gly
370 375 380

Lys Glu Leu Val Gln Thr Ala Asn Ser Asp Pro Gly Ile Ala Val Gly
385 390 395 400

Phe Asp Glu Phe Gly Ser Val Asp Phe Ser Gly Thr Phe Tyr Val Asn
405 410 415

Thr Asp Arg Asp Asp Asp Tyr Ala Gly Phe Val Phe Gly Tyr Gln Ser
420 425 430

Ser Ser Arg Phe Tyr Val Val Met Trp Lys Gln Val Thr Gln Thr Tyr
435 440 445

Trp Glu Asp Gln Pro Thr Arg Ala Tyr Gly Tyr Ser Gly Val Ser Leu
450 455 460

Lys Val Val Asn Ser Thr Thr Gly Thr Gly Glu His Leu Arg Asn Ala
465 470 475 480

Leu Trp His Xaa Gly Asn Thr Pro Gly Gln Val Arg Thr Leu Trp His
485 490 495

Asp Pro Arg Asn Ile Gly Trp Lys Asp Tyr Thr Ala Tyr Arg Trp His
500 505 510

Leu Thr His Arg Pro Lys Thr Gly Tyr Ile Arg Val Leu Val His Glu
515 520 525

Gly Lys Gln Val Met Ala Asp Ser Gly Pro Ile Tyr Asp Gln Thr Tyr
530 535 540

Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser Gln Glu Met Val Tyr
545 550 555 560

Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Ile
565 570

<210> 1032
<211> 114
<212> PRT
<213> Homo sapiens

<400> 1032
Gly Arg Gly Thr Ala Thr Phe Pro Thr Gly His Glu Phe Val Gly Pro
1 5 10 15

Cys Leu Gly Arg Ala Glu Ala Phe Trp Arg Ser Lys Met Gly Arg Lys
20 25 30

Asp Ala Ala Thr Ile Lys Leu Pro Val Asp Gln Tyr Arg Lys Gln Ile
35 40 45

Gly Lys Gln Asp Tyr Lys Lys Thr Lys Pro Ile Leu Arg Ala Thr Lys
50 55 60

Leu Lys Ala Glu Ala Lys Lys Thr Ala Ile Gly Ile Lys Glu Val Gly
65 70 75 80

Leu Val Leu Ala Ala Ile Leu Ala Leu Leu Leu Ala Phe Tyr Ala Phe
85 90 95

Phe Tyr Leu Arg Leu Thr Thr Asp Val Asp Pro Asp Leu Asp Gln Asp
100 105 110

Glu Asp

<210> 1033
<211> 243
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (88)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (101)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1033

His Arg Arg Asp Glu Ala Leu Gln Ser Leu Arg Phe Arg Arg Arg Pro
1 5 10 15

Gly Ala Gln Ala Ala Asp Ala Cys Gly Pro Arg Ala Asp Leu Gly Gly
20 25 30

Pro Arg Glu Pro Ala Ala Gly Gly Arg Ala Ala Trp His Arg Pro Ala
35 40 45

Ala Arg Gly Gln Ser Pro Arg Arg Cys His Ala Gly Val His Arg Ser
50 55 60

Gln Cys His Leu Cys Arg Leu Gly Ala Ala Glu Arg Phe Arg Gly Ile
65 70 75 80

Val Ala Leu Leu Ala Ser Arg Xaa Leu Leu Arg Pro Pro Leu His Trp
85 90 95

Val Leu Leu Ala Xaa Ala Leu Val Asn Leu Leu Leu Ser Val Ala Cys
100 105 110

Ser Leu Gly Leu Leu Leu Ala Val Ser Leu Thr Val Ala Asn Gly Gly
115 120 125

Arg Arg Leu Ile Ala Asp Cys His Pro Gly Leu Leu Asp Pro Leu Val
130 135 140

Pro Leu Asp Glu Gly Pro Gly His Thr Asp Cys Pro Phe Asp Pro Thr
145 150 155 160

Arg Ile Tyr Asp Thr Ala Leu Ala Leu Trp Ile Pro Ser Leu Leu Met
165 170 175

Ser Ala Gly Glu Ala Ala Leu Ser Gly Tyr Cys Cys Val Ala Ala Leu
180 185 190

Thr Leu Arg Gly Val Gly Pro Cys Arg Lys Asp Gly Leu Gln Gly Gln
195 200 205

Leu Glu Glu Met Thr Glu Leu Glu Ser Pro Lys Cys Lys Arg Gln Glu
210 215 220

Asn Glu Gln Leu Leu Asp Gln Asn Gln Glu Ile Arg Ala Ser Gln Arg
225 230 235 240

Ser Trp Val

<210> 1034
<211> 173
<212> PRT
<213> Homo sapiens

<400> 1034
Tyr Thr Trp His Ser Glu Lys Met Asp Leu Lys Asp Lys Asn Gly Gly
1 5 10 15

Pro Gly Arg Cys Asn Ser His Arg Leu Lys Val Ser Ser Gly Leu Cys
20 25 30

Lys Thr His Glu Ile Gly Phe Asp Pro Leu Ala Leu Lys Cys Pro Leu
35 40 45

Arg Ser Arg Thr Ala Pro Trp Trp Pro Leu Asp Arg Val Ser Phe Asp
50 55 60

Leu His His Leu Val Ile Gly Asn Phe Phe Val Gly Asn Arg Lys Ile
65 70 75 80

Phe Leu Asp Tyr Leu Val Tyr Gly Phe Ala His Asn Asn Arg Trp Lys
85 90 95

Leu Leu Val Gln Ser Trp Ser Asp Gly Cys Val His Arg Thr Phe Gly
100 105 110

Leu Val Lys Ser Phe Ser Lys Ala Ser Phe Cys Ile Phe Ile Thr Lys
115 120 125

Gln Arg Lys Ser Ser Glu Asp Leu Ala Leu Lys Gln Ile Cys Ala Asn
130 135 140

Thr Ala Arg Val Ile Leu Lys Leu Lys His Phe His Phe Val Ser Tyr
145 150 155 160

Met Cys Thr Phe Leu Phe Thr Cys Glu Asn Gly His Leu
165 170

<210> 1035
<211> 241
<212> PRT
<213> Homo sapiens

<400> 1035
Ser Phe Ser Glu Met Ala Gly Val Ser Ala Cys Ile Lys Tyr Ser Met
1 5 10 15

Phe Thr Phe Asn Phe Leu Phe Trp Leu Cys Gly Ile Leu Ile Leu Ala
20 25 30

Leu Ala Ile Trp Val Arg Val Ser Asn Asp Ser Gln Ala Ile Phe Gly
35 40 45

Ser Glu Asp Val Gly Ser Ser Ser Tyr Val Ala Val Asp Ile Leu Ile
50 55 60

Ala Val Gly Ala Ile Ile Met Ile Leu Gly Phe Leu Gly Cys Cys Gly
65 70 75 80

Ala Ile Lys Glu Ser Arg Cys Met Leu Leu Leu Phe Phe Ile Gly Leu
85 90 95

Leu Leu Ile Leu Leu Leu Gln Val Ala Thr Gly Ile Leu Gly Ala Val
100 105 110

Phe Lys Ser Lys Ser Asp Arg Ile Val Asn Glu Thr Leu Tyr Glu Asn
115 120 125

Thr Lys Leu Leu Ser Ala Thr Gly Glu Ser Glu Lys Gln Phe Gln Glu
130 135 140

Ala Ile Ile Val Phe Gln Glu Glu Phe Lys Cys Cys Gly Leu Val Asn
145 150 155 160

Gly Ala Ala Asp Trp Gly Asn Asn Phe Gln His Tyr Pro Glu Leu Cys
165 170 175

Ala Cys Leu Asp Lys Gln Arg Pro Cys Gln Ser Tyr Asn Gly Lys Gln
180 185 190

Val Tyr Lys Glu Thr Cys Ile Ser Phe Ile Lys Asp Phe Leu Ala Lys
195 200 205

Asn Leu Ile Ile Val Ile Gly Ile Ser Phe Gly Leu Ala Val Ile Glu
210 215 220

Ile Leu Gly Leu Val Phe Ser Met Val Leu Tyr Cys Gln Ile Gly Asn
225 230 235 240

Lys

<210> 1036
<211> 335
<212> PRT

<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1036
Pro Thr Xaa Gly Arg Ala Glu Glu Ala Lys Met Ala Ala Ala Ala Ala
1 5 10 15

Ser Leu Arg Gly Val Val Leu Gly Pro Arg Gly Ala Gly Leu Pro Gly
20 25 30

Ala Arg Ala Arg Gly Leu Leu Cys Ser Ala Arg Pro Gly Gln Leu Pro
35 40 45

Leu Arg Thr Pro Gln Ala Val Ala Leu Ser Ser Lys Ser Gly Leu Ser
50 55 60

Arg Gly Arg Lys Val Met Leu Ser Ala Leu Gly Met Leu Ala Ala Gly
65 70 75 80

Gly Ala Gly Leu Ala Val Ala Leu His Ser Ala Val Ser Ala Ser Asp
85 90 95

Leu Glu Leu His Pro Pro Ser Tyr Pro Trp Ser His Arg Gly Leu Leu
100 105 110

Ser Ser Leu Asp His Thr Ser Ile Arg Arg Gly Phe Gln Val Tyr Lys
115 120 125

Gln Val Cys Ala Ser Cys His Ser Met Asp Phe Val Ala Tyr Arg His
130 135 140

Leu Val Gly Val Cys Tyr Thr Glu Asp Glu Ala Lys Glu Leu Ala Ala
145 150 155 160

Glu Val Glu Val Gln Asp Gly Pro Asn Glu Asp Gly Glu Met Phe Met
165 170 175

Arg Pro Gly Lys Leu Phe Asp Tyr Phe Pro Lys Pro Tyr Pro Asn Ser
180 185 190

Glu Ala Ala Arg Ala Ala Asn Asn Gly Ala Leu Pro Pro Asp Leu Ser
195 200 205

Tyr Ile Val Arg Ala Arg His Gly Gly Glu Asp Tyr Val Phe Ser Leu
210 215 220

Leu Thr Gly Tyr Cys Glu Pro Pro Thr Gly Val Ser Leu Arg Glu Gly

225 230 235 240

Leu Tyr Phe Asn Pro Tyr Phe Pro Gly Gln Ala Ile Ala Met Ala Pro
245 250 255

Pro Ile Tyr Thr Asp Val Leu Glu Phe Asp Asp Gly Thr Pro Ala Thr
260 265 270

Met Ser Gln Ile Ala Lys Asp Val Cys Thr Phe Leu Arg Trp Ala Ser
275 280 285

Glu Pro Glu His Asp His Arg Lys Arg Met Gly Leu Lys Met Leu Met
290 295 300

Met Met Ala Leu Leu Val Pro Leu Val Tyr Thr Ile Lys Arg His Lys
305 310 315 320

Trp Ser Val Leu Lys Ser Arg Lys Leu Ala Tyr Arg Pro Pro Lys
325 330 335

<210> 1037
<211> 511
<212> PRT
<213> Homo sapiens

<400> 1037
His Gln Leu Gln Gly Pro Leu Pro Leu Arg Ala Leu Pro Trp His Ser
1 5 10 15

Ser Arg Ser Arg Val Thr Cys Thr Arg Cys Phe Ser Trp Met His Pro
20 25 30

Ser Pro Met His Pro Leu Arg Ala Gly Ser Lys Ser Gln Gly Ser Arg
35 40 45

Ser Pro Ala Pro Ser Pro Met Arg Ala Ala Asn Arg Ser His Ser Ala
50 55 60

Gly Arg Thr Pro Gly Arg Thr Pro Gly Lys Ser Ser Ser Lys Val Gln
65 70 75 80

Thr Thr Pro Ser Lys Pro Gly Gly Asp Arg Tyr Ile Pro His Arg Ser
85 90 95

Ala Ala Gln Met Glu Val Ala Ser Phe Leu Leu Ser Lys Glu Asn Gln
100 105 110

Pro Glu Asn Ser Gln Thr Pro Thr Lys Lys Glu His Gln Lys Ala Trp
115 120 125

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Ala Leu Asn Leu Asn Gly Phe Asp Val Glu Glu Ala Lys Ile Leu Arg
    130                 135                 140

Leu Ser Gly Lys Pro Gln Asn Ala Pro Glu Gly Tyr Gln Asn Arg Leu
145                 150                 155                 160

Lys Val Leu Tyr Ser Gln Lys Ala Thr Pro Gly Ser Ser Arg Lys Thr
                165                 170                 175

Cys Arg Tyr Ile Pro Ser Leu Pro Asp Arg Ile Leu Asp Ala Pro Glu
            180                 185                 190

Ile Arg Asn Asp Tyr Tyr Leu Asn Leu Val Asp Trp Ser Ser Gly Asn
        195                 200                 205

Val Leu Ala Val Ala Leu Asp Asn Ser Val Tyr Leu Trp Ser Ala Ser
    210                 215                 220

Ser Gly Asp Ile Leu Gln Leu Leu Gln Met Glu Gln Pro Gly Glu Tyr
225                 230                 235                 240

Ile Ser Ser Val Ala Trp Ile Lys Glu Gly Asn Tyr Leu Ala Val Gly
                245                 250                 255

Thr Ser Ser Ala Glu Val Gln Leu Trp Asp Val Gln Gln Gln Lys Arg
            260                 265                 270

Leu Arg Asn Met Thr Ser His Ser Ala Arg Val Gly Ser Leu Ser Trp
        275                 280                 285

Asn Ser Tyr Ile Leu Ser Ser Gly Ser Arg Ser Gly His Ile His His
    290                 295                 300

His Asp Val Arg Val Ala Glu His His Val Ala Thr Leu Ser Gly His
305                 310                 315                 320

Ser Gln Glu Val Cys Gly Leu Arg Trp Ala Pro Asp Gly Arg His Leu
                325                 330                 335

Ala Ser Gly Gly Asn Asp Asn Leu Val Asn Val Trp Pro Ser Ala Pro
            340                 345                 350

Gly Glu Gly Gly Trp Val Pro Leu Gln Thr Phe Thr Gln His Gln Gly
        355                 360                 365

Ala Val Lys Ala Val Ala Trp Cys Pro Trp Gln Ser Asn Val Leu Ala
    370                 375                 380

Thr Gly Gly Gly Thr Ser Asp Arg His Ile Arg Ile Trp Asn Val Cys
385                 390                 395                 400
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Ser Gly Ala Cys Leu Ser Ala Val Asp Ala His Ser Gln Val Cys Ser
405 410 415

Ile Leu Trp Ser Pro His Tyr Lys Glu Leu Ile Ser Gly His Gly Phe
420 425 430

Ala Gln Asn Gln Leu Val Ile Trp Lys Tyr Pro Thr Met Ala Lys Val
435 440 445

Ala Glu Leu Lys Gly His Thr Ser Arg Val Leu Ser Leu Thr Met Ser
450 455 460

Pro Asp Gly Ala Thr Val Ala Ser Ala Ala Ala Asp Glu Thr Leu Arg
465 470 475 480

Leu Trp Arg Cys Phe Glu Leu Asp Pro Ala Arg Arg Arg Glu Arg Glu
485 490 495

Lys Ala Ser Ala Ala Lys Ser Ser Leu Ile His Gln Gly Ile Arg
500 505 510

<210> 1038
<211> 209
<212> PRT
<213> Homo sapiens

<400> 1038
His Glu Pro Pro Ser Ala Ser Ser Val Ala Gly Asp Leu Gly Arg Gly
1 5 10 15

Thr Arg Thr Glu Val Glu Ala Arg Ala Ala Arg Pro Gly Ala Glu Ser
20 25 30

Ala Pro Ala Ala Ala Met Pro Asp Ser Trp Asp Lys Asp Val Tyr Pro
35 40 45

Glu Pro Pro Arg Arg Thr Pro Val Gln Pro Asn Pro Ile Val Tyr Met
50 55 60

Met Lys Ala Phe Asp Leu Ile Val Asp Arg Pro Val Thr Leu Val Arg
65 70 75 80

Glu Phe Ile Glu Arg Gln His Ala Lys Asn Arg Tyr Tyr Tyr Tyr His
85 90 95

Arg Gln Tyr Arg Arg Val Pro Asp Ile Thr Glu Cys Lys Glu Glu Asp
100 105 110

```
Ile Met Cys Met Tyr Glu Ala Glu Met Gln Trp Lys Arg Asp Tyr Lys
        115                 120                 125

Val Asp Gln Glu Ile Ile Asn Ile Met Gln Asp Arg Leu Lys Ala Cys
    130                 135                 140

Gln Gln Arg Glu Gly Gln Asn Tyr Gln Gln Asn Cys Ile Lys Glu Val
145                 150                 155                 160

Glu Gln Phe Thr Gln Val Ala Lys Ala Tyr Gln Asp Arg Tyr Gln Asp
                165                 170                 175

Leu Gly Ala Tyr Ser Ser Ala Arg Lys Cys Leu Ala Lys Gln Arg Gln
            180                 185                 190

Arg Met Leu Gln Glu Arg Lys Ala Ala Lys Glu Ala Ala Ala Thr
        195                 200                 205

Ser



<210> 1039
<211> 219
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (153)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1039
Leu Ala Ala Pro Asp Leu Ser Lys Pro Arg Gly Tyr His Trp Asp Thr
  1               5                  10                  15

Ser Asp Trp Met Pro Ser Val Pro Leu Pro Asp Ile Gln Glu Phe Pro
             20                  25                  30

Asn Tyr Glu Val Ile Asp Glu Gln Thr Pro Leu Tyr Ser Ala Asp Pro
         35                  40                  45

Asn Ala Ile Asp Thr Asp Tyr Tyr Pro Gly Gly Tyr Asp Ile Glu Ser
     50                  55                  60

Asp Phe Pro Pro Pro Pro Glu Asp Phe Pro Ala Ala Asp Glu Leu Pro
 65                  70                  75                  80

Pro Leu Pro Pro Glu Phe Ser Asn Gln Phe Glu Ser Ile His Pro Pro
                 85                  90                  95
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Arg Asp Met Pro Ala Ala Gly Ser Leu Gly Ser Ser Ser Arg Asn Arg
100 105 110

Gln Arg Phe Asn Leu Asn Gln Tyr Leu Pro Asn Phe Tyr Pro Leu Asp
115 120 125

Met Ser Glu Pro Gln Thr Lys Gly Thr Gly Glu Asn Ser Thr Cys Arg
130 135 140

Glu Pro His Ala Pro Tyr Pro Pro Xaa Tyr Gln Arg His Phe Glu Ala
145 150 155 160

Pro Ala Val Glu Ser Met Pro Met Ser Val Tyr Ala Ser Thr Ala Ser
165 170 175

Cys Ser Asp Val Ser Ala Cys Cys Glu Val Glu Ser Glu Val Met Met
180 185 190

Ser Asp Tyr Glu Ser Gly Asp Asp Gly His Phe Glu Glu Val Thr Ile
195 200 205

Pro Pro Leu Asp Ser Gln Gln His Thr Glu Val
210 215

<210> 1040
<211> 178
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1040
Phe Asp Leu Pro Tyr Arg Ala Glu Phe Gly Xaa Pro Gly Pro Pro Leu
1 5 10 15

Ser Ala Ala Cys Ser Trp Lys Phe Arg Leu Gly Cys Leu Leu Gly Ala
20 25 30

Met Glu Ser Asp Phe Tyr Leu Arg Tyr Tyr Val Gly His Lys Gly Lys
35 40 45

Phe Gly His Glu Phe Leu Glu Phe Glu Phe Arg Pro Asp Gly Lys Leu
50 55 60

Arg Tyr Ala Asn Asn Ser Asn Tyr Lys Asn Asp Val Met Ile Arg Lys

65 70 75 80

Glu Ala Tyr Val His Lys Ser Val Met Glu Glu Leu Lys Arg Ile Ile
85 90 95

Asp Asp Ser Glu Ile Thr Lys Glu Asp Asp Ala Leu Trp Pro Pro Pro
100 105 110

Asp Arg Val Gly Arg Gln Glu Leu Glu Ile Val Ile Gly Asp Glu His
115 120 125

Ile Ser Phe Thr Thr Ser Lys Ile Gly Ser Leu Ile Asp Val Asn Gln
130 135 140

Ser Lys Asp Pro Glu Gly Leu Arg Val Phe Tyr Tyr Leu Val Gln Asp
145 150 155 160

Leu Lys Cys Leu Val Phe Ser Leu Ile Gly Leu His Phe Lys Ile Lys
165 170 175

Pro Ile

<210> 1041
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1041
Leu Val Pro Asn Ser Ala Arg Ala Gly Ala Ser Tyr Ala Ala Ala Ala
1 5 10 15

Val Thr Met Ala His Tyr Lys Ala Ala Asp Ser Lys Arg Glu Gln Phe
20 25 30

Arg Arg Tyr Leu Glu Lys Ser Gly Val Leu Asp Thr Leu Thr Lys Val
35 40 45

Leu Val Ala Leu Tyr Glu Glu Pro Glu Lys Pro Asn Ser Ala Leu Asp
50 55 60

Phe Leu Lys His His Leu Gly Ala Ala Thr Pro Glu Asn Pro Glu Ile
65 70 75 80

Glu Leu Leu Arg Leu Glu Leu Ala Glu Met Lys Glu Lys Tyr Glu Ala
85 90 95

Ile Val Glu Glu Asn Lys Lys Leu Lys Ala Lys Leu Ala Gln Tyr Glu
100 105 110

Pro Pro Gln Glu Glu Lys Arg Ala Glu
115 120

<210> 1042
<211> 253
<212> PRT
<213> Homo sapiens

<400> 1042
Val Asp Pro Arg Val Arg Pro Arg Ser Val Asn Gly Glu Leu Gln Lys
1 5 10 15

Ala Ile Asp Leu Phe Thr Asp Ala Ile Lys Leu Asn Pro Arg Leu Ala
20 25 30

Ile Leu Tyr Ala Lys Arg Ala Ser Val Phe Val Lys Leu Gln Lys Pro
35 40 45

Asn Ala Ala Ile Arg Asp Cys Asp Arg Ala Ile Glu Ile Asn Pro Asp
50 55 60

Ser Ala Gln Pro Tyr Lys Trp Arg Gly Lys Ala His Arg Leu Leu Gly
65 70 75 80

His Trp Glu Glu Ala Ala His Asp Leu Ala Leu Ala Cys Lys Leu Asp
85 90 95

Tyr Asp Glu Asp Ala Ser Ala Met Leu Lys Glu Val Gln Pro Arg Ala
100 105 110

Gln Lys Ile Ala Glu His Arg Arg Lys Tyr Glu Arg Lys Arg Glu Glu
115 120 125

Arg Glu Ile Lys Glu Arg Ile Glu Arg Val Lys Lys Ala Arg Glu Glu
130 135 140

His Glu Arg Ala Gln Arg Glu Glu Glu Ala Arg Arg Gln Ser Gly Ala
145 150 155 160

Gln Tyr Gly Ser Phe Pro Gly Gly Phe Pro Gly Gly Met Pro Gly Asn
165 170 175

Phe Pro Gly Gly Met Pro Gly Met Gly Gly Gly Met Pro Gly Met Ala
180 185 190

Gly Met Pro Gly Leu Asn Glu Ile Leu Ser Asp Pro Glu Val Leu Ala
195 200 205

Ala Met Gln Asp Pro Glu Val Met Val Ala Phe Gln Asp Val Ala Gln
    210   215   220

Asn Pro Ala Asn Met Ser Lys Tyr Gln Ser Asn Pro Lys Val Met Asn
225   230   235   240

Leu Ile Ser Lys Leu Ser Ala Lys Phe Gly Gly Gln Ala
                245   250

<210> 1043
<211> 343
<212> PRT
<213> Homo sapiens

<400> 1043
Met Lys Thr Cys Gln Glu Glu Lys Leu Met Gly His Leu Gly Val Val
  1   5   10   15

Leu Tyr Glu Tyr Leu Gly Glu Glu Tyr Pro Glu Val Leu Gly Ser Ile
             20   25   30

Leu Gly Ala Leu Lys Ala Ile Val Asn Val Ile Gly Met His Lys Met
         35   40   45

Thr Pro Pro Ile Lys Asp Leu Leu Pro Arg Leu Thr Pro Ile Leu Lys
     50   55   60

Asn Arg His Glu Lys Val Gln Glu Asn Cys Ile Asp Leu Val Gly Arg
 65   70   75   80

Ile Ala Asp Arg Gly Ala Glu Tyr Val Ser Ala Arg Glu Trp Met Arg
                 85   90   95

Ile Cys Phe Glu Leu Leu Glu Leu Leu Lys Ala His Lys Lys Ala Ile
            100   105   110

Arg Arg Ala Thr Val Asn Thr Phe Gly Tyr Ile Ala Lys Ala Ile Gly
        115   120   125

Pro His Asp Val Leu Ala Thr Leu Leu Asn Asn Leu Lys Val Gln Glu
    130   135   140

Arg Gln Asn Arg Val Cys Thr Thr Val Ala Ile Ala Ile Val Ala Glu
145   150   155   160

Thr Cys Ser Pro Phe Thr Val Leu Pro Ala Leu Met Asn Glu Tyr Arg
                165   170   175

Val Pro Glu Leu Asn Val Gln Asn Gly Val Leu Lys Ser Leu Ser Phe

180 185 190

Leu Phe Glu Tyr Ile Gly Glu Met Gly Lys Asp Tyr Ile Tyr Ala Val
195 200 205

Thr Pro Leu Leu Glu Asp Ala Leu Met Asp Arg Asp Leu Val His Arg
210 215 220

Gln Thr Ala Ser Ala Val Val Gln His Met Ser Leu Gly Val Tyr Gly
225 230 235 240

Phe Gly Cys Glu Asp Ser Leu Asn His Leu Leu Asn Tyr Val Trp Pro
245 250 255

Asn Val Phe Glu Thr Ser Pro His Val Ile Gln Ala Val Met Gly Ala
260 265 270

Leu Glu Gly Leu Arg Val Ala Ile Gly Pro Cys Arg Met Leu Gln Tyr
275 280 285

Cys Leu Gln Gly Leu Phe His Pro Ala Arg Lys Val Arg Asp Val Tyr
290 295 300

Trp Lys Ile Tyr Asn Ser Ile Tyr Ile Gly Ser Gln Asp Ala Leu Ile
305 310 315 320

Ala His Tyr Pro Arg Ile Tyr Asn Asp Asp Lys Asn Thr Tyr Ile Arg
325 330 335

Tyr Glu Leu Asp Tyr Ile Leu
340

<210> 1044
<211> 268
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (20)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1044
Leu Arg Arg Pro Tyr Ala Arg Tyr Asn Gly Leu Tyr Arg Ser Gly Ile
1 5 10 15

Arg Gly Arg Xaa Asn Leu Glu Ser Thr Arg Val Arg Glu Leu Pro Gly
20 25 30

Gly Ala Met Ser Cys Ile Asn Leu Pro Thr Val Leu Pro Gly Ser Pro
35 40 45

Ser Lys Thr Arg Gly Gln Ile Gln Val Ile Leu Gly Pro Met Phe Ser
50 55 60

Gly Lys Ser Thr Glu Leu Met Arg Arg Val Arg Arg Phe Gln Ile Ala
65 70 75 80

Gln Tyr Lys Cys Leu Val Ile Lys Tyr Ala Lys Asp Thr Arg Tyr Ser
85 90 95

Ser Ser Phe Cys Thr His Asp Arg Asn Thr Met Glu Ala Leu Pro Ala
100 105 110

Cys Leu Leu Arg Asp Val Ala Gln Glu Ala Leu Gly Val Ala Val Ile
115 120 125

Gly Ile Asp Glu Gly Gln Phe Phe Pro Asp Ile Val Glu Phe Cys Glu
130 135 140

Ala Met Ala Asn Ala Gly Lys Thr Val Ile Val Ala Ala Leu Asp Gly
145 150 155 160

Thr Phe Gln Arg Lys Pro Phe Gly Ala Ile Leu Asn Leu Val Pro Leu
165 170 175

Ala Glu Ser Val Val Lys Leu Thr Ala Val Cys Met Glu Cys Phe Arg
180 185 190

Glu Ala Ala Tyr Thr Lys Arg Leu Gly Thr Glu Lys Glu Val Glu Val
195 200 205

Ile Gly Gly Ala Asp Lys Tyr His Ser Val Cys Arg Leu Cys Tyr Phe
210 215 220

Lys Lys Ala Ser Gly Gln Pro Ala Gly Pro Asp Asn Lys Glu Asn Cys
225 230 235 240

Pro Val Pro Gly Lys Pro Gly Glu Ala Val Ala Ala Arg Lys Leu Phe
245 250 255

Ala Pro Gln Gln Ile Leu Gln Cys Ser Pro Ala Asn
260 265

<210> 1045
<211> 139
<212> PRT
<213> Homo sapiens

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<220>
<221> SITE
<222> (128)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1045
Pro Gly Gln Ser Arg Trp Gln Gly Pro Pro Leu Pro Leu Cys Gln Ala
 1               5                  10                  15

Gly Ser Ala Lys Ser Gly Glu Pro Gly Ala Gly Gly Lys Ala Gly Asp
            20                  25                  30

Ser Pro Ala Leu Pro Pro Pro Pro Leu Gly Ala Gln Gln Leu Leu Arg
        35                  40                  45

Lys Val Trp His Pro Trp Arg Gly Gly Ala Pro Gly Trp Ala Gly Ser
    50                  55                  60

Arg Trp Pro Gly Ala Trp Arg Cys Ala Ala Gly Ala Cys Met Ala Pro
65                  70                  75                  80

Arg Gly Thr Gln Ala Glu Glu Ser Pro Phe Val Gly Asn Pro Gly Asn
                85                  90                  95

Ile Thr Gly Ala Arg Gly Leu Thr Gly Thr Leu Arg Cys Gln Leu Gln
            100                 105                 110

Val Gln Gly Glu Pro Pro Glu Val His Trp Leu Arg Asp Gly Gln Xaa
        115                 120                 125

Leu Glu Leu Ala Asp Ser Thr Gln Thr Gln Val
    130                 135


<210> 1046
<211> 416
<212> PRT
<213> Homo sapiens

<400> 1046
Ser Pro Ser Glu Arg Leu Gln Arg Gly Arg Glu Glu Gln Pro Ala Gly
 1               5                  10                  15

Gly Gly Gly Glu Ser Val Ser Ser Trp Glu Glu Gln Asn Arg Gly Gly
            20                  25                  30

Ala Pro Ala Gly Ala Gly Gly Gly Pro Thr Met Ala Ile Arg Lys Lys
        35                  40                  45
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Ser Thr Lys Ser Pro Pro Val Leu Ser His Glu Phe Val Leu Gln Asn
     50                  55                  60

His Ala Asp Ile Val Ser Cys Val Ala Met Val Phe Leu Leu Gly Leu
 65                  70                  75                  80

Met Phe Glu Ile Thr Ala Lys Ala Ser Ile Ile Phe Val Thr Leu Gln
                 85                  90                  95

Tyr Asn Val Thr Leu Pro Ala Thr Glu Glu Gln Ala Thr Glu Ser Val
            100                 105                 110

Ser Leu Tyr Tyr Tyr Gly Ile Lys Asp Leu Ala Thr Val Phe Phe Tyr
        115                 120                 125

Met Leu Val Ala Ile Ile Ile His Ala Val Ile Gln Glu Tyr Met Leu
    130                 135                 140

Asp Lys Ile Asn Arg Arg Met His Phe Ser Lys Thr Lys His Ser Lys
145                 150                 155                 160

Phe Asn Glu Ser Gly Gln Leu Ser Ala Phe Tyr Leu Phe Ala Cys Val
                165                 170                 175

Trp Gly Thr Phe Ile Leu Ile Ser Glu Asn Tyr Ile Ser Asp Pro Thr
            180                 185                 190

Ile Leu Trp Arg Ala Tyr Pro His Asn Leu Met Thr Phe Gln Met Lys
        195                 200                 205

Phe Phe Tyr Ile Ser Gln Leu Ala Tyr Trp Leu His Ala Phe Pro Glu
    210                 215                 220

Leu Tyr Phe Gln Lys Thr Lys Lys Glu Asp Ile Pro Arg Gln Leu Val
225                 230                 235                 240

Tyr Ile Gly Leu Tyr Leu Phe His Ile Ala Gly Ala Tyr Leu Leu Asn
                245                 250                 255

Leu Asn His Leu Gly Leu Val Leu Leu Val Leu His Tyr Phe Val Glu
            260                 265                 270

Phe Leu Phe His Ile Ser Arg Leu Phe Tyr Phe Ser Asn Glu Lys Tyr
        275                 280                 285

Gln Lys Gly Phe Ser Leu Trp Ala Val Leu Phe Val Leu Gly Arg Leu
    290                 295                 300

Leu Thr Leu Ile Leu Ser Val Leu Thr Val Gly Phe Gly Leu Ala Arg
305                 310                 315                 320
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Ala Glu Asn Gln Lys Leu Asp Phe Ser Thr Gly Asn Phe Asn Val Leu
                325                 330                 335

Ala Val Arg Ile Ala Val Leu Ala Ser Ile Cys Val Thr Gln Ala Phe
            340                 345                 350

Met Met Trp Lys Phe Ile Asn Phe Gln Leu Arg Arg Trp Arg Glu His
        355                 360                 365

Ser Ala Phe Gln Ala Pro Ala Val Lys Lys Lys Pro Thr Val Thr Lys
    370                 375                 380

Gly Arg Ser Ser Lys Lys Gly Thr Glu Asn Gly Val Asn Gly Thr Leu
385                 390                 395                 400

Thr Ser Asn Val Ala Asp Ser Pro Arg Asn Lys Lys Glu Lys Ser Ser
                405                 410                 415



<210> 1047
<211> 466
<212> PRT
<213> Homo sapiens

<400> 1047
Pro Ala Ser Ser Gly Leu Leu Pro Leu Ser Arg Ser Asn Leu Tyr Ser
  1               5                  10                  15

Gly Arg Thr Gly Ile Pro Arg Ala Pro Pro Ala Leu Ala Ala Leu Ala
             20                  25                  30

Thr Ala Pro Gly Arg Arg Ala Pro Val His Thr Gly Ser Leu Leu Gly
         35                  40                  45

Thr Asn Ser Ser Thr Met Gly Leu Ala Trp Gly Leu Gly Val Leu Phe
     50                  55                  60

Leu Met His Val Cys Gly Thr Asn Arg Ile Pro Glu Ser Gly Gly Asp
 65                  70                  75                  80

Asn Ser Val Phe Asp Ile Phe Glu Leu Thr Gly Ala Ala Arg Lys Gly
                 85                  90                  95

Ser Gly Arg Arg Leu Val Lys Gly Pro Asp Pro Ser Ser Pro Ala Phe
            100                 105                 110

Arg Ile Glu Asp Ala Asn Leu Ile Pro Pro Val Pro Asp Asp Lys Phe
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115 120 125

Gln Asp Leu Val Asp Ala Val Arg Ala Glu Lys Gly Phe Leu Leu Leu
130 135 140

Ala Ser Leu Arg Gln Met Lys Lys Thr Arg Gly Thr Leu Leu Ala Leu
145 150 155 160

Glu Arg Lys Asp His Ser Gly Gln Val Phe Ser Val Val Ser Asn Gly
165 170 175

Lys Ala Gly Thr Leu Asp Leu Ser Leu Thr Val Gln Gly Lys Gln His
180 185 190

Val Val Ser Val Glu Glu Ala Leu Leu Ala Thr Gly Gln Trp Lys Ser
195 200 205

Ile Thr Leu Phe Val Gln Glu Asp Arg Ala Gln Leu Tyr Ile Asp Cys
210 215 220

Glu Lys Met Glu Asn Ala Glu Leu Asp Val Pro Ile Gln Ser Val Phe
225 230 235 240

Thr Arg Asp Leu Ala Ser Ile Ala Arg Leu Arg Ile Ala Lys Gly Gly
245 250 255

Val Asn Asp Asn Phe Gln Gly Val Leu Gln Asn Val Arg Phe Val Phe
260 265 270

Gly Thr Thr Pro Glu Asp Ile Leu Arg Asn Lys Gly Cys Ser Ser Ser
275 280 285

Thr Ser Val Leu Leu Thr Leu Asp Asn Asn Val Val Asn Gly Ser Ser
290 295 300

Pro Ala Ile Arg Thr Asn Tyr Ile Gly His Lys Thr Lys Asp Leu Gln
305 310 315 320

Ala Ile Cys Gly Ile Ser Cys Asp Glu Leu Ser Ser Met Val Leu Glu
325 330 335

Leu Arg Gly Leu Arg Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg
340 345 350

Lys Val Thr Glu Glu Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro
355 360 365

Pro Leu Cys Tyr His Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp
370 375 380

Thr Val Asp Ser Cys Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile

385 390 395 400

Cys Lys Lys Val Ser Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val
405 410 415

Pro Asp Gly Glu Cys Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp
420 425 430

Asp Gly Trp Ser Pro Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys
435 440 445

Gly Asn Gly Ile Gln Gln Arg Gly Arg Ser Cys Asp Ser Ala Gln Gln
450 455 460

Pro Met
465

<210> 1048
<211> 217
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (122)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (186)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (200)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1048
Asp Pro Arg Val Arg Gln Ser His Ile Ser Asp Thr Ser Val Val Val
1 5 10 15

Lys Leu Asp Asn Ser Arg Asp Leu Asn Met Asp Cys Ile Ile Ala Glu
20 25 30

Ile Lys Ala Gln Tyr Asp Asp Ile Val Thr Arg Ser Arg Ala Glu Ala
35 40 45

Glu Ser Trp Tyr Arg Ser Lys Cys Glu Glu Met Lys Ala Thr Val Ile
50 55 60

Arg His Gly Glu Thr Leu Arg Arg Thr Lys Glu Glu Ile Asn Glu Leu
65 70 75 80

Asn Arg Met Ile Gln Arg Leu Thr Ala Glu Val Glu Asn Ala Lys Cys
85 90 95

Gln Asn Ser Lys Leu Glu Ala Ala Val Ala Gln Ser Glu Gln Gln Gly
100 105 110

Glu Ala Ala Leu Ser Asp Ala Arg Cys Xaa Leu Ala Glu Leu Glu Gly
115 120 125

Ala Leu Gln Lys Ala Lys Gln Asp Met Ala Cys Leu Ile Arg Glu Tyr
130 135 140

Gln Glu Val Met Asn Ser Lys Leu Gly Leu Asp Ile Glu Ile Ala Thr
145 150 155 160

Tyr Arg Arg Leu Leu Glu Gly Glu Glu Gln Arg Leu Cys Glu Gly Ile
165 170 175

Gly Ala Val Asn Val Cys Val Ser Ser Xaa Arg Gly Gly Val Val Cys
180 185 190

Gly Asp Leu Cys Val Ser Gly Xaa Arg Pro Val Thr Ala Val Ser Ala
195 200 205

Ala Leu Arg Ala Thr Gly Thr Trp Arg
210 215

<210> 1049
<211> 406
<212> PRT
<213> Homo sapiens

<400> 1049
Gly Ser Ala Ala Ala Arg Tyr Leu Ser Ala Thr Trp Arg Asn Trp Ile
1 5 10 15

Ser Leu Pro Pro Ala Gly Leu Pro Ala Thr Ala Gly Leu Arg His Ser
20 25 30

Gly Ser Leu Met Ala Ala Thr Cys Glu Ile Ser Asn Ile Phe Ser Asn
35 40 45

Tyr Phe Ser Ala Met Tyr Ser Ser Glu Asp Ser Thr Leu Ala Ser Val
50 55 60

Pro Pro Ala Ala Thr Phe Gly Ala Asp Asp Leu Val Leu Thr Leu Ser
65 70 75 80

Asn Pro Gln Met Ser Leu Glu Gly Thr Glu Lys Ala Ser Trp Leu Gly
85 90 95

Glu Gln Pro Gln Phe Trp Ser Lys Thr Gln Val Leu Asp Trp Ile Ser
100 105 110

Tyr Gln Val Glu Lys Asn Lys Tyr Asp Ala Ser Ala Ile Asp Phe Ser
115 120 125

Arg Cys Asp Met Asp Gly Ala Thr Leu Cys Asn Cys Ala Leu Glu Glu
130 135 140

Leu Arg Leu Val Phe Gly Pro Leu Gly Asp Gln Leu His Ala Gln Leu
145 150 155 160

Arg Asp Leu Thr Ser Ser Ser Ser Asp Glu Leu Ser Trp Ile Ile Glu
165 170 175

Leu Leu Glu Lys Asp Gly Met Ala Phe Gln Glu Ala Leu Asp Pro Gly
180 185 190

Pro Phe Asp Gln Gly Ser Pro Phe Ala Gln Glu Leu Leu Asp Asp Gly
195 200 205

Gln Gln Ala Ser Pro Tyr His Pro Gly Ser Cys Gly Ala Gly Ala Pro
210 215 220

Ser Pro Gly Ser Ser Asp Val Ser Thr Ala Gly Thr Gly Ala Ser Arg
225 230 235 240

Ser Ser His Ser Ser Asp Ser Gly Gly Ser Asp Val Asp Leu Asp Pro
245 250 255

Thr Asp Gly Lys Leu Phe Pro Ser Asp Gly Phe Arg Asp Cys Lys Lys
260 265 270

Gly Asp Pro Lys His Gly Lys Arg Lys Arg Gly Arg Pro Arg Lys Leu
275 280 285

Ser Lys Glu Tyr Trp Asp Cys Leu Glu Gly Lys Lys Ser Lys His Ala
290 295 300

Pro Arg Gly Thr His Leu Trp Glu Phe Ile Arg Asp Ile Leu Ile His
305 310 315 320

Pro Glu Leu Asn Glu Gly Leu Met Lys Trp Glu Asn Arg His Glu Gly
325 330 335

Val Phe Lys Phe Leu Arg Ser Glu Ala Val Ala Gln Leu Trp Gly Gln
340 345 350

Lys Lys Lys Asn Ser Asn Met Thr Tyr Glu Lys Leu Ser Arg Ala Met
355 360 365

Arg Tyr Tyr Tyr Lys Arg Glu Ile Leu Glu Arg Val Asp Gly Arg Arg
370 375 380

Leu Val Tyr Lys Phe Gly Lys Asn Ser Ser Gly Trp Lys Glu Glu Glu
385 390 395 400

Val Leu Gln Ser Arg Asn
405

<210> 1050
<211> 251
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (53)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (86)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1050
Arg Pro Ala Leu Asp Thr Cys Cys Pro Phe Pro Ala Arg Ile Leu Gly
1 5 10 15

Ser Phe Pro Leu Ser Gln His Leu Gly Pro Ala Phe Asp Thr Thr Pro
20 25 30

Arg Leu Pro Thr Leu Arg Ala Trp Ser Leu Pro Gln Gly Pro Leu Ser
35 40 45

Trp Ala Met Ala Xaa Lys Gly Val Leu Gly Pro Gly Gln Leu Gly Ala
50 55 60

Val Ala Ile Leu Leu Tyr Leu Gly Leu Leu Arg Ser Gly Thr Gly Ala
65 70 75 80

Glu Gly Ala Glu Ala Xaa Cys Gly Val Ala Pro Gln Ala Arg Ile Thr
85 90 95

Gly Gly Ser Ser Ala Val Ala Gly Gln Trp Pro Trp Gln Val Ser Ile
100 105 110

Thr Tyr Glu Gly Val His Val Cys Gly Gly Ser Leu Val Ser Glu Gln
115 120 125

Trp Val Leu Ser Ala Ala His Cys Phe Pro Ser Glu His His Lys Glu
130 135 140

Ala Tyr Glu Val Lys Leu Gly Ala His Gln Leu Asp Ser Tyr Ser Glu
145 150 155 160

Asp Ala Lys Val Ser Thr Leu Lys Asp Ile Ile Pro His Pro Ser Tyr
165 170 175

Leu Gln Glu Gly Ser Gln Gly Asp Ile Ala Leu Leu Gln Leu Ser Arg
180 185 190

Pro Ile Thr Phe Ser Arg Tyr Ile Arg Pro Ile Cys Leu Pro Ala Ala
195 200 205

Asn Ala Ser Phe Pro Asn Gly Leu His Cys Thr Val Thr Gly Trp Gly
210 215 220

His Val Ala Pro Ser Val Ser Leu Leu Thr Pro Lys Pro Leu Gln Gln
225 230 235 240

Leu Glu Val Pro Leu Ile Ser Arg Glu Thr Trp
245 250

<210> 1051
<211> 171
<212> PRT
<213> Homo sapiens

<400> 1051
His Tyr Arg Arg Tyr Ala Cys Arg Tyr Arg Ser Gly Ile Arg Gly Arg
1 5 10 15

Val Asp Ile Arg Arg Arg Ser Ser Arg Arg Pro Arg Glu Pro Pro Gly
20 25 30

Pro Ser Arg Arg Arg Arg Arg Arg Arg Pro Asp Pro Arg Thr Met Pro
35 40 45

Ser Glu Lys Thr Phe Lys Gln Arg Arg Thr Phe Glu Gln Arg Val Glu
50 55 60

Asp Val Arg Leu Ile Arg Glu Gln His Pro Thr Lys Ile Pro Val Ile

65 70 75 80

Ile Glu Arg Tyr Lys Gly Glu Lys Gln Leu Pro Val Leu Asp Lys Thr
85 90 95

Lys Phe Leu Val Pro Asp His Val Asn Met Ser Glu Leu Ile Lys Ile
100 105 110

Ile Arg Arg Arg Leu Gln Leu Asn Ala Asn Gln Ala Phe Phe Leu Leu
115 120 125

Val Asn Gly His Ser Met Val Ser Val Ser Thr Pro Ile Ser Glu Val
130 135 140

Tyr Glu Ser Glu Lys Asp Glu Asp Gly Phe Leu Tyr Met Val Tyr Ala
145 150 155 160

Ser Gln Glu Thr Phe Gly Met Lys Leu Ser Val
165 170

<210> 1052
<211> 189
<212> PRT
<213> Homo sapiens

<400> 1052
Gly Gly Pro Thr Cys Ser Ala Arg Cys Glu Pro Val Arg Pro Pro Pro
1 5 10 15

Ala Pro Glu Gln Pro Ala Ser Leu His Arg Leu Leu Ser Val Leu Ser
20 25 30

Pro Arg Ala Ala Ile Ala Val Met Leu Gly Ala Ala Leu Arg Arg Cys
35 40 45

Ala Val Ala Ala Thr Thr Arg Ala Asp Pro Arg Gly Leu Leu His Ser
50 55 60

Ala Arg Thr Pro Gly Pro Ala Val Ala Ile Gln Ser Val Arg Cys Tyr
65 70 75 80

Ser His Gly Ser Gln Glu Thr Asp Glu Glu Phe Asp Ala Arg Trp Val
85 90 95

Thr Tyr Phe Asn Lys Pro Asp Ile Asp Ala Trp Glu Leu Arg Lys Gly
100 105 110

Ile Asn Thr Leu Val Thr Tyr Asp Met Val Pro Glu Pro Lys Ile Ile
115 120 125

Asp Ala Ala Leu Arg Ala Cys Arg Arg Leu Asn Asp Phe Ala Ser Thr
    130   135   140

Val Arg Ile Leu Glu Val Val Lys Asp Lys Ala Gly Pro His Lys Glu
145   150   155   160

Ile Tyr Pro Tyr Val Ile Gln Glu Leu Arg Pro Thr Leu Asn Glu Leu
                165   170   175

Gly Ile Ser Thr Pro Glu Glu Leu Gly Leu Asp Lys Val
            180   185

<210> 1053
<211> 315
<212> PRT
<213> Homo sapiens

<400> 1053
Arg His Ser Ala Ser Pro Arg Cys Arg Leu Pro Pro Thr Glu Pro Val
  1   5   10   15

Ser Gly Leu Arg Ala Ser Gly Glu Met Leu Leu Pro Leu Leu Leu Leu
            20   25   30

Leu Pro Met Cys Trp Ala Val Glu Val Lys Arg Pro Arg Gly Val Ser
        35   40   45

Leu Thr Asn His His Phe Tyr Asp Glu Ser Lys Pro Phe Thr Cys Leu
    50   55   60

Asp Gly Ser Ala Thr Ile Pro Phe Asp Gln Val Asn Asp Asp Tyr Cys
65   70   75   80

Asp Cys Lys Asp Gly Ser Asp Glu Pro Gly Thr Ala Ala Cys Pro Asn
                85   90   95

Gly Ser Phe His Cys Thr Asn Thr Gly Tyr Lys Pro Leu Tyr Ile Pro
            100   105   110

Ser Asn Arg Val Asn Asp Gly Val Cys Asp Cys Cys Asp Gly Thr Asp
        115   120   125

Glu Tyr Asn Ser Gly Val Ile Cys Glu Asn Thr Cys Lys Glu Lys Gly
    130   135   140

Arg Lys Glu Arg Glu Ser Leu Gln Gln Met Ala Glu Val Thr Arg Glu
145   150   155   160

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Gly Phe Arg Leu Lys Lys Ile Leu Ile Glu Asp Trp Lys Lys Ala Arg
                165                 170                 175

Glu Glu Lys Gln Lys Lys Leu Ile Glu Leu Gln Ala Gly Lys Lys Ser
            180                 185                 190

Leu Glu Asp Gln Val Glu Met Leu Arg Thr Val Lys Glu Glu Ala Glu
        195                 200                 205

Lys Pro Glu Arg Glu Ala Lys Glu Gln His Gln Lys Leu Trp Glu Glu
    210                 215                 220

Gln Leu Ala Ala Ala Lys Ala Gln Gln Glu Gln Glu Leu Ala Ala Asp
225                 230                 235                 240

Ala Phe Lys Glu Leu Asp Asp Asp Met Asp Gly Thr Val Ser Val Thr
                245                 250                 255

Glu Leu Gln Thr His Pro Glu Leu Asp Thr Asp Gly Asp Gly Ala Leu
            260                 265                 270

Ser Glu Ala Glu Ala Gln Ala Leu Leu Ser Gly Asp Thr Gln Thr Asp
        275                 280                 285

Ala Thr Ser Phe Tyr Asp Arg Val Trp Gly Pro Gly Gly Ala Gly Pro
    290                 295                 300

His Ser Gln Ala Pro Thr Ala Phe Lys Asp Gly
305                 310                 315


<210> 1054
<211> 138
<212> PRT
<213> Homo sapiens

<400> 1054
Val Trp Lys Val Ile Val Trp Ser His Ser Ser Leu Ile Thr Leu Leu
  1               5                  10                  15

Gly Ile Leu Glu Glu Lys Gly Ser Lys Thr Tyr Thr His Thr Pro Thr
             20                  25                  30

Gln Ser Asn Ser Val Phe Lys Gln Ile Pro Arg Ile Leu Gly Pro Gly
         35                  40                  45

Leu Asn Lys Ala Gly Lys Phe Pro Ser Leu Leu Thr His Asn Glu Asn
     50                  55                  60

Met Val Ala Lys Val Asp Glu Val Lys Ser Thr Ile Lys Phe Gln Met
```

65 70 75 80

Lys Lys Val Leu Cys Leu Ala Val Ala Val Gly His Val Lys Met Thr
85 90 95

Asp Asp Glu Leu Val Tyr Asn Ile His Leu Ala Val Asn Phe Leu Val
100 105 110

Ser Leu Leu Lys Lys Asn Trp Gln Asn Val Arg Ala Leu Tyr Ile Lys
115 120 125

Ser Thr Met Gly Lys Pro Gln Arg Leu Tyr
130 135

<210> 1055
<211> 243
<212> PRT
<213> Homo sapiens

<400> 1055
Gly Thr Arg Glu Glu Ala Gly Val Asp Leu Val Ser Pro Thr Pro Leu
1 5 10 15

Thr Pro Pro Asp Pro Gly Ala Ala Ser Ala Thr Ala Thr Ala Pro Ala
20 25 30

Pro Ala Ala Ala Arg Arg Gly Glu Ala Met Ala Lys Val Ser Val Leu
35 40 45

Asn Val Ala Val Leu Glu Asn Pro Ser Pro Phe His Ser Pro Phe Arg
50 55 60

Phe Glu Ile Ser Phe Glu Cys Ser Glu Ala Leu Ala Asp Asp Leu Glu
65 70 75 80

Trp Lys Ile Ile Tyr Val Gly Ser Ala Glu Ser Glu Glu Phe Asp Gln
85 90 95

Ile Leu Asp Ser Val Leu Val Gly Pro Val Pro Ala Gly Arg His Met
100 105 110

Phe Val Phe Gln Ala Asp Ala Pro Asn Pro Ser Leu Ile Pro Glu Thr
115 120 125

Asp Ala Val Gly Val Thr Val Val Leu Ile Thr Cys Thr Tyr His Gly
130 135 140

Gln Glu Phe Ile Arg Val Gly Tyr Tyr Val Asn Asn Glu Tyr Leu Asn
145 150 155 160

Pro Glu Leu Arg Glu Asn Pro Pro Met Lys Pro Asp Phe Ser Gln Leu
165 170 175

Gln Arg Asn Ile Leu Ala Ser Asn Pro Arg Val Thr Arg Phe His Ile
180 185 190

Asn Trp Asp Asn Asn Met Asp Arg Leu Glu Ala Ile Glu Thr Gln Asp
195 200 205

Pro Ser Leu Gly Cys Gly Leu Pro Leu Asn Cys Thr Pro Ile Lys Gly
210 215 220

Leu Gly Leu Pro Gly Cys Ile Pro Gly Leu Leu Pro Glu Asn Ser Met
225 230 235 240

Asp Cys Ile

<210> 1056
<211> 211
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1056
His Glu Pro Arg Arg Leu Leu Xaa Asp Ala Glu Gly Pro Glu Glu Thr
1 5 10 15

Val Arg Leu Trp Pro Ala Ala Arg Ala Ala Met Asp Ala Ala Glu Val
20 25 30

Glu Phe Leu Ala Glu Lys Glu Leu Val Thr Ile Ile Pro Asn Phe Ser
35 40 45

Leu Asp Lys Ile Tyr Leu Ile Gly Gly Asp Leu Gly Pro Phe Asn Pro
50 55 60

Gly Leu Pro Val Glu Val Pro Leu Trp Leu Ala Ile Asn Leu Lys Gln
65 70 75 80

Arg Gln Lys Cys Arg Leu Leu Pro Pro Glu Trp Met Asp Val Glu Lys
85 90 95

Leu Glu Lys Met Arg Asp His Glu Arg Lys Glu Glu Thr Phe Thr Pro

100 105 110

Met Pro Ser Pro Tyr Tyr Met Glu Leu Thr Lys Leu Leu Leu Asn His
115 120 125

Ala Ser Asp Asn Ile Pro Lys Ala Asp Glu Ile Arg Thr Leu Val Lys
130 135 140

Asp Met Trp Asp Thr Arg Ile Ala Lys Leu Arg Val Ser Ala Asp Ser
145 150 155 160

Phe Val Arg Gln Gln Glu Ala His Ala Lys Leu Asp Asn Leu Thr Leu
165 170 175

Met Glu Ile Asn Thr Ser Gly Thr Phe Leu Thr Gln Ala Leu Asn His
180 185 190

Met Tyr Lys Leu Arg Thr Asn Leu Gln Pro Leu Glu Ser Thr Gln Ser
195 200 205

Gln Asp Phe
210

<210> 1057
<211> 407
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (343)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1057
Val Ile Leu Gly Ala Gly Leu Arg Asp Lys Asp Met Trp Ile Pro Val
1 5 10 15

Val Gly Leu Pro Arg Arg Leu Arg Leu Ser Ala Leu Ala Gly Ala Gly
20 25 30

Arg Phe Cys Ile Leu Gly Ser Glu Ala Ala Thr Arg Lys His Leu Pro
35 40 45

Ala Arg Asn His Cys Gly Leu Ser Asp Ser Ser Pro Gln Leu Trp Pro
50 55 60

Glu Pro Asp Phe Arg Asn Pro Pro Arg Lys Ala Ser Lys Ala Ser Leu
65 70 75 80

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Asp Phe Lys Arg Tyr Val Thr Asp Arg Arg Leu Ala Glu Thr Leu Ala
                85                  90                  95

Gln Ile Tyr Leu Gly Lys Pro Ser Arg Pro Pro His Leu Leu Leu Glu
            100                 105                 110

Cys Asn Pro Gly Pro Gly Ile Leu Thr Gln Ala Leu Leu Glu Ala Gly
        115                 120                 125

Ala Lys Val Val Ala Leu Glu Ser Asp Lys Thr Phe Ile Pro His Leu
    130                 135                 140

Glu Ser Leu Gly Lys Asn Leu Asp Gly Lys Leu Arg Val Ile His Cys
145                 150                 155                 160

Asp Phe Phe Lys Leu Asp Pro Arg Ser Gly Gly Val Ile Lys Pro Pro
                165                 170                 175

Ala Met Ser Ser Arg Gly Leu Phe Lys Asn Leu Gly Ile Glu Ala Val
            180                 185                 190

Pro Trp Thr Ala Asp Ile Pro Leu Lys Val Val Gly Met Phe Pro Ser
        195                 200                 205

Arg Gly Glu Lys Arg Ala Leu Trp Lys Leu Ala Tyr Asp Leu Tyr Ser
    210                 215                 220

Cys Thr Ser Ile Tyr Lys Phe Gly Arg Ile Glu Val Asn Met Phe Ile
225                 230                 235                 240

Gly Glu Lys Glu Phe Gln Lys Leu Met Ala Asp Pro Gly Asn Pro Asp
                245                 250                 255

Leu Tyr His Val Leu Ser Val Ile Trp Gln Leu Ala Cys Glu Ile Lys
            260                 265                 270

Val Leu His Met Glu Pro Trp Ser Ser Phe Asp Ile Tyr Thr Arg Lys
        275                 280                 285

Gly Pro Leu Glu Asn Pro Lys Arg Arg Glu Leu Leu Asp Gln Leu Gln
    290                 295                 300

Gln Lys Leu Tyr Leu Ile Gln Met Ile Pro Arg Gln Asn Leu Phe Thr
305                 310                 315                 320

Lys Asn Leu Thr Pro Met Asn Tyr Asn Ile Phe Phe His Leu Leu Lys
                325                 330                 335

His Cys Phe Gly Arg Arg Xaa Ala Thr Val Ile Asp His Leu Arg Ser
            340                 345                 350
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Leu Thr Pro Leu Asp Ala Arg Asp Ile Leu Met Gln Ile Gly Lys Gln
355 360 365

Glu Asp Glu Lys Val Val Asn Met His Pro Gln Asp Phe Lys Thr Leu
370 375 380

Phe Glu Thr Ile Glu Arg Ser Lys Asp Cys Ala Tyr Lys Trp Leu Tyr
385 390 395 400

Asp Glu Thr Leu Glu Asp Arg
405

<210> 1058
<211> 89
<212> PRT
<213> Homo sapiens

<400> 1058
Ser Ser Trp Val Gly Gly Ser Leu Arg Gln Ala Ala Thr Leu Glu Gly
1 5 10 15

Glu Gln Gly Ser Ala Val Ser Ala Ala Ser His Ala Arg Ser Asp Leu
20 25 30

Ser Leu Gly Thr Pro Gln Glu Pro Glu Asp Ser Ser Gly Gln Cys Arg
35 40 45

Trp Gly Val Gly Gly Glu Ser Gly Arg Glu Ala Leu Arg Ala Pro Ser
50 55 60

Pro Thr Thr Asn Leu Ala Leu Val Val Ile Phe Arg Gln Asn Phe Val
65 70 75 80

Val Phe Phe Pro Phe Tyr Asp Gly Phe
85

<210> 1059
<211> 457
<212> PRT
<213> Homo sapiens

<400> 1059
Gly Thr Arg Pro Ser Ser Cys Ser Gln Thr Glu Ala Gln Pro Pro Ser
1 5 10 15

Pro Val Ser Ile Thr Ser Ala Ala Ser Met Ser Asp Lys Leu Pro Tyr
20 25 30

Lys Val Ala Asp Ile Gly Leu Ala Ala Trp Gly Arg Lys Ala Leu Asp
35 40 45

Ile Ala Glu Asn Glu Met Pro Gly Leu Met Arg Met Arg Glu Arg Tyr
50 55 60

Ser Ala Ser Lys Pro Leu Lys Gly Ala Arg Ile Ala Gly Cys Leu His
65 70 75 80

Met Thr Val Glu Thr Ala Val Leu Ile Glu Thr Leu Val Thr Leu Gly
85 90 95

Ala Glu Val Gln Trp Ser Ser Cys Asn Ile Phe Ser Thr Gln Asp His
100 105 110

Ala Ala Ala Ala Ile Ala Lys Ala Gly Ile Pro Val Tyr Ala Trp Lys
115 120 125

Gly Glu Thr Asp Glu Glu Tyr Leu Trp Cys Ile Glu Gln Thr Leu Tyr
130 135 140

Phe Lys Asp Gly Pro Leu Asn Met Ile Leu Asp Asp Gly Gly Asp Leu
145 150 155 160

Thr Asn Leu Ile His Thr Lys Tyr Pro Gln Leu Leu Pro Gly Ile Arg
165 170 175

Gly Ile Ser Glu Glu Thr Thr Thr Gly Val His Asn Leu Tyr Lys Met
180 185 190

Met Ala Asn Gly Ile Leu Lys Val Pro Ala Ile Asn Val Asn Asp Ser
195 200 205

Val Thr Lys Ser Lys Phe Asp Asn Leu Tyr Gly Cys Arg Glu Ser Leu
210 215 220

Ile Asp Gly Ile Lys Arg Ala Thr Asp Val Met Ile Ala Gly Lys Val
225 230 235 240

Ala Val Val Ala Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Gln Ala
245 250 255

Leu Arg Gly Phe Gly Ala Arg Val Ile Ile Thr Glu Ile Asp Pro Ile
260 265 270

Asn Ala Leu Gln Ala Ala Met Glu Gly Tyr Glu Val Thr Thr Met Asp
275 280 285

Glu Ala Cys Gln Glu Gly Asn Ile Phe Val Thr Thr Thr Gly Cys Ile
290 295 300

Asp Ile Ile Leu Gly Arg His Phe Glu Gln Met Lys Asp Asp Ala Ile
305 310 315 320

Val Cys Asn Ile Gly His Phe Asp Val Glu Ile Asp Val Lys Trp Leu
325 330 335

Asn Glu Asn Ala Val Glu Lys Val Asn Ile Lys Pro Gln Val Asp Arg
340 345 350

Tyr Arg Leu Lys Asn Gly Arg Arg Ile Ile Leu Leu Ala Glu Gly Arg
355 360 365

Leu Val Asn Leu Gly Cys Ala Met Gly His Pro Ser Phe Val Met Ser
370 375 380

Asn Ser Phe Thr Asn Gln Val Met Ala Gln Ile Glu Leu Trp Thr His
385 390 395 400

Pro Asp Lys Tyr Pro Val Gly Val His Phe Leu Pro Lys Lys Leu Asp
405 410 415

Glu Ala Val Ala Glu Ala His Leu Gly Lys Leu Asn Val Lys Leu Thr
420 425 430

Lys Leu Thr Glu Lys Gln Ala Gln Tyr Leu Gly Met Ser Cys Asp Gly
435 440 445

Pro Phe Lys Pro Asp His Tyr Arg Tyr
450 455

<210> 1060
<211> 511
<212> PRT
<213> Homo sapiens

<400> 1060
Glu Gly Val Met Ala Asp Gly Gln Val Ala Glu Leu Leu Leu Arg Arg
1 5 10 15

Leu Glu Ala Ser Asp Gly Gly Leu Asp Ser Ala Glu Leu Ala Ala Glu
20 25 30

Leu Gly Met Glu His Gln Ala Val Val Gly Ala Val Lys Ser Leu Gln
35 40 45

Ala Leu Gly Glu Val Ile Glu Ala Glu Leu Arg Ser Thr Lys His Trp
50 55 60

Glu Leu Thr Ala Glu Gly Glu Glu Ile Ala Arg Glu Gly Ser His Glu
65 70 75 80

Ala Arg Val Phe Arg Ser Ile Pro Pro Glu Gly Leu Ala Gln Ser Glu
85 90 95

Leu Met Arg Leu Pro Ser Gly Lys Val Gly Phe Ser Lys Ala Met Ser
100 105 110

Asn Lys Trp Ile Arg Val Asp Lys Ser Ala Ala Asp Gly Pro Arg Val
115 120 125

Phe Arg Val Val Asp Ser Met Glu Asp Glu Val Gln Arg Arg Leu Gln
130 135 140

Leu Val Arg Gly Gly Gln Ala Glu Lys Leu Gly Glu Lys Glu Arg Ser
145 150 155 160

Glu Leu Arg Lys Arg Lys Leu Leu Ala Glu Val Thr Leu Lys Thr Tyr
165 170 175

Trp Val Ser Lys Gly Ser Ala Phe Ser Thr Ser Ile Ser Lys Gln Glu
180 185 190

Thr Glu Leu Ser Pro Glu Met Ile Ser Ser Gly Ser Trp Arg Asp Arg
195 200 205

Pro Phe Lys Pro Tyr Asn Phe Leu Ala His Gly Val Leu Pro Asp Ser
210 215 220

Gly His Leu His Pro Leu Leu Lys Val Arg Ser Gln Phe Arg Gln Ile
225 230 235 240

Phe Leu Glu Met Gly Phe Thr Glu Met Pro Thr Asp Asn Phe Ile Glu
245 250 255

Ser Ser Phe Trp Asn Phe Asp Ala Leu Phe Gln Pro Gln Gln His Pro
260 265 270

Ala Arg Asp Gln His Asp Thr Phe Phe Leu Arg Asp Pro Ala Glu Ala
275 280 285

Leu Gln Leu Pro Met Asp Tyr Val Gln Arg Val Lys Arg Thr His Ser
290 295 300

Gln Gly Gly Tyr Gly Ser Gln Gly Tyr Lys Tyr Asn Trp Lys Leu Asp
305 310 315 320

Glu Ala Arg Lys Asn Leu Leu Arg Thr His Thr Thr Ser Ala Ser Ala
325 330 335

Arg Ala Leu Tyr Arg Leu Ala Gln Lys Lys Pro Phe Thr Pro Val Lys
340 345 350

Tyr Phe Ser Ile Asp Arg Val Phe Arg Asn Glu Thr Leu Asp Ala Thr
355 360 365

His Leu Ala Glu Phe His Gln Ile Glu Gly Val Val Ala Asp His Gly
370 375 380

Leu Thr Leu Gly His Leu Met Gly Val Leu Arg Glu Phe Phe Thr Lys
385 390 395 400

Leu Gly Ile Thr Gln Leu Arg Phe Lys Pro Ala Tyr Asn Pro Tyr Thr
405 410 415

Glu Pro Ser Met Glu Val Phe Ser Tyr His Gln Gly Leu Lys Lys Trp
420 425 430

Val Glu Val Gly Asn Ser Gly Val Phe Arg Pro Glu Met Leu Leu Pro
435 440 445

Met Gly Leu Pro Glu Asn Val Ser Val Ile Ala Trp Gly Leu Ser Leu
450 455 460

Glu Arg Pro Thr Met Ile Lys Tyr Gly Ile Asn Asn Ile Arg Glu Leu
465 470 475 480

Val Gly His Lys Val Asn Leu Gln Met Val Tyr Asp Ser Pro Leu Cys
485 490 495

Arg Leu Asp Ala Glu Pro Arg Pro Pro Pro Thr Gln Glu Ala Ala
500 505 510

<210> 1061
<211> 228
<212> PRT
<213> Homo sapiens

<400> 1061
Arg Ala Ala Ser Thr Pro Arg Ala Ala Pro Gly Ala Ala Leu Leu Ser
1 5 10 15

Pro Pro Gly Leu Arg Ala Ala Pro Ala Ala Leu Val Met Gly Glu Gly
20 25 30

Thr Cys Glu Lys Arg Arg Asp Ala Glu Tyr Gly Ala Ser Pro Glu Gln
35 40 45

Val Ala Asp Asn Gly Asp Asp His Ser Glu Gly Gly Leu Val Glu Asn

50 55 60

His Val Asp Ser Thr Met Asn Met Leu Gly Gly Gly Gly Ser Ala Gly
65 70 75 80

Arg Lys Pro Leu Lys Ser Gly Met Lys Glu Leu Ala Val Phe Arg Glu
85 90 95

Lys Val Thr Glu Gln His Arg Gln Met Gly Lys Gly Gly Lys His His
100 105 110

Leu Gly Leu Glu Glu Pro Lys Lys Leu Arg Pro Pro Pro Ala Arg Thr
115 120 125

Pro Cys Gln Gln Glu Leu Asp Gln Val Leu Glu Arg Ile Ser Thr Met
130 135 140

Arg Leu Pro Asp Glu Arg Gly Pro Leu Glu His Leu Tyr Ser Leu His
145 150 155 160

Ile Pro Asn Cys Asp Lys His Gly Leu Tyr Asn Leu Lys Gln Cys Lys
165 170 175

Met Ser Leu Asn Gly Gln Arg Gly Glu Cys Trp Cys Val Asn Pro Asn
180 185 190

Thr Gly Lys Leu Ile Gln Gly Ala Pro Thr Ile Arg Gly Asp Pro Glu
195 200 205

Cys His Leu Phe Tyr Asn Glu Gln Gln Glu Ala Arg Gly Val His Thr
210 215 220

Gln Arg Met Gln
225

<210> 1062
<211> 324
<212> PRT
<213> Homo sapiens

<400> 1062
Pro Arg Val Met Ala Met Ala Thr Lys Gly Gly Thr Val Lys Ala Ala
1 5 10 15

Ser Gly Phe Asn Ala Met Glu Asp Ala Gln Thr Leu Arg Lys Ala Met
20 25 30

Lys Gly Leu Gly Thr Asp Glu Asp Ala Ile Ile Ser Val Leu Ala Tyr
35 40 45

Arg Asn Thr Ala Gln Arg Gln Glu Ile Arg Thr Ala Tyr Lys Ser Thr
50 55 60

Ile Gly Arg Asp Leu Ile Asp Asp Leu Lys Ser Glu Leu Ser Gly Asn
65 70 75 80

Phe Glu Gln Val Ile Val Gly Met Met Thr Pro Thr Val Leu Tyr Asp
85 90 95

Val Gln Glu Leu Arg Arg Ala Met Lys Gly Ala Gly Thr Asp Glu Gly
100 105 110

Cys Leu Ile Glu Ile Leu Ala Ser Arg Thr Pro Glu Glu Ile Arg Arg
115 120 125

Ile Ser Gln Thr Tyr Gln Gln Gln Tyr Gly Arg Ser Leu Glu Asp Asp
130 135 140

Ile Arg Ser Asp Thr Ser Phe Met Phe Gln Arg Val Leu Val Ser Leu
145 150 155 160

Ser Ala Gly Gly Arg Asp Glu Gly Asn Tyr Leu Asp Asp Ala Leu Val
165 170 175

Arg Gln Asp Ala Gln Asp Leu Tyr Glu Ala Gly Glu Lys Lys Trp Gly
180 185 190

Thr Asp Glu Val Lys Phe Leu Thr Val Leu Cys Ser Arg Asn Arg Asn
195 200 205

His Leu Leu His Val Phe Asp Glu Tyr Lys Arg Ile Ser Gln Lys Asp
210 215 220

Ile Glu Gln Ser Ile Lys Ser Glu Thr Ser Gly Ser Phe Glu Asp Ala
225 230 235 240

Leu Leu Ala Ile Val Lys Cys Met Arg Asn Lys Ser Ala Tyr Phe Ala
245 250 255

Glu Lys Leu Tyr Lys Ser Met Lys Gly Leu Gly Thr Asp Asp Asn Thr
260 265 270

Leu Ile Arg Val Met Val Ser Arg Ala Glu Ile Asp Met Leu Asp Ile
275 280 285

Arg Ala His Phe Lys Arg Leu Tyr Gly Lys Ser Leu Tyr Ser Phe Ile
290 295 300

Lys Gly Asp Thr Ser Gly Asp Tyr Arg Lys Val Leu Leu Val Leu Cys
305 310 315 320

Gly Gly Asp Asp

<210> 1063
<211> 355
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (37)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1063
Xaa Tyr Xaa Ile Pro Gly Ser Thr His Ala Ser Gly Lys Ile Leu Gly
1 5 10 15

Ser Gly Ile Ser Ser Ser Ser Val Leu His Gly Met Val Phe Lys Lys
20 25 30

Glu Thr Glu Val Xaa Val Thr Ser Val Lys Asp Ala Lys Ile Ala Val
35 40 45

Tyr Ser Cys Pro Phe Asp Gly Met Ile Thr Glu Thr Lys Gly Thr Val
50 55 60

Leu Ile Lys Thr Ala Glu Glu Leu Met Asn Phe Ser Lys Gly Glu Glu
65 70 75 80

Asn Leu Met Asp Ala Gln Val Lys Ala Ile Ala Asp Thr Gly Ala Asn
85 90 95

Val Val Val Thr Gly Gly Lys Val Ala Asp Met Ala Leu His Tyr Ala
100 105 110

Asn Lys Tyr Asn Ile Met Leu Val Arg Leu Asn Ser Lys Trp Asp Leu
115 120 125

Arg Arg Leu Cys Lys Thr Val Gly Ala Thr Ala Leu Pro Arg Leu Thr
    130   135   140

Pro Pro Val Leu Glu Glu Met Gly His Cys Asp Ser Val Tyr Leu Ser
145   150   155   160

Glu Val Gly Asp Thr Gln Val Val Val Phe Lys His Glu Lys Glu Asp
                165   170   175

Gly Ala Ile Ser Thr Ile Val Leu Arg Gly Ser Thr Asp Asn Leu Met
            180   185   190

Asp Asp Ile Glu Arg Ala Val Asp Asp Gly Val Asn Thr Phe Lys Val
        195   200   205

Leu Thr Arg Asp Lys Arg Leu Val Pro Gly Gly Gly Ala Thr Glu Ile
    210   215   220

Glu Leu Ala Lys Gln Ile Thr Ser Tyr Gly Glu Thr Cys Pro Gly Leu
225   230   235   240

Glu Gln Tyr Ala Ile Lys Lys Phe Ala Glu Ala Phe Glu Ala Ile Pro
                245   250   255

Arg Ala Leu Ala Glu Asn Ser Gly Val Lys Ala Asn Glu Val Ile Ser
            260   265   270

Lys Leu Tyr Ala Val His Gln Glu Gly Asn Lys Asn Val Gly Leu Asp
        275   280   285

Ile Glu Ala Glu Val Pro Ala Val Lys Asp Met Leu Glu Ala Gly Ile
    290   295   300

Leu Asp Thr Tyr Leu Gly Lys Tyr Trp Ala Ile Lys Leu Ala Thr Asn
305   310   315   320

Ala Ala Val Thr Val Leu Arg Val Asp Gln Ile Ile Met Ala Lys Pro
                325   330   335

Ala Gly Gly Pro Lys Pro Pro Ser Gly Lys Lys Asp Trp Asp Asp Asp
            340   345   350

Gln Asn Asp
        355

<210> 1064
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1064
Ser Pro Phe Thr Leu His Cys Cys His Ser Thr Leu Tyr Asp Gly Arg
1 5 10 15

Thr Gly Ser Ser Arg Glu Asn Cys Thr Val Thr Thr Val Phe Phe Thr
20 25 30

Leu Phe Gln Gly Ser Leu Ser Pro Asp Ile Glu Glu Ile Ser Phe Arg
35 40 45

Pro Glu Thr Gln Arg Pro His Ser Pro Val Ile Lys Pro Arg Phe His
50 55 60

Ser Gly Pro Arg Ser Gly Ala Trp Pro Leu Leu Phe Gly Ser His Trp
65 70 75 80

Glu Ala His Trp Pro Trp Ile Ile Ser Ser Cys Thr Pro Gly Val Leu
85 90 95

Pro Ala Cys Leu Leu Ser Trp Thr Ala Val Cys Lys Lys Val Thr Lys
100 105 110

Thr

<210> 1065
<211> 634
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (325)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1065
Val Gln Gly Phe Glu Ser Ala Thr Phe Leu Gly Tyr Phe Lys Ser Gly
1 5 10 15

Leu Lys Tyr Lys Lys Gly Gly Val Ala Ser Gly Phe Lys His Val Val
20 25 30

Pro Asn Glu Val Val Val Gln Arg Leu Phe Gln Val Lys Gly Arg Arg
35 40 45

Val Val Arg Ala Thr Glu Val Pro Val Ser Trp Glu Ser Phe Asn Asn
50 55 60

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Gly Asp Cys Phe Ile Leu Asp Leu Gly Asn Asn Ile His Gln Trp Cys
65                  70                  75                  80

Gly Ser Asn Ser Asn Arg Tyr Glu Arg Leu Lys Ala Thr Gln Val Ser
                85                  90                  95

Lys Gly Ile Arg Asp Asn Glu Arg Ser Gly Arg Ala Arg Val His Val
            100                 105                 110

Ser Glu Glu Gly Thr Glu Pro Glu Ala Met Leu Gln Val Leu Gly Pro
        115                 120                 125

Lys Pro Ala Leu Pro Ala Gly Thr Glu Asp Thr Ala Lys Glu Asp Ala
    130                 135                 140

Ala Asn Arg Lys Leu Ala Lys Leu Tyr Lys Val Ser Asn Gly Ala Gly
145                 150                 155                 160

Thr Met Ser Val Ser Leu Val Ala Asp Glu Asn Pro Phe Ala Gln Gly
                165                 170                 175

Ala Leu Lys Ser Glu Asp Cys Phe Ile Leu Asp His Gly Lys Asp Gly
            180                 185                 190

Lys Ile Phe Val Trp Lys Gly Lys Gln Ala Asn Thr Glu Glu Arg Lys
        195                 200                 205

Ala Ala Leu Lys Thr Ala Ser Asp Phe Ile Thr Lys Met Asp Tyr Pro
    210                 215                 220

Lys Gln Thr Gln Val Ser Val Leu Pro Glu Gly Gly Glu Thr Pro Leu
225                 230                 235                 240

Phe Lys Gln Phe Phe Lys Asn Trp Arg Asp Pro Asp Gln Thr Asp Gly
                245                 250                 255

Leu Gly Leu Ser Tyr Leu Ser Ser His Ile Ala Asn Val Glu Arg Val
            260                 265                 270

Pro Phe Asp Ala Ala Thr Leu His Thr Ser Thr Ala Met Ala Ala Gln
        275                 280                 285

His Gly Met Asp Asp Asp Gly Thr Gly Gln Lys Gln Ile Trp Arg Ile
    290                 295                 300

Glu Gly Ser Asn Lys Val Pro Val Asp Pro Ala Thr Tyr Gly Gln Phe
305                 310                 315                 320

Tyr Gly Gly Asp Xaa Tyr Ile Ile Leu Tyr Asn Tyr Arg His Gly Gly
                325                 330                 335
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Arg Gln Gly Gln Ile Ile Tyr Asn Trp Gln Gly Ala Gln Ser Thr Gln
            340                 345                 350

Asp Glu Val Ala Ala Ser Ala Ile Leu Thr Ala Gln Leu Asp Glu Glu
        355                 360                 365

Leu Gly Gly Thr Pro Val Gln Ser Arg Val Val Gln Gly Lys Glu Pro
    370                 375                 380

Ala His Leu Met Ser Leu Phe Gly Gly Lys Pro Met Ile Ile Tyr Lys
385                 390                 395                 400

Gly Gly Thr Ser Arg Glu Gly Gly Gln Thr Ala Pro Ala Ser Thr Arg
                405                 410                 415

Leu Phe Gln Val Arg Ala Asn Ser Ala Gly Ala Thr Arg Ala Val Glu
            420                 425                 430

Val Leu Pro Lys Ala Gly Ala Leu Asn Ser Asn Asp Ala Phe Val Leu
        435                 440                 445

Lys Thr Pro Ser Ala Ala Tyr Leu Trp Val Gly Thr Gly Ala Ser Glu
    450                 455                 460

Ala Glu Lys Thr Gly Ala Gln Glu Leu Leu Arg Val Leu Arg Ala Gln
465                 470                 475                 480

Pro Val Gln Val Ala Glu Gly Ser Glu Pro Asp Gly Phe Trp Glu Ala
                485                 490                 495

Leu Gly Gly Lys Ala Ala Tyr Arg Thr Ser Pro Arg Leu Lys Asp Lys
            500                 505                 510

Lys Met Asp Ala His Pro Pro Arg Leu Phe Ala Cys Ser Asn Lys Ile
        515                 520                 525

Gly Arg Phe Val Ile Glu Glu Val Pro Gly Glu Leu Met Gln Glu Asp
    530                 535                 540

Leu Ala Thr Asp Asp Val Met Leu Leu Asp Thr Trp Asp Gln Val Phe
545                 550                 555                 560

Val Trp Val Gly Lys Asp Ser Gln Glu Glu Glu Lys Thr Glu Ala Leu
                565                 570                 575

Thr Ser Ala Lys Arg Tyr Ile Glu Thr Asp Pro Ala Asn Arg Asp Arg
            580                 585                 590

Arg Thr Pro Ile Thr Val Val Lys Gln Gly Phe Glu Pro Pro Ser Phe
        595                 600                 605
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Val Gly Trp Phe Leu Gly Trp Asp Asp Asp Tyr Trp Ser Val Asp Pro
610 615 620

Leu Asp Arg Ala Met Ala Glu Leu Ala Ala
625 630

<210> 1066
<211> 117
<212> PRT
<213> Homo sapiens

<400> 1066
Arg Ala Arg Gly Arg Cys Arg Arg Ser Pro Asp Gly Val Gly Ile Glu
1 5 10 15

Ala Pro Arg Lys Lys Val Lys Tyr Gln Glu Ile Gln Val Glu Glu Pro
20 25 30

Tyr Tyr Asp Cys His Glu Cys Thr Glu Thr Phe Thr Ser Ser Thr Ala
35 40 45

Phe Ser Glu His Leu Lys Thr His Ala Ser Met Ile Ile Phe Glu Pro
50 55 60

Ala Asn Ala Phe Gly Glu Cys Ser Gly Tyr Ile Glu Arg Ala Ser Thr
65 70 75 80

Ser Thr Gly Gly Ala Asn Gln Ala Asp Glu Lys Tyr Phe Lys Cys Asp
85 90 95

Val Cys Gly Gln Leu Phe Asn Asp Arg Leu Ser Leu Ala Arg His Gln
100 105 110

Asn Thr His Thr Gly
115

<210> 1067
<211> 192
<212> PRT
<213> Homo sapiens

<400> 1067
Pro Glu Gln Arg Gly Ser Ser Met Ala His Gly Pro Gly Ala Leu Met
1 5 10 15

Leu Lys Cys Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu
20 25 30

Leu Met Ser Tyr Ala Asn Asp Ala Phe Pro Glu Ser Thr Cys Pro Pro
35 40 45

Ser Ser Thr Thr Thr Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser
50 55 60

Tyr Pro Met Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn Pro
65 70 75 80

Ala Ser Phe Gln Asn Val Lys Glu Glu Trp Val Pro Glu Leu Lys Glu
85 90 95

Tyr Ala Pro Asn Val Pro Phe Leu Leu Ile Gly Thr Gln Ile Asp Leu
100 105 110

Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Asn Asp Met Lys Glu Lys
115 120 125

Pro Ile Cys Val Glu Gln Gly Gln Lys Leu Ala Lys Glu Ile Gly Ala
130 135 140

Cys Cys Tyr Val Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys Thr
145 150 155 160

Val Phe Asp Glu Ala Ile Ile Ala Ile Leu Thr Pro Lys Lys His Thr
165 170 175

Val Lys Lys Arg Ile Gly Ser Arg Cys Ile Asn Cys Cys Leu Ile Thr
180 185 190

<210> 1068
<211> 360
<212> PRT
<213> Homo sapiens

<400> 1068
Ser Arg Trp Ala Arg Arg Asp Pro Gln Glu Arg Arg Glu Arg Gly Thr
1 5 10 15

Arg Val Gln Ser Ser Gly Thr Trp Ile Gly Ala Gly Ala Met Gly Gly
20 25 30

Glu Gln Glu Glu Glu Arg Phe Asp Gly Met Leu Leu Ala Met Ala Gln
35 40 45

```
Gln His Glu Gly Gly Val Gln Glu Leu Val Asn Thr Phe Phe Ser Phe
     50                  55                  60

Leu Arg Arg Lys Thr Asp Phe Phe Ile Gly Gly Glu Glu Gly Met Ala
 65                  70                  75                  80

Glu Lys Leu Ile Thr Gln Thr Phe Ser His His Asn Gln Leu Ala Gln
                 85                  90                  95

Lys Thr Arg Arg Glu Lys Arg Ala Arg Gln Glu Ala Glu Arg Arg Glu
            100                 105                 110

Lys Ala Glu Arg Ala Ala Arg Leu Ala Lys Glu Ala Lys Ser Glu Thr
        115                 120                 125

Ser Gly Pro Gln Ile Lys Glu Leu Thr Asp Glu Glu Ala Glu Arg Leu
    130                 135                 140

Gln Leu Glu Ile Asp Gln Lys Lys Asp Ala Glu Asn His Glu Ala Gln
145                 150                 155                 160

Leu Lys Asn Gly Ser Leu Asp Ser Pro Gly Lys Gln Asp Thr Glu Glu
                165                 170                 175

Asp Glu Glu Glu Asp Glu Lys Asp Lys Gly Lys Leu Lys Pro Asn Leu
            180                 185                 190

Gly Asn Gly Ala Asp Leu Pro Asn Tyr Arg Trp Thr Gln Thr Leu Ser
        195                 200                 205

Glu Leu Asp Leu Ala Val Pro Phe Cys Val Asn Phe Arg Leu Lys Gly
    210                 215                 220

Lys Asp Met Val Val Asp Ile Gln Arg Arg His Leu Arg Val Gly Leu
225                 230                 235                 240

Lys Gly Gln Pro Ala Ile Ile Asp Gly Glu Leu Tyr Asn Glu Val Lys
                245                 250                 255

Val Glu Glu Ser Ser Trp Leu Ile Glu Asp Gly Lys Val Val Thr Val
            260                 265                 270

His Leu Glu Lys Ile Asn Lys Met Glu Trp Trp Ser Arg Leu Val Ser
        275                 280                 285

Ser Asp Pro Glu Ile Asn Thr Lys Lys Ile Asn Pro Glu Asn Ser Lys
    290                 295                 300

Leu Ser Asp Leu Asp Ser Glu Thr Arg Ser Met Val Glu Lys Met Met
305                 310                 315                 320
```

Tyr Asp Gln Arg Gln Lys Ser Met Gly Leu Pro Thr Ser Asp Glu Gln
325 330 335

Lys Lys Gln Glu Ile Leu Lys Lys Phe Met Asp Gln His Pro Glu Met
340 345 350

Asp Phe Ser Lys Ala Lys Phe Asn
355 360

<210> 1069
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (52)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1069
Val Trp Leu Ser Trp Asp Gln Glu Lys Ile Pro Val Leu Asp Gln Glu
1 5 10 15

Ala Ala Asp Gly Ser Ser Thr Leu Gly Gly Gly Ala Gly Thr Met Gly
20 25 30

Leu Ser Ala Arg Tyr Gly Pro Gln Phe Thr Leu Gln His Val Pro Asp
35 40 45

Tyr Arg Gln Xaa Val Tyr Ile Pro Gly Ser Asn Ala Thr Leu Thr Asn
50 55 60

Ala Ala Gly Lys Arg Gly Trp Gln Gly Pro Ser Arg Trp Gln Trp Gln
65 70 75 80

Gln Glu Glu Val Gly Gln Glu Gly Glu Glu Val Thr Trp Arg Pro Gly
85 90 95

Gln Glu Pro Gln Gly Gly Leu Ser Pro Thr Ser Pro Ala Ser Pro Tyr
100 105 110

Leu His Pro Gly Leu Arg Val Ser Gly Leu Thr Pro Arg Ile Leu Val
115 120 125

Gly Ala Lys Ala Met Leu Pro Leu Gly Asn Arg Asn Lys Cys Pro Val
130 135 140

Ser Thr Tyr Pro Phe Pro Pro Arg Gly Leu Asn Met Gln Lys Gln Phe
145 150 155 160

Arg Trp Glu Pro Pro Ser Asn Gln Leu Leu Tyr Pro Trp Gly
165 170

<210> 1070
<211> 445
<212> PRT
<213> Homo sapiens

<400> 1070
Pro Arg Gly Leu Thr Gly Leu Trp Arg Ser Ser Leu Pro Ile Arg Lys
1 5 10 15

Leu Gln Leu Pro Pro Asp Ala Leu Lys Met Ala Thr Ser Leu Gly Ser
20 25 30

Asn Thr Tyr Asn Arg Gln Asn Trp Glu Asp Ala Asp Phe Pro Ile Leu
35 40 45

Cys Gln Thr Cys Leu Gly Glu Asn Pro Tyr Ile Arg Met Thr Lys Glu
50 55 60

Lys Tyr Gly Lys Glu Cys Lys Ile Cys Ala Arg Pro Phe Thr Val Phe
65 70 75 80

Arg Trp Cys Pro Gly Val Arg Met Arg Phe Lys Lys Thr Glu Val Cys
85 90 95

Gln Thr Cys Ser Lys Leu Lys Asn Val Cys Gln Thr Cys Leu Leu Asp
100 105 110

Leu Glu Tyr Gly Leu Pro Ile Gln Val Arg Asp Ala Gly Leu Ser Phe
115 120 125

Lys Asp Asp Met Pro Lys Ser Asp Val Asn Lys Glu Tyr Tyr Thr Gln
130 135 140

Asn Met Glu Arg Glu Ile Ser Asn Ser Asp Gly Thr Arg Pro Val Gly
145 150 155 160

Met Leu Gly Lys Ala Thr Ser Thr Ser Asp Met Leu Leu Lys Leu Ala
165 170 175

Arg Thr Thr Pro Tyr Tyr Lys Arg Asn Arg Pro His Ile Cys Ser Phe
180 185 190

Trp Val Lys Gly Glu Cys Lys Arg Gly Glu Glu Cys Pro Tyr Arg His
195 200 205

Glu Lys Pro Thr Asp Pro Asp Asp Pro Leu Ala Asp Gln Asn Ile Lys
    210   215   220

Asp Arg Tyr Tyr Gly Ile Asn Asp Pro Val Ala Asp Lys Leu Leu Lys
225   230   235   240

Arg Ala Ser Thr Met Pro Arg Leu Asp Pro Pro Glu Asp Lys Thr Ile
                245   250   255

Thr Thr Leu Tyr Val Gly Gly Leu Gly Asp Thr Ile Thr Glu Thr Asp
            260   265   270

Leu Arg Asn His Phe Tyr Gln Phe Gly Glu Ile Arg Thr Ile Thr Val
        275   280   285

Val Gln Arg Gln Gln Cys Ala Phe Ile Gln Phe Ala Thr Arg Gln Ala
    290   295   300

Ala Glu Val Ala Ala Glu Lys Ser Phe Asn Lys Leu Ile Val Asn Gly
305   310   315   320

Arg Arg Leu Asn Val Lys Trp Gly Arg Ser Gln Ala Ala Arg Gly Lys
                325   330   335

Glu Lys Glu Lys Asp Gly Thr Thr Asp Ser Gly Ile Lys Leu Glu Pro
            340   345   350

Val Pro Gly Leu Pro Gly Ala Leu Pro Pro Pro Pro Ala Ala Glu Glu
        355   360   365

Glu Ala Ser Ala Asn Tyr Phe Asn Leu Pro Pro Ser Gly Pro Pro Ala
    370   375   380

Val Val Asn Ile Ala Leu Pro Pro Pro Pro Gly Ile Ala Pro Pro Pro
385   390   395   400

Pro Pro Gly Phe Gly Pro His Met Phe His Pro Met Gly Pro Pro Pro
                405   410   415

Pro Phe Met Arg Ala Pro Gly Pro Ile His Tyr Pro Ser Gln Asp Pro
            420   425   430

Gln Arg Met Gly Ala His Ala Gly Lys His Ser Ser Pro
        435   440   445

<210> 1071
<211> 346
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (286)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (287)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (291)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (294)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1071

```
Trp Ser Arg Leu Cys Leu Leu Lys Gln Tyr Leu Phe Thr Met Lys Leu
  1               5                  10                  15

Gln Ser Pro Glu Phe Gln Ser Leu Phe Thr Glu Gly Leu Lys Ser Leu
             20                  25                  30

Thr Glu Leu Phe Val Lys Glu Asn His Glu Leu Arg Ile Ala Gly Gly
         35                  40                  45

Ala Val Arg Asp Leu Leu Asn Gly Val Lys Pro Gln Asp Ile Asp Phe
     50                  55                  60

Ala Thr Thr Ala Thr Pro Thr Gln Met Lys Glu Met Phe Gln Ser Ala
 65                  70                  75                  80

Gly Ile Arg Met Ile Asn Asn Arg Gly Glu Lys His Gly Thr Ile Thr
                 85                  90                  95

Ala Arg Leu His Glu Glu Asn Phe Glu Ile Thr Thr Leu Arg Ile Asp
            100                 105                 110

Val Thr Thr Asp Gly Arg His Ala Glu Val Glu Phe Thr Thr Asp Trp
        115                 120                 125

Gln Lys Asp Ala Glu Arg Arg Asp Leu Thr Ile Asn Ser Met Phe Leu
    130                 135                 140

Gly Phe Asp Gly Thr Leu Phe Asp Tyr Phe Asn Gly Tyr Glu Asp Leu
145                 150                 155                 160
```

Lys Asn Lys Lys Val Arg Phe Val Gly His Ala Lys Gln Arg Ile Gln
165 170 175

Glu Asp Tyr Leu Arg Ile Leu Arg Tyr Phe Arg Phe Tyr Gly Arg Ile
180 185 190

Val Asp Lys Pro Gly Asp His Asp Pro Glu Thr Leu Glu Ala Ile Ala
195 200 205

Glu Asn Ala Lys Gly Leu Ala Gly Ile Ser Gly Glu Arg Ile Trp Val
210 215 220

Glu Leu Lys Lys Ile Leu Val Gly Asn His Val Asn His Leu Ile His
225 230 235 240

Leu Ile Tyr Asp Leu Asp Val Ala Pro Tyr Ile Gly Leu Pro Ala Asn
245 250 255

Ala Ser Leu Glu Glu Phe Asp Lys Val Ser Lys Asn Val Asp Gly Phe
260 265 270

Ser Pro Lys Pro Val Thr Leu Leu Ala Ser Leu Phe Lys Xaa Xaa Asp
275 280 285

Asp Val Xaa Lys Leu Xaa Leu Arg Leu Lys Ile Ala Lys Glu Glu Lys
290 295 300

Asn Leu Gly Leu Phe Ile Val Lys Asn Arg Lys Asp Leu Ile Lys Ala
305 310 315 320

Thr Asp Ser Ser Asp Pro Leu Lys Pro Tyr Gln Asp Phe Ile Ile Asp
325 330 335

Ser Arg Glu Pro Asp Ala His Ser Cys Met
340 345

<210> 1072
<211> 404
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (77)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (81)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1072
Glu Asp Ser Leu Asn Leu Asp Leu Thr Pro Arg Met Leu Arg Arg Leu
1 5 10 15

Leu Glu Arg Pro Cys Thr Leu Ala Leu Leu Val Gly Ser Gln Leu Ala
20 25 30

Val Met Met Tyr Leu Ser Leu Gly Gly Phe Arg Ser Leu Ser Ala Leu
35 40 45

Phe Gly Arg Asp Gln Gly Pro Thr Phe Asp Tyr Ser His Pro Arg Asp
50 55 60

Val Tyr Ser Asn Leu Ser His Leu Pro Gly Ala Pro Xaa Gly Pro Pro
65 70 75 80

Xaa Pro Gln Gly Leu Pro Tyr Cys Pro Glu Arg Ser Pro Leu Leu Val
85 90 95

Gly Pro Val Ser Val Ser Phe Ser Pro Val Pro Ser Leu Ala Glu Ile
100 105 110

Val Glu Arg Asn Pro Arg Val Glu Pro Gly Gly Arg Tyr Arg Pro Ala
115 120 125

Gly Cys Glu Pro Arg Ser Arg Thr Ala Ile Ile Val Pro His Arg Ala
130 135 140

Arg Glu His His Leu Arg Leu Leu Leu Tyr His Leu His Pro Phe Leu
145 150 155 160

Gln Arg Gln Gln Leu Ala Tyr Gly Ile Tyr Val Ile His Gln Ala Gly
165 170 175

Asn Gly Thr Phe Asn Arg Ala Lys Leu Leu Asn Val Gly Val Arg Glu
180 185 190

Ala Leu Arg Asp Glu Glu Trp Asp Cys Leu Phe Leu His Asp Val Asp
195 200 205

Leu Leu Pro Glu Asn Asp His Asn Leu Tyr Val Cys Asp Pro Arg Gly
210 215 220

Pro Arg His Val Ala Val Ala Met Asn Lys Phe Gly Tyr Ser Leu Pro
225 230 235 240

Tyr Pro Gln Tyr Phe Gly Gly Val Ser Ala Leu Thr Pro Asp Gln Tyr
245 250 255

Leu Lys Met Asn Gly Phe Pro Asn Glu Tyr Trp Gly Trp Gly Gly Glu
260 265 270

Asp Asp Asp Ile Ala Thr Arg Val Arg Leu Ala Gly Met Lys Ile Ser
275 280 285

Arg Pro Pro Thr Ser Val Gly His Tyr Lys Met Val Lys His Arg Gly
290 295 300

Asp Lys Gly Asn Glu Glu Asn Pro His Arg Phe Asp Leu Leu Val Arg
305 310 315 320

Thr Gln Asn Ser Trp Thr Gln Asp Gly Met Asn Ser Leu Thr Tyr Gln
325 330 335

Leu Leu Ala Arg Glu Leu Gly Pro Leu Tyr Thr Asn Ile Thr Ala Asp
340 345 350

Ile Gly Thr Asp Pro Arg Gly Pro Arg Ala Pro Ser Gly Pro Arg Tyr
355 360 365

Pro Pro Gly Ser Ser Gln Ala Phe Arg Gln Glu Met Leu Gln Arg Arg
370 375 380

Pro Pro Ala Arg Pro Gly Pro Leu Ser Thr Ala Asn His Thr Ala Leu
385 390 395 400

Arg Gly Ser His

<210> 1073
<211> 217
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (68)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1073
Asn Lys Glu Gln Leu Met Asp Lys Ser Gly Ile Asp Ser Leu Asp His
1 5 10 15

Val Thr Ser Asp Ala Val Glu Leu Ala Asn Arg Ser Asp Asn Ser Ser
20 25 30

Asp Ser Ser Leu Phe Lys Thr Gln Cys Ile Pro Tyr Ser Pro Lys Gly

35 40 45

Glu Lys Arg Asn Pro Ile Arg Lys Phe Val Arg Thr Pro Glu Ser Val
50 55 60

His Ala Ser Xaa Ser Ser Ser Asp Ser Ser Phe Glu Pro Ile Pro Leu
65 70 75 80

Thr Ile Lys Ala Ile Phe Glu Arg Phe Lys Asn Arg Lys Lys Arg Tyr
85 90 95

Lys Lys Lys Lys Lys Arg Arg Tyr Gln Pro Thr Gly Arg Pro Arg Gly
100 105 110

Arg Pro Glu Gly Arg Arg Asn Pro Ile Tyr Ser Leu Ile Asp Lys Lys
115 120 125

Lys Gln Phe Arg Ser Arg Gly Ser Gly Phe Pro Phe Leu Glu Ser Glu
130 135 140

Asn Glu Lys Asn Ala Pro Trp Arg Lys Ile Leu Thr Phe Glu Gln Ala
145 150 155 160

Val Ala Arg Gly Phe Phe Asn Tyr Ile Glu Lys Leu Lys Tyr Glu His
165 170 175

His Leu Lys Glu Ser Leu Lys Gln Met Asn Val Gly Glu Asp Leu Glu
180 185 190

Asn Glu Asp Phe Asp Ser Arg Arg Tyr Lys Phe Leu Asp Asp Asp Gly
195 200 205

Ser Ile Ser Pro Ile Glu Glu Ser Thr
210 215

<210> 1074
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (110)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (122)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (123)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (125)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (128)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (147)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1074

```
Thr His Tyr Arg Ala Lys Leu Val Arg Leu Pro Gly Thr Gly Ser Gly
  1               5                  10                  15

Asn Ser Arg Val Asp Pro Arg Val Arg Glu Gln Pro Ser Pro Ala Ser
             20                  25                  30

Ser Ala Pro Gly Gln Leu Asn Ser Cys Gln Asp Val Leu Pro Ala Glu
         35                  40                  45

Pro Ala Ala Val Pro Thr Pro Thr Gln Val Ser Leu Thr Gln Val Ser
     50                  55                  60

Pro Lys Glu Pro Ser Thr Val Ser Ala Ser Ser Phe Leu Trp Leu Cys
 65                  70                  75                  80

Pro Lys Leu Trp Gly Leu Trp Pro Ser Ser Glu Gly Gly Cys Phe Leu
                 85                  90                  95

Asn His His Arg Arg His His Arg Cys Arg Arg Gln Arg Xaa Asn Ser
            100                 105                 110

Cys Asp Arg Ala Val Val Ser Lys Ala Xaa Xaa Leu Xaa Ala Ala Xaa
        115                 120                 125

Phe Trp Gly Leu Leu Leu Ile Gln Ile Leu Met Leu Arg Gln Ala Ile
    130                 135                 140

Phe Gly Xaa Asn Lys Asn Ser Gln Glu Ala Lys Asn Ser Pro Ile Trp
145                 150                 155                 160
```

Lys

<210> 1075
<211> 221
<212> PRT
<213> Homo sapiens

<400> 1075

```
Ser Ser Ser Trp His Ala Arg Tyr Thr Val Leu Thr Tyr Leu Gln Thr
  1               5                  10                  15

Met Val Phe Tyr Asn Leu Phe Ile Phe Leu Asn Asn Glu Asp Ala Val
             20                  25                  30

Lys Asp Ile Arg Trp Leu Val Ile Ser Leu Leu Glu Asp Glu Gln Leu
         35                  40                  45

Glu Val Arg Glu Met Ala Ala Thr Thr Leu Ser Gly Leu Leu Gln Cys
     50                  55                  60

Asn Phe Leu Thr Met Asp Ser Pro Met Gln Ile His Phe Glu Gln Leu
 65                  70                  75                  80

Cys Lys Thr Lys Leu Pro Lys Lys Arg Lys Arg Asp Pro Gly Ser Val
                 85                  90                  95

Gly Asp Thr Ile Pro Ser Ala Glu Leu Val Lys Arg His Ala Gly Val
            100                 105                 110

Leu Gly Leu Gly Ala Cys Val Leu Ser Ser Pro Tyr Asp Val Pro Thr
        115                 120                 125

Trp Met Pro Gln Leu Leu Met Asn Leu Ser Ala His Leu Asn Asp Pro
    130                 135                 140

Gln Pro Ile Glu Met Thr Val Lys Lys Thr Leu Ser Asn Phe Arg Arg
145                 150                 155                 160

Leu Thr Met Thr Thr Gly Arg Asn Ile Asn Ser Asn Ser Leu Met Thr
                165                 170                 175

Asn Cys Leu Phe Ser Pro Ile Phe Leu Cys His His Ala Ile Met His
            180                 185                 190

Arg Lys Met Thr Ser Pro His Phe Arg Leu Phe Ser Ser Lys Ile Pro
        195                 200                 205
```

His Pro Gln Val Pro Ser Val Val Ala Leu Cys Lys Phe
210 215 220

<210> 1076
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (135)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (163)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (166)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1076
Ala Arg Gly Ala Arg Val Arg Ala Cys Ala Ser Leu Gly Ser Trp Arg
1 5 10 15

Gly Pro Arg Gly Glu Gly Trp Lys Met Ser Met Asp Val Thr Phe Leu
20 25 30

Gly Thr Gly Ala Ala Tyr Pro Ser Pro Thr Arg Gly Ala Ser Ala Val
35 40 45

Val Leu Arg Cys Glu Gly Glu Xaa Trp Leu Phe Asp Cys Gly Glu Gly
50 55 60

Thr Gln Thr Gln Leu Met Lys Ser Gln Leu Lys Ala Gly Arg Ile Thr
65 70 75 80

Lys Ile Phe Ile Thr His Leu His Gly Asp His Phe Phe Gly Leu Pro
85 90 95

Gly Leu Leu Cys Thr Ile Ser Leu Gln Ser Gly Ser Met Val Ser Lys
100 105 110

Gln Pro Ile Glu Ile Tyr Gly Pro Val Gly Phe Gly Thr Leu Ser Gly
115 120 125

Glu Pro Trp Asn Ser Leu Xaa Arg Glu Leu Val Phe His Tyr Val Val
130 135 140

His Glu Leu Val Pro Thr Ala Asp Gln Cys Pro Ala Glu Gly Thr Lys
145 150 155 160

Arg Ile Xaa Ala Cys Xaa
165

<210> 1077
<211> 239
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (25)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1077
Gly Leu Arg Ala Leu Ser Gln His Thr Asp Leu Ser Pro Leu Ser Pro
1 5 10 15

Lys Thr Pro Ala Pro Ser Met Arg Xaa Lys Met Gly Asn Gly Thr Glu
20 25 30

Glu Asp Tyr Asn Phe Val Phe Lys Val Val Leu Ile Gly Glu Ser Gly
35 40 45

Val Gly Lys Thr Asn Leu Leu Ser Arg Phe Thr Arg Asn Glu Phe Ser
50 55 60

His Asp Ser Arg Thr Thr Ile Gly Val Glu Phe Ser Thr Arg Thr Val
65 70 75 80

Met Leu Gly Thr Ala Ala Val Lys Ala Gln Ile Trp Asp Thr Ala Gly
85 90 95

Leu Glu Arg Tyr Arg Ala Ile Thr Ser Ala Tyr Tyr Arg Gly Ala Val
100 105 110

Gly Ala Leu Leu Val Phe Asp Leu Thr Lys His Gln Thr Tyr Ala Val
115 120 125

Val Glu Arg Trp Leu Lys Glu Leu Tyr Asp His Ala Glu Ala Thr Ile

130 135 140

Val Val Met Leu Val Gly Asn Lys Ser Asp Leu Ser Gln Ala Arg Glu
145 150 155 160

Val Pro Thr Glu Glu Ala Arg Met Phe Ala Glu Asn Asn Gly Leu Leu
165 170 175

Phe Leu Glu Thr Ser Ala Leu Asp Ser Thr Asn Val Glu Leu Ala Phe
180 185 190

Glu Thr Val Leu Lys Glu Ile Phe Ala Lys Val Ser Lys Gln Arg Gln
195 200 205

Asn Ser Ile Arg Thr Asn Ala Ile Thr Ser Gly Ser Ala Gln Ala Gly
210 215 220

Gln Glu Pro Gly Pro Gly Glu Lys Arg Ala Cys Cys Ile Ser Leu
225 230 235

<210> 1078
<211> 171
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (123)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1078
Ile Leu Lys Gly Ser Ser Gly Ser Val Trp Leu Arg Asn Leu Gln Leu
1 5 10 15

Gly Leu Phe Gly Thr Ala Leu Gly Leu Val Gly Leu Trp Trp Ala Glu
20 25 30

Gly Thr Ala Val Ala Thr Arg Gly Phe Phe Phe Gly Tyr Thr Pro Ala
35 40 45

Val Trp Gly Val Val Leu Asn Gln Ala Phe Gly Gly Leu Leu Val Ala
50 55 60

Val Val Val Lys Tyr Ala Asp Asn Ile Leu Lys Gly Phe Ala Thr Ser
65 70 75 80

Leu Ser Ile Val Leu Ser Thr Val Ala Ser Ile Arg Leu Phe Gly Phe
85 90 95

His Val Asp Pro Leu Phe Ala Leu Gly Ala Gly Leu Val Ile Gly Ala
100 105 110

Val Tyr Leu Tyr Ser Leu Pro Arg Gly Ala Xaa Lys Ala Ile Ala Ser
115 120 125

Ala Ser Ala Ser Ala Ser Gly Pro Cys Val His Gln Gln Pro Pro Gly
130 135 140

Gln Pro Pro Pro Pro Gln Leu Ser Ser His Arg Gly Asp Leu Ile Thr
145 150 155 160

Glu Pro Phe Leu Pro Lys Ser Val Leu Val Lys
165 170

<210> 1079
<211> 141
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (59)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1079
Arg Arg Val Cys His Ser Ser Pro His Leu Ser Ser Pro Arg Ala Ala
1 5 10 15

Cys Glu Gln Gln Ala Val Ala Leu Thr Leu Gln Glu Asp Arg Ala Ser
20 25 30

Leu Thr Leu Ser Gly Gly Pro Ser Ala Leu Ala Phe Asp Leu Ser Lys
35 40 45

Val Pro Gly Pro Glu Ala Ala Pro Arg Leu Xaa Ala Leu Thr Leu Gly
50 55 60

Leu Ala Lys Arg Val Trp Ser Leu Glu Arg Arg Leu Ala Ala Ala Glu
65 70 75 80

Glu Thr Ala Val Ser Pro Arg Lys Ser Pro Arg Pro Ala Gly Pro Gln
85 90 95

Leu Phe Leu Pro Asp Pro Asp Pro Gln Arg Gly Gly Pro Gly Pro Gly
100 105 110

Val Arg Arg Arg Cys Pro Gly Glu Ser Leu Ile Asn Pro Gly Phe Lys
115 120 125

Ser Lys Lys Pro Ala Gly Gly Val Asp Phe Asp Glu Thr
    130   135   140

<210> 1080
<211> 359
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1080
Ala Val Glu Ser Arg Xaa Pro Gly Trp Asn His His Gly Ile Gln Phe
  1   5   10   15

Pro Cys Gly Ser Val Trp Leu Glu His Ala Ile Ala Met Ile Cys Gly
            20   25   30

Asn Val Cys Leu Trp Lys Gly Ala Pro Thr Thr Ser Leu Ile Ser Val
        35   40   45

Ala Val Thr Lys Ile Ile Ala Lys Val Leu Glu Asp Asn Lys Leu Pro
    50   55   60

Gly Ala Ile Cys Ser Leu Thr Cys Gly Gly Ala Asp Ile Gly Thr Ala
65   70   75   80

Met Ala Lys Asp Glu Arg Val Asn Leu Leu Ser Phe Thr Gly Ser Thr
                85   90   95

Gln Val Gly Lys Gln Val Gly Leu Met Val Gln Glu Arg Phe Gly Arg
            100   105   110

Ser Leu Leu Glu Leu Gly Gly Asn Asn Ala Ile Ile Ala Phe Glu Asp
        115   120   125

Ala Asp Leu Ser Leu Val Val Pro Ser Ala Leu Phe Ala Ala Val Gly
    130   135   140

Thr Ala Gly Gln Arg Cys Thr Thr Ala Arg Arg Leu Phe Ile His Glu
145   150   155   160

Ser Ile His Asp Glu Val Val Asn Arg Leu Lys Lys Ala Tyr Ala Gln
                165   170   175

Ile Arg Val Gly Asn Pro Trp Asp Pro Asn Val Leu Tyr Gly Pro Leu

180 185 190

His Thr Lys Gln Ala Val Ser Met Phe Leu Gly Ala Val Glu Glu Ala
195 200 205

Lys Lys Glu Gly Gly Thr Val Val Tyr Gly Gly Lys Val Met Asp Arg
210 215 220

Pro Gly Asn Tyr Val Glu Pro Thr Ile Val Thr Gly Leu Gly His Asp
225 230 235 240

Ala Ser Ile Ala His Thr Glu Thr Phe Ala Pro Ile Leu Tyr Val Phe
245 250 255

Lys Phe Lys Asn Glu Glu Glu Val Phe Ala Trp Asn Asn Glu Val Lys
260 265 270

Gln Gly Leu Ser Ser Ser Ile Phe Thr Lys Asp Leu Gly Arg Ile Phe
275 280 285

Arg Trp Leu Gly Pro Lys Gly Ser Asp Cys Gly Ile Val Asn Val Asn
290 295 300

Ile Pro Thr Ser Gly Ala Glu Ile Gly Gly Ala Phe Gly Gly Glu Lys
305 310 315 320

His Thr Gly Gly Gly Arg Glu Ser Gly Ser Asp Ala Trp Lys Gln Tyr
325 330 335

Met Arg Arg Ser Thr Cys Thr Ile Asn Tyr Ser Lys Asp Leu Pro Leu
340 345 350

Ala Gln Gly Ile Lys Phe Gln
355

<210> 1081
<211> 138
<212> PRT
<213> Homo sapiens

<400> 1081
Ala Val Pro Leu Leu Gly Arg Pro Thr Arg Pro Val Gly Pro Arg Ala
1 5 10 15

Ala Leu Thr Met Thr Gln Gln Gly Ala Ala Leu Gln Asn Tyr Asn Asn
20 25 30

Glu Leu Val Lys Cys Ile Glu Glu Leu Cys Gln Lys Arg Glu Glu Leu
35 40 45

Cys Arg Gln Ile Gln Glu Glu Glu Asp Glu Lys Gln Arg Leu Gln Asn
50 55 60

Glu Val Arg Gln Leu Thr Glu Lys Leu Ala Arg Val Asn Glu Asn Leu
65 70 75 80

Ala Arg Lys Ile Ala Ser Arg Asn Glu Phe Asp Arg Thr Ile Ala Glu
85 90 95

Thr Glu Ala Ala Tyr Leu Lys Ile Leu Glu Ser Ser Gln Thr Leu Leu
100 105 110

Ser Val Leu Lys Arg Glu Ala Gly Asn Leu Thr Lys Ala Thr Ala Pro
115 120 125

Asp Gln Lys Ser Ser Gly Gly Arg Asp Ser
130 135

<210> 1082
<211> 339
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1082
Ser Pro Ile Ser Asn Cys Glu Ile Thr Ile Thr Asp Pro Gly Lys Phe
1 5 10 15

Tyr Asn Ser Asn Ser Val Phe Ser Arg Gly Asn Met Ala Lys Val Phe
20 25 30

Ser Phe Ile Leu Val Thr Thr Ala Leu Xaa Met Gly Arg Glu Ile Ser
35 40 45

Ala Leu Glu Asp Cys Ala Gln Glu Gln Met Arg Leu Arg Ala Gln Val
50 55 60

Arg Leu Leu Glu Thr Arg Val Lys Gln Gln Gln Val Lys Ile Lys Gln
65 70 75 80

Leu Leu Gln Glu Asn Glu Val Gln Phe Leu Asp Lys Gly Asp Glu Asn
85 90 95

Thr Val Val Asp Leu Gly Ser Lys Arg Gln Tyr Ala Asp Cys Ser Glu

100 105 110

Ile Phe Asn Asp Gly Tyr Lys Leu Ser Gly Phe Tyr Lys Ile Lys Pro
115 120 125

Leu Gln Ser Pro Ala Glu Phe Ser Val Tyr Cys Asp Met Ser Asp Gly
130 135 140

Gly Gly Trp Thr Val Ile Gln Arg Arg Ser Asp Gly Ser Glu Asn Phe
145 150 155 160

Asn Arg Gly Trp Lys Asp Tyr Glu Asn Gly Phe Gly Asn Phe Val Gln
165 170 175

Lys His Gly Glu Tyr Trp Leu Gly Asn Lys Asn Leu His Phe Leu Thr
180 185 190

Thr Gln Glu Asp Tyr Thr Leu Lys Ile Asp Leu Ala Asp Phe Glu Lys
195 200 205

Asn Ser Arg Tyr Ala Gln Tyr Lys Asn Phe Lys Val Gly Asp Glu Lys
210 215 220

Asn Phe Tyr Glu Leu Asn Ile Gly Glu Tyr Ser Gly Thr Ala Gly Asp
225 230 235 240

Ser Leu Ala Gly Asn Phe His Pro Glu Val Gln Trp Trp Ala Ser His
245 250 255

Gln Arg Met Lys Phe Ser Thr Trp Asp Arg Asp His Asp Asn Tyr Glu
260 265 270

Gly Asn Cys Ala Glu Glu Asp Gln Ser Gly Trp Trp Phe Asn Arg Cys
275 280 285

His Ser Ala Asn Leu Asn Gly Val Tyr Tyr Ser Gly Pro Tyr Thr Ala
290 295 300

Lys Thr Asp Asn Gly Ile Val Trp Tyr Thr Trp His Gly Trp Trp Tyr
305 310 315 320

Ser Leu Lys Ser Val Val Met Lys Ile Arg Pro Asn Asp Phe Ile Pro
325 330 335

Asn Val Ile

<210> 1083
<211> 256

<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1083

```
Lys Ser Leu Asn Gly Pro Ala Asp Phe Glu Lys Arg Val Glu Gly Gly
 1               5                  10                  15

Gly Arg Pro Arg Ala Pro Leu Val Asn Ala Leu Leu Thr Ala Pro Glu
            20                  25                  30

Phe Leu Ile Tyr Thr Gly Cys Met Val Cys Val Phe Leu Phe Cys Phe
        35                  40                  45

Ser Pro Pro Ala Gly Leu Phe Xaa Gly Trp Gly Gly Gly Phe Ala Met
    50                  55                  60

Ser Asp Asp Asp Ser Arg Ala Ser Thr Ser Ser Ser Ser Ser Ser Ser
65                  70                  75                  80

Ser Asn Gln Gln Thr Glu Lys Glu Thr Asn Thr Pro Lys Lys Lys Glu
                85                  90                  95

Ser Lys Val Ser Met Ser Lys Asn Ser Lys Leu Leu Ser Thr Ser Ala
            100                 105                 110

Lys Arg Ile Gln Lys Glu Leu Ala Asp Ile Thr Leu Asp Pro Pro Pro
        115                 120                 125

Asn Cys Ser Ala Gly Pro Lys Gly Asp Asn Ile Tyr Glu Trp Arg Ser
    130                 135                 140

Thr Ile Leu Gly Pro Pro Gly Ser Val Tyr Glu Gly Gly Val Phe Phe
145                 150                 155                 160

Leu Asp Ile Thr Phe Thr Pro Glu Tyr Pro Phe Lys Pro Pro Lys Val
                165                 170                 175

Thr Phe Arg Thr Arg Ile Tyr His Cys Asn Ile Asn Ser Gln Gly Val
            180                 185                 190

Ile Cys Leu Asp Ile Leu Lys Asp Asn Trp Ser Pro Ala Leu Thr Ile
        195                 200                 205

Ser Lys Val Leu Leu Ser Ile Cys Ser Leu Leu Thr Asp Cys Asn Pro
    210                 215                 220
```

Ala Asp Pro Leu Val Gly Ser Ile Ala Thr Gln Tyr Met Thr Asn Arg
225 230 235 240

Ala Glu His Asp Arg Met Ala Arg Gln Trp Thr Lys Arg Tyr Ala Thr
245 250 255

<210> 1084
<211> 176
<212> PRT
<213> Homo sapiens

<400> 1084
Glu Lys Cys Val Ser Phe Ser Ala Val Leu Lys Ser Leu Ser Pro Val
1 5 10 15

Asp Pro Val Glu Pro Ile Ser Asn Ser Glu Pro Ser Met Asn Ser Asp
20 25 30

Met Gly Lys Val Ser Lys Asn Asp Thr Glu Glu Glu Ser Asn Lys Ser
35 40 45

Ala Thr Thr Asp Asn Glu Ile Ser Arg Thr Glu Tyr Leu Cys Glu Asn
50 55 60

Ser Leu Glu Gly Lys Asn Lys Asp Asn Ser Ser Asn Glu Val Phe Pro
65 70 75 80

Gln Gly Ala Glu Glu Arg Met Cys Tyr Gln Cys Glu Ser Glu Asp Glu
85 90 95

Pro Gln Ala Asp Gly Ser Gly Leu Thr Thr Ala Pro Pro Thr Pro Arg
100 105 110

Asp Ser Leu Gln Pro Ser Ile Lys Gln Arg Leu Ala Arg Leu Gln Leu
115 120 125

Ser Pro Asp Phe Thr Phe Thr Ala Gly Leu Ala Ala Glu Val Ala Ala
130 135 140

Arg Ser Leu Ser Phe Thr Thr Met Gln Glu Gln Thr Phe Gly Asp Glu
145 150 155 160

Glu Glu Glu Gln Ile Ile Glu Glu Asn Lys Asn Glu Ile Glu Glu Lys
165 170 175

<210> 1085
<211> 220
<212> PRT
<213> Homo sapiens

<400> 1085
His Arg Lys Ser Arg Pro Ala Asn His Cys Val Tyr Phe Tyr Gly Asp
1 5 10 15

Glu Ile Ser Phe Ser Cys His Glu Thr Ser Arg Phe Ser Ala Ile Cys
20 25 30

Gln Gly Asp Gly Thr Trp Ser Pro Arg Thr Pro Ser Cys Gly Asp Ile
35 40 45

Cys Asn Phe Pro Pro Lys Ile Ala His Gly His Tyr Lys Gln Ser Ser
50 55 60

Ser Tyr Ser Phe Phe Lys Glu Glu Ile Ile Tyr Glu Cys Asp Lys Gly
65 70 75 80

Tyr Ile Leu Val Gly Gln Ala Lys Leu Ser Cys Ser Tyr Ser His Trp
85 90 95

Ser Ala Pro Ala Pro Gln Cys Lys Ala Leu Cys Arg Lys Pro Glu Leu
100 105 110

Val Asn Gly Arg Leu Ser Val Asp Lys Asp Gln Tyr Val Glu Pro Glu
115 120 125

Asn Val Thr Ile Gln Cys Asp Ser Gly Tyr Gly Val Val Gly Pro Gln
130 135 140

Ser Ile Thr Cys Ser Gly Asn Arg Thr Trp Tyr Pro Glu Val Pro Lys
145 150 155 160

Cys Glu Trp Glu Thr Pro Glu Gly Cys Glu Gln Val Leu Thr Gly Lys
165 170 175

Arg Leu Met Gln Cys Leu Pro Asn Pro Glu Asp Val Lys Met Ala Leu
180 185 190

Glu Val Tyr Lys Leu Ser Leu Glu Ile Glu Gln Leu Glu Leu Gln Arg
195 200 205

Asp Ser Ala Arg Gln Ser Thr Leu Asp Lys Glu Leu
210 215 220

<210> 1086
<211> 133
<212> PRT
<213> Homo sapiens

<400> 1086
Val Lys Pro Ser Gly Gly Glu Gly Asp Val Ala Gln Arg Pro Arg Asp
1   5   10   15

Arg Leu Ser Ser Arg Leu Leu Gly Ser Pro Ala Trp Arg Arg Arg Leu
            20   25   30

Met Thr Glu Gly Pro Leu Ala Gly Ala Pro Val Cys Ile Phe Glu Gly
        35   40   45

Pro Gly Pro Pro Gly Gly Ala Gly Ser Tyr Ser Trp Gly Leu Gly Phe
    50   55   60

Arg Arg Ala Gly Gly Gly Ala Gly Leu Lys Ala Ala Leu Val Tyr Gly
65   70   75   80

Val Val Thr Gln Ser His Trp Gln Arg Trp Gly Leu Ala Val Ala Trp
                85   90   95

Gln Tyr Leu Gly Ile Ala Ser Thr Gly Asn Lys Asp Gly His Glu Gln
            100   105   110

Ser Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
        115   120   125

Lys Lys Lys Lys Lys
    130

<210> 1087
<211> 289
<212> PRT
<213> Homo sapiens

<400> 1087
Ile Leu Thr Tyr Lys Met Lys Gln Asp Ala Ser Arg Asn Ala Ala Tyr
1   5   10   15

Thr Val Asp Cys Glu Asp Tyr Val His Val Val Glu Phe Asn Pro Phe
            20   25   30

Glu Asn Gly Asp Ser Gly Asn Leu Ile Ala Tyr Gly Gly Asn Asn Tyr

35 40 45

Val Val Ile Gly Thr Cys Thr Phe Gln Glu Glu Glu Ala Asp Val Glu
50 55 60

Gly Ile Gln Tyr Lys Thr Leu Arg Thr Phe His His Gly Val Arg Val
65 70 75 80

Asp Gly Ile Ala Trp Ser Pro Glu Thr Arg Leu Asp Ser Leu Pro Pro
85 90 95

Val Ile Lys Phe Cys Thr Ser Ala Ala Asp Met Lys Ile Arg Leu Phe
100 105 110

Thr Ser Asp Leu Gln Asp Lys Asn Glu Tyr Lys Val Leu Glu Gly His
115 120 125

Thr Asp Phe Ile Asn Gly Leu Val Phe Asp Pro Lys Glu Gly Gln Glu
130 135 140

Ile Ala Ser Val Ser Asp Asp His Thr Cys Arg Ile Trp Asn Leu Glu
145 150 155 160

Gly Val Gln Thr Ala His Phe Val Leu His Ser Pro Gly Met Ser Val
165 170 175

Cys Trp His Pro Glu Glu Thr Phe Lys Leu Met Val Ala Glu Lys Asn
180 185 190

Gly Thr Ile Arg Phe Tyr Asp Leu Leu Ala Gln Gln Ala Ile Leu Ser
195 200 205

Leu Glu Ser Glu Gln Val Pro Leu Met Ser Ala His Trp Cys Leu Lys
210 215 220

Asn Thr Phe Lys Val Gly Ala Val Ala Gly Asn Asp Trp Leu Ile Trp
225 230 235 240

Asp Ile Thr Arg Ser Ser Tyr Pro Gln Asn Lys Arg Pro Val His Met
245 250 255

Asp Arg Ala Cys Leu Phe Arg Trp Ser Thr Ile Ser Glu Asn Leu Phe
260 265 270

Ala Thr Thr Gly Tyr Pro Gly Lys Met Gln Ala Ser Phe Lys Phe Ile
275 280 285

Ile

<210> 1088
<211> 836
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (677)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1088
Pro Thr Arg Pro Asn Trp Thr Gly Met Thr Asn Leu Leu Asp Ile Pro
1   5   10   15

Gly Leu Ser Ser Leu Ser Asp Thr Met Ile Met Asp Ser Ile Ala Ala
            20   25   30

Phe Leu Val Leu Pro Asn Arg Leu Leu Val Pro Leu Val Pro Asp Leu
        35   40   45

Gln Asp Val Ala Gln Leu Arg Ser Pro Leu Pro Arg Gly Ile Ile Arg
    50   55   60

Ile His Leu Leu Ala Ala Arg Gly Leu Ser Ser Lys Asp Lys Tyr Val
65   70   75   80

Lys Gly Leu Ile Glu Gly Lys Ser Asp Pro Tyr Ala Leu Val Arg Leu
                85   90   95

Gly Thr Gln Thr Phe Cys Ser Arg Val Ile Asp Glu Glu Leu Asn Pro
            100   105   110

Gln Trp Gly Glu Thr Tyr Glu Val Met Val His Glu Val Pro Gly Gln
        115   120   125

Glu Ile Glu Val Glu Val Phe Asp Lys Asp Pro Asp Lys Asp Asp Phe
    130   135   140

Leu Gly Arg Met Lys Leu Asp Val Gly Lys Val Leu Gln Ala Ser Val
145   150   155   160

Leu Asp Asp Trp Phe Pro Leu Gln Gly Gly Gln Gly Gln Val His Leu
                165   170   175

Arg Leu Glu Trp Leu Ser Leu Leu Ser Asp Ala Glu Lys Leu Glu Gln
            180   185   190

Val Leu Gln Trp Asn Trp Gly Val Ser Ser Arg Pro Asp Pro Pro Ser
        195   200   205

Ala Ala Ile Leu Val Val Tyr Leu Asp Arg Ala Gln Asp Leu Pro Leu
    210   215   220

Lys Lys Gly Asn Lys Glu Pro Asn Pro Met Val Gln Leu Ser Ile Gln
225   230   235   240

Asp Val Thr Gln Glu Ser Lys Ala Val Tyr Ser Thr Asn Cys Pro Val
                245   250   255

Trp Glu Glu Ala Phe Arg Phe Phe Leu Gln Asp Pro Gln Ser Gln Glu
            260   265   270

Leu Asp Val Gln Val Lys Asp Asp Ser Arg Ala Leu Thr Leu Gly Ala
        275   280   285

Leu Thr Leu Pro Leu Ala Arg Leu Leu Thr Ala Pro Glu Leu Ile Leu
    290   295   300

Asp Gln Trp Phe Gln Leu Ser Ser Ser Gly Pro Asn Ser Arg Leu Tyr
305   310   315   320

Met Lys Leu Val Met Arg Ile Leu Tyr Leu Asp Ser Ser Glu Ile Cys
                325   330   335

Phe Pro Thr Val Pro Gly Cys Pro Gly Ala Trp Asp Val Asp Ser Glu
            340   345   350

Asn Pro Gln Arg Gly Ser Ser Val Asp Ala Pro Pro Arg Pro Cys His
        355   360   365

Thr Thr Pro Asp Ser Gln Phe Gly Thr Glu His Val Leu Arg Ile His
    370   375   380

Val Leu Glu Ala Gln Asp Leu Ile Ala Lys Asp Arg Phe Leu Gly Gly
385   390   395   400

Leu Val Lys Gly Lys Ser Asp Pro Tyr Val Lys Leu Lys Leu Ala Gly
                405   410   415

Arg Ser Phe Arg Ser His Val Val Arg Glu Asp Leu Asn Pro Arg Trp
            420   425   430

Asn Glu Val Phe Glu Val Ile Val Thr Ser Val Pro Gly Gln Glu Leu
        435   440   445

Glu Val Glu Val Phe Asp Lys Asp Leu Asp Lys Asp Asp Phe Leu Gly
    450   455   460

Arg Cys Lys Val Arg Leu Thr Thr Val Leu Asn Ser Gly Phe Leu Asp
465   470   475   480

Glu Trp Leu Thr Leu Glu Asp Val Pro Ser Gly Arg Leu His Leu Arg
485 490 495

Leu Glu Arg Leu Thr Pro Arg Pro Thr Ala Ala Glu Leu Glu Glu Val
500 505 510

Leu Gln Val Asn Ser Leu Ile Gln Thr Gln Lys Ser Ala Glu Leu Ala
515 520 525

Ala Ala Leu Leu Ser Ile Tyr Met Glu Arg Ala Glu Asp Leu Pro Leu
530 535 540

Arg Lys Gly Thr Lys His Leu Ser Pro Tyr Ala Thr Leu Thr Val Gly
545 550 555 560

Asp Ser Ser His Lys Thr Lys Thr Ile Ser Gln Thr Ser Ala Pro Val
565 570 575

Trp Asp Glu Ser Ala Ser Phe Leu Ile Arg Lys Pro His Thr Glu Ser
580 585 590

Leu Glu Leu Gln Val Arg Gly Glu Gly Thr Gly Val Leu Gly Ser Leu
595 600 605

Ser Leu Pro Leu Ser Glu Leu Leu Val Ala Asp Gln Leu Cys Leu Asp
610 615 620

Arg Trp Phe Thr Leu Ser Ser Gly Gln Gly Gln Val Leu Leu Arg Ala
625 630 635 640

Gln Leu Gly Ile Leu Val Ser Gln His Ser Gly Val Glu Ala His Ser
645 650 655

His Ser Tyr Ser His Ser Ser Ser Ser Leu Ser Glu Glu Pro Glu Leu
660 665 670

Ser Gly Gly Pro Xaa His Ile Thr Ser Ser Ala Pro Glu Leu Arg Gln
675 680 685

Arg Leu Thr His Val Asp Ser Pro Leu Glu Ala Pro Ala Gly Pro Leu
690 695 700

Gly Gln Val Lys Leu Thr Leu Trp Tyr Tyr Ser Glu Glu Arg Lys Leu
705 710 715 720

Val Ser Ile Val His Gly Cys Arg Ser Leu Arg Gln Asn Gly Arg Asp
725 730 735

Pro Pro Asp Pro Tyr Val Ser Leu Leu Leu Leu Pro Asp Lys Asn Arg
740 745 750

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Gly Thr Lys Arg Arg Thr Ser Gln Lys Lys Arg Thr Leu Ser Pro Glu
        755                 760                 765

Phe Asn Glu Arg Phe Glu Trp Glu Leu Pro Leu Asp Glu Ala Gln Arg
    770                 775                 780

Arg Lys Leu Asp Val Ser Val Lys Ser Asn Ser Ser Phe Met Ser Arg
785                 790                 795                 800

Glu Arg Glu Leu Leu Gly Lys Val Gln Leu Asp Leu Ala Glu Thr Asp
                805                 810                 815

Leu Ser Gln Gly Val Ala Arg Trp Tyr Asp Leu Met Asp Asn Lys Asp
            820                 825                 830

Lys Gly Ser Ser
        835



<210> 1089
<211> 409
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (65)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (393)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (406)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1089
Arg Ser Ser Val Ala Ser Val His Thr Trp Arg Gln Arg Arg Gln Val
  1               5                  10                  15

Xaa Val Phe Val Leu Pro Ser Thr Ala Asn Met Lys Arg Pro Lys Leu
            20                  25                  30
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Lys Lys Ala Ser Lys Arg Met Thr Cys His Lys Arg Tyr Lys Ile Gln
35 40 45

Lys Lys Val Arg Glu His His Arg Lys Leu Arg Lys Glu Ala Lys Lys
50 55 60

Xaa Gly His Lys Lys Pro Arg Lys Asp Pro Gly Val Pro Asn Ser Ala
65 70 75 80

Pro Phe Lys Glu Ala Leu Leu Arg Glu Ala Glu Leu Arg Lys Gln Arg
85 90 95

Leu Glu Glu Leu Lys Gln Gln Gln Lys Leu Asp Arg Gln Lys Glu Leu
100 105 110

Glu Lys Lys Arg Lys Leu Glu Thr Asn Pro Asp Ile Lys Pro Ser Asn
115 120 125

Val Glu Pro Met Glu Lys Glu Phe Gly Leu Cys Lys Thr Glu Asn Lys
130 135 140

Ala Lys Ser Gly Lys Gln Asn Ser Lys Lys Leu Tyr Cys Gln Glu Leu
145 150 155 160

Lys Lys Val Ile Glu Ala Ser Asp Val Val Leu Glu Val Leu Asp Ala
165 170 175

Arg Asp Pro Leu Gly Cys Arg Cys Pro Gln Val Glu Glu Ala Ile Val
180 185 190

Gln Ser Gly Gln Lys Lys Leu Val Leu Ile Leu Asn Lys Ser Asp Leu
195 200 205

Val Pro Lys Glu Asn Leu Glu Ser Trp Leu Asn Tyr Leu Lys Lys Glu
210 215 220

Leu Pro Thr Val Val Phe Arg Ala Ser Thr Lys Pro Lys Asp Lys Gly
225 230 235 240

Lys Ile Thr Lys Arg Val Lys Ala Lys Lys Asn Ala Ala Pro Phe Arg
245 250 255

Ser Glu Val Cys Phe Gly Lys Glu Gly Leu Trp Lys Leu Leu Gly Gly
260 265 270

Phe Gln Glu Thr Cys Ser Lys Ala Ile Arg Val Gly Val Ile Gly Phe
275 280 285

Pro Asn Val Gly Lys Ser Ser Ile Ile Asn Ser Leu Lys Gln Glu Gln
290 295 300

Met Cys Asn Val Gly Val Ser Met Gly Leu Thr Arg Ser Met Gln Val
305 310 315 320

Val Pro Leu Asp Lys Gln Ile Thr Ile Ile Asp Ser Pro Ser Phe Ile
325 330 335

Val Ser Pro Leu Asn Ser Ser Ser Ala Leu Ala Leu Arg Ser Pro Ala
340 345 350

Ser Ile Glu Val Val Lys Pro Met Glu Ala Ala Ser Ala Ile Leu Ser
355 360 365

Gln Ala Asp Ala Arg Gln Val Val Leu Lys Tyr Thr Val Pro Gly Tyr
370 375 380

Arg Asn Ser Leu Gly Ile Phe Tyr Xaa Ala Cys Ser Glu Lys Arg Tyr
385 390 395 400

Ala Pro Lys Arg Trp Xaa Pro Lys Cys
405

<210> 1090
<211> 161
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1090
Pro Lys Asn Trp Xaa Thr Ala Arg Ala Asp His His Ala Ser Met Asn
1 5 10 15

Trp Val Pro Cys Gly His Ser Tyr Phe Gly Ala Thr Leu Asn Ser Phe
20 25 30

Ile His Val Leu Met Tyr Ser Tyr Tyr Gly Leu Ser Ser Val Pro Ser
35 40 45

Met Arg Pro Tyr Leu Trp Trp Xaa Glu Val His His Ser Gly Ala Ala
50 55 60

Ala Ser Val Cys Ala Asp Asn His Pro Asp Gln Leu Arg Gly His Leu
65 70 75 80

Ala Val His Ile Pro Ser Trp Leu Val Val Phe Pro Asp Trp Ile His
85 90 95

Asp Phe Pro Asp Cys Ser Leu His Lys Leu Leu His Ser Asp Leu Gln
100 105 110

Gln Glu Arg Gly Leu Pro Lys Glu Arg Pro Pro Glu Gly Pro Pro Glu
115 120 125

Trp Val His Gly Cys Cys Glu Trp Thr His Gln Gln Leu Phe Thr Pro
130 135 140

Gly Lys Gln Cys Glu Ala Lys Glu Ala Ala Glu Gly Leu Lys Ser Lys
145 150 155 160

Asn

<210> 1091
<211> 118
<212> PRT
<213> Homo sapiens

<400> 1091
Ser Lys Asn Ser Ala Arg Glu Glu Met Ala Ala Ser Ser Ser Ser Ser
1 5 10 15

Ser Ala Gly Gly Val Ser Gly Ser Ser Val Thr Gly Ser Gly Phe Ser
20 25 30

Val Ser Asp Leu Ala Pro Pro Arg Lys Ala Leu Phe Thr Tyr Pro Lys
35 40 45

Gly Ala Gly Glu Met Leu Glu Asp Gly Ser Glu Arg Phe Leu Cys Glu
50 55 60

Ser Val Phe Ser Tyr Gln Val Ala Ser Thr Leu Lys Gln Val Lys His
65 70 75 80

Asp Gln Gln Val Ala Arg Met Glu Lys Leu Ala Gly Leu Val Glu Glu
85 90 95

Leu Glu Ala Asp Glu Trp Arg Phe Lys Pro Ile Glu Gln Leu Leu Gly
100 105 110

Phe Thr Pro Ser Ser Gly
115

<210> 1092
<211> 198
<212> PRT
<213> Homo sapiens

<400> 1092
Ala Pro Phe Leu Ala Ala Gly Val Ser Met Gly Gly Met Leu Leu Leu
1 5 10 15

Asn Tyr Leu Gly Lys Ile Gly Ser Lys Thr Pro Leu Met Ala Ala Ala
20 25 30

Thr Phe Ser Val Gly Trp Asn Thr Phe Ala Cys Ser Glu Ser Leu Glu
35 40 45

Lys Pro Leu Asn Trp Leu Leu Phe Asn Tyr Tyr Leu Thr Thr Cys Leu
50 55 60

Gln Ser Ser Val Asn Lys His Arg His Met Phe Val Lys Gln Val Asp
65 70 75 80

Met Asp His Val Met Lys Ala Lys Ser Ile Arg Glu Phe Asp Lys Arg
85 90 95

Phe Thr Ser Val Met Phe Gly Tyr Gln Thr Ile Asp Asp Tyr Tyr Thr
100 105 110

Asp Ala Ser Pro Ser Pro Arg Leu Lys Ser Val Gly Ile Pro Val Leu
115 120 125

Cys Leu Asn Ser Val Asp Asp Val Phe Ser Pro Ser His Ala Ile Pro
130 135 140

Ile Glu Thr Ala Lys Gln Asn Pro Asn Val Ala Leu Val Leu Thr Ser
145 150 155 160

Tyr Gly Gly His Ile Gly Phe Leu Glu Gly Ile Trp Pro Arg Gln Ser
165 170 175

Thr Tyr Met Asp Arg Val Phe Lys Gln Phe Val Gln Ala Met Val Glu
180 185 190

His Gly His Glu Leu Ser
195

<210> 1093
<211> 36
<212> PRT
<213> Homo sapiens

<400> 1093
Pro Gly Trp Ser Arg Ser Pro Gly Trp Ser Arg Ser Pro Gly Trp Ser
1 5 10 15

Arg Ser Pro Asp Val Val Ile His Pro Pro Arg Pro Pro Lys Met Leu
20 25 30

Gly Leu Gln Val
35

<210> 1094
<211> 615
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (21)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (113)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (132)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (155)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (156)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (157)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1094
Tyr Xaa Gln Leu Val Leu Leu Gln Val Pro Val Arg Ile Pro Gly Ser
1   5   10   15

Thr His Ala Ser Xaa Asp Ala Trp Val Ala Arg Gln Leu Ala Lys Pro
            20   25   30

Asp Asn Thr Leu Phe Val Asn Arg Thr Leu Phe Asp Gln Val Leu Glu
        35   40   45

Phe Leu Cys Ser Pro Asp Asp Asp Ser Arg His Ser Glu Arg Gln Gln
    50   55   60

Val Leu Leu Glu Leu Leu Gln Ala Gly Gly Ile Val Gln Phe Glu Glu
65   70   75   80

Ser Arg Leu Ile Arg Met Ala Glu Lys Ala Glu Phe Tyr Gln Ile Cys
                85   90   95

Glu Phe Met Tyr Glu Arg Glu His Gln Tyr Asp Lys Ile Ile Asp Cys
            100   105   110

Xaa Leu Arg Asp Pro Leu Arg Glu Glu Glu Val Phe Asn Tyr Ile His
        115   120   125

Asn Ile Leu Xaa Ile Pro Gly His Ser Ala Glu Glu Lys Gln Ser Val
    130   135   140

Trp Gln Lys Ala Met Asp His Ile Glu Glu Xaa Xaa Xaa Leu Lys Pro
145   150   155   160

Cys Lys Ala Ala Glu Leu Val Ala Thr His Phe Ser Gly His Ile Glu
                165   170   175

Thr Val Ile Lys Lys Leu Gln Asn Gln Val Leu Leu Phe Lys Phe Leu
            180   185   190

Arg Ser Leu Leu Asp Pro Arg Glu Gly Ile His Val Asn Gln Glu Leu
        195   200   205

Leu Gln Ile Ser Pro Cys Ile Thr Glu Gln Phe Ile Glu Leu Leu Cys
    210   215   220

Gln Phe Asn Pro Thr Gln Val Ile Glu Thr Leu Gln Val Leu Glu Cys

225 230 235 240

Tyr Arg Leu Glu Glu Thr Ile Gln Ile Thr Gln Lys Tyr Gln Leu His
245 250 255

Glu Val Thr Ala Tyr Leu Leu Glu Lys Lys Gly Asp Ile His Gly Ala
260 265 270

Phe Leu Ile Met Leu Glu Arg Leu Gln Ser Lys Leu Gln Glu Val Thr
275 280 285

His Gln Gly Glu Asn Thr Lys Glu Asp Pro Ser Leu Lys Asp Val Glu
290 295 300

Asp Thr Met Val Glu Thr Ile Ala Leu Cys Gln Arg Asn Ser His Asn
305 310 315 320

Leu Asn Gln Gln Gln Arg Glu Ala Leu Trp Phe Pro Leu Leu Glu Ala
325 330 335

Met Met Ala Pro Gln Lys Leu Ser Ser Ser Ala Ile Pro His Leu His
340 345 350

Ser Glu Ala Leu Lys Ser Leu Thr Met Gln Val Leu Asn Ser Met Ala
355 360 365

Ala Phe Ile Ala Leu Pro Ser Ile Leu Gln Arg Ile Leu Gln Asp Pro
370 375 380

Val Tyr Gly Lys Gly Lys Leu Gly Glu Ile Gln Gly Leu Ile Leu Gly
385 390 395 400

Met Leu Asp Thr Phe Asn Tyr Glu Gln Thr Leu Leu Glu Thr Thr Thr
405 410 415

Ser Leu Leu Asn Gln Asp Leu His Trp Ser Leu Cys Asn Leu Arg Ala
420 425 430

Ser Val Thr Arg Gly Leu Asn Pro Lys Gln Asp Tyr Cys Ser Ile Cys
435 440 445

Leu Gln Gln Tyr Lys Arg Arg Gln Glu Met Ala Asp Glu Ile Ile Val
450 455 460

Phe Ser Cys Gly His Leu Tyr His Ser Phe Cys Leu Gln Asn Lys Glu
465 470 475 480

Cys Thr Val Glu Phe Glu Gly Gln Thr Arg Trp Thr Cys Tyr Lys Cys
485 490 495

Ser Ser Ser Asn Lys Val Gly Lys Leu Ser Glu Asn Ser Ser Glu Ile

500 505 510

Lys Lys Gly Arg Ile Thr Pro Ser Gln Val Lys Met Ser Pro Ser Tyr
515 520 525

His Gln Ser Lys Gly Asp Pro Thr Ala Lys Lys Gly Thr Ser Glu Pro
530 535 540

Val Leu Asp Pro Gln Gln Ile Gln Ala Phe Asp Gln Leu Cys Arg Leu
545 550 555 560

Tyr Arg Gly Ser Ser Arg Leu Ala Leu Leu Thr Glu Leu Ser Gln Asn
565 570 575

Arg Ser Ser Glu Ser Tyr Arg Pro Phe Ser Gly Ser Gln Ser Ala Pro
580 585 590

Ala Phe Asn Ser Ile Phe Gln Asn Glu Asn Phe Gln Leu Gln Leu Ile
595 600 605

Pro Pro Pro Val Thr Glu Asp
610 615

<210> 1095
<211> 264
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1095
Trp Xaa Ser Thr Thr Ile Trp Lys Ala Gly Pro Pro Ala Gly Thr Gly
1 5 10 15

Pro Glu Phe Pro Gly Arg Pro Thr Arg Pro Xaa Thr Arg Gly Phe Trp
20 25 30

Phe Cys Ser Ser Val Trp Val Ser Ser Arg Leu Leu Lys Met Asn Arg
35 40 45

Leu Phe Gly Lys Ala Lys Pro Lys Ala Pro Pro Pro Ser Leu Thr Asp

50 55 60

Cys Ile Gly Thr Val Asp Ser Arg Ala Glu Ser Ile Asp Lys Lys Ile
65 70 75 80

Ser Arg Leu Asp Ala Glu Leu Val Lys Tyr Lys Asp Gln Ile Lys Lys
85 90 95

Met Arg Glu Gly Pro Ala Lys Asn Met Val Lys Gln Lys Ala Leu Arg
100 105 110

Val Leu Lys Gln Lys Arg Met Tyr Glu Gln Gln Arg Asp Asn Leu Ala
115 120 125

Gln Gln Ser Phe Asn Met Glu Gln Ala Asn Tyr Thr Ile Gln Ser Leu
130 135 140

Lys Asp Thr Lys Thr Thr Val Asp Ala Met Lys Leu Gly Val Lys Glu
145 150 155 160

Met Lys Lys Ala Tyr Lys Gln Val Lys Ile Asp Gln Ile Glu Asp Leu
165 170 175

Gln Asp Gln Leu Glu Asp Met Met Glu Asp Ala Asn Glu Ile Gln Glu
180 185 190

Ala Leu Ser Arg Ser Tyr Gly Thr Pro Glu Leu Asp Glu Asp Asp Leu
195 200 205

Glu Ala Glu Leu Asp Ala Leu Gly Asp Glu Leu Leu Ala Asp Glu Asp
210 215 220

Ser Ser Tyr Leu Asp Glu Ala Ala Ser Ala Pro Ala Ile Pro Glu Gly
225 230 235 240

Val Pro Thr Asp Thr Lys Asn Lys Asp Gly Val Leu Val Asp Glu Phe
245 250 255

Gly Leu Pro Gln Ile Pro Ala Ser
260

<210> 1096
<211> 244
<212> PRT
<213> Homo sapiens

<400> 1096
Ser Cys Cys Phe Leu Lys Arg Leu Gln Ala Ser Phe Pro Arg Thr Ala
1 5 10 15

Val Ser Phe Glu Pro Leu Ala Gly Asp Met Pro Arg Gly Arg Lys Ser
20 25 30

Arg Arg Arg Arg Asn Ala Arg Ala Ala Glu Glu Asn Arg Asn Asn Arg
35 40 45

Lys Ile Gln Ala Ser Glu Ala Ser Glu Thr Pro Met Ala Ala Ser Val
50 55 60

Val Ala Ser Thr Pro Glu Asp Asp Leu Ser Gly Pro Glu Glu Asp Pro
65 70 75 80

Ser Thr Pro Glu Glu Ala Ser Thr Thr Pro Glu Glu Ala Ser Ser Thr
85 90 95

Ala Gln Ala Gln Lys Pro Ser Val Pro Arg Ser Asn Phe Gln Gly Thr
100 105 110

Lys Lys Ser Leu Leu Met Ser Ile Leu Ala Leu Ile Phe Ile Met Gly
115 120 125

Asn Ser Ala Lys Glu Ala Leu Val Trp Lys Val Leu Gly Lys Leu Gly
130 135 140

Met Gln Pro Gly Arg Gln His Ser Ile Phe Gly Asp Pro Lys Lys Ile
145 150 155 160

Val Thr Glu Glu Phe Val Arg Arg Gly Tyr Leu Ile Tyr Lys Pro Val
165 170 175

Pro Arg Ser Ser Pro Val Glu Tyr Glu Phe Phe Trp Gly Pro Arg Ala
180 185 190

His Val Glu Ser Ser Lys Leu Lys Val Met His Phe Val Ala Arg Val
195 200 205

Arg Asn Arg Cys Ser Lys Asp Trp Pro Cys Asn Tyr Asp Trp Asp Ser
210 215 220

Asp Asp Asp Ala Glu Val Glu Ala Ile Leu Asn Ser Gly Ala Arg Gly
225 230 235 240

Tyr Ser Ala Pro

<210> 1097
<211> 132
<212> PRT

<213> Homo sapiens

<400> 1097
Ala Thr Met Val Arg Met Asn Val Leu Ala Asp Ala Leu Lys Ser Ile
1 5 10 15

Asn Asn Ala Glu Lys Arg Gly Lys Arg Gln Val Leu Ile Arg Pro Cys
20 25 30

Ser Lys Val Ile Val Arg Phe Leu Thr Val Met Met Lys His Gly Tyr
35 40 45

Ile Gly Glu Phe Glu Ile Ile Asp Asp His Arg Ala Gly Lys Ile Val
50 55 60

Val Asn Leu Thr Gly Arg Leu Asn Lys Cys Gly Val Ile Ser Pro Arg
65 70 75 80

Phe Asp Val Gln Leu Lys Asp Leu Glu Lys Trp Gln Asn Asn Leu Leu
85 90 95

Pro Ser Arg Gln Phe Gly Phe Ile Val Leu Thr Thr Ser Ala Gly Ile
100 105 110

Met Asp His Glu Glu Ala Arg Arg Lys His Thr Gly Gly Lys Ile Leu
115 120 125

Gly Phe Phe Phe
130

<210> 1098
<211> 371
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (44)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (186)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1098
Ala Arg His Thr Pro Ala Gln Arg His Asp His Pro Gln Glu Gly Asn
1 5 10 15

Ile Pro Val Cys Val Gln Leu Ala Val Cys Ala Leu Pro Leu Pro Val
20 25 30

Val Pro Gly Pro Glu His Cys Gly Pro Gln Arg Xaa Leu Gln Pro Leu
35 40 45

Val Tyr Pro Leu Ala Gln Val Ile Ile Gly Cys Ile Lys Leu Ile Pro
50 55 60

Thr Ala Arg Phe Tyr Pro Leu Arg Met His Cys Ile Arg Ala Leu Thr
65 70 75 80

Leu Leu Ser Gly Ser Ser Gly Ala Phe Ile Pro Val Leu Pro Phe Ile
85 90 95

Leu Glu Met Phe Gln Gln Val Asp Phe Asn Arg Lys Pro Gly Arg Met
100 105 110

Ser Ser Lys Pro Ile Asn Phe Ser Val Ile Leu Lys Leu Ser Asn Val
115 120 125

Asn Leu Gln Glu Lys Ala Tyr Arg Asp Gly Leu Val Glu Gln Leu Tyr
130 135 140

Asp Leu Thr Leu Glu Tyr Leu His Ser Gln Ala His Cys Ile Gly Phe
145 150 155 160

Pro Glu Leu Val Leu Pro Val Val Leu Gln Leu Lys Ser Phe Leu Arg
165 170 175

Glu Cys Lys Val Ala Asn Tyr Cys Arg Xaa Val Gln Gln Leu Leu Gly
180 185 190

Lys Val Gln Glu Asn Ser Ala Tyr Ile Cys Ser Arg Arg Gln Arg Val
195 200 205

Ser Phe Gly Val Ser Glu Gln Gln Ala Val Glu Ala Trp Glu Lys Leu
210 215 220

Thr Arg Glu Glu Gly Thr Pro Leu Thr Leu Tyr Tyr Ser His Trp Arg
225 230 235 240

Lys Leu Arg Asp Arg Glu Ile Gln Leu Glu Ile Ser Gly Lys Glu Arg
245 250 255

Leu Glu Asp Leu Asn Phe Pro Glu Ile Lys Arg Arg Lys Met Ala Asp
260 265 270

Arg Lys Asp Glu Asp Arg Lys Gln Phe Lys Asp Leu Phe Asp Leu Asn
275 280 285

Ser Ser Glu Glu Asp Asp Thr Glu Gly Phe Ser Glu Arg Gly Ile Leu
290 295 300

Arg Pro Leu Ser Thr Arg His Gly Val Glu Asp Asp Glu Glu Asp Glu
305 310 315 320

Glu Glu Gly Glu Glu Asp Ser Ser Asn Ser Glu Gly Glu Trp Ser Trp
325 330 335

Asp Gly Asp Pro Asp Ala Glu Ala Gly Leu Ala Pro Gly Glu Leu Gln
340 345 350

Gln Leu Ala Gln Gly Pro Glu Asp Glu Leu Glu Asp Leu Gln Leu Ser
355 360 365

Glu Asp Asp
370

<210> 1099
<211> 321
<212> PRT
<213> Homo sapiens

<400> 1099
Glu Arg Thr Leu Gly Gln Pro Gly Phe Leu Gly Cys Pro Arg Gln Pro
1 5 10 15

His Thr Ala Met His Tyr Pro Thr Ala Leu Leu Phe Leu Ile Leu Ala
20 25 30

Asn Gly Ala Gln Ala Phe Arg Ile Cys Ala Phe Asn Ala Gln Arg Leu
35 40 45

Thr Leu Ala Lys Val Ala Arg Glu Gln Val Met Asp Thr Leu Val Arg
50 55 60

Ile Leu Ala Arg Cys Asp Ile Met Val Leu Gln Glu Val Val Asp Ser
65 70 75 80

Ser Gly Ser Ala Ile Pro Leu Leu Leu Arg Glu Leu Asn Arg Phe Asp
85 90 95

Gly Ser Gly Pro Tyr Ser Thr Leu Ser Ser Pro Gln Leu Gly Arg Ser
100 105 110

Thr Tyr Met Glu Thr Tyr Val Tyr Phe Tyr Arg Ser His Lys Thr Gln
115 120 125

Val Leu Ser Ser Tyr Val Tyr Asn Asp Glu Asp Asp Val Phe Ala Arg

130 135 140

Glu Pro Phe Val Ala Gln Phe Ser Leu Pro Ser Asn Val Leu Pro Ser
145 150 155 160

Leu Val Leu Val Pro Leu His Thr Thr Pro Lys Ala Val Glu Lys Glu
165 170 175

Leu Asn Ala Leu Tyr Asp Val Phe Leu Glu Val Ser Gln His Trp Gln
180 185 190

Ser Lys Asp Val Ile Leu Leu Gly Asp Phe Asn Ala Asp Cys Ala Ser
195 200 205

Leu Thr Lys Lys Arg Leu Asp Lys Leu Glu Leu Arg Thr Glu Pro Gly
210 215 220

Phe His Trp Val Ile Ala Asp Gly Glu Asp Thr Thr Val Arg Ala Ser
225 230 235 240

Thr His Cys Thr Tyr Asp Arg Val Val Leu His Gly Glu Arg Cys Arg
245 250 255

Ser Leu Leu His Thr Ala Ala Ala Phe Asp Phe Pro Thr Ser Phe Gln
260 265 270

Leu Thr Glu Glu Glu Ala Leu Asn Ile Ser Asp His Tyr Pro Val Glu
275 280 285

Val Glu Leu Lys Leu Ser Gln Ala His Ser Val Gln Pro Leu Ser Leu
290 295 300

Thr Val Leu Leu Leu Leu Ser Leu Leu Ser Pro Gln Leu Cys Pro Ala
305 310 315 320

Ala

<210> 1100
<211> 60
<212> PRT
<213> Homo sapiens

<400> 1100
Leu Leu Leu Cys Val Phe Tyr Ile Ala Cys Phe Cys Lys Asn Met Leu
1 5 10 15

Gly Asp Glu Arg Leu Val Leu Glu Arg Lys Cys Ser Ser Val Gln Arg
20 25 30

Met His Phe Leu Pro Leu Ile Leu Glu Lys Thr Phe Thr Val Ile Tyr
35 40 45

Met Val Phe Cys Lys Arg Thr Ile Asn Arg Thr Phe
50 55 60

<210> 1101
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (162)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (170)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1101
Phe Gly Thr Ser Tyr Ile Gly Gly Leu Leu Ser Ala Phe Tyr Leu Thr
1 5 10 15

Gly Glu Glu Val Phe Arg Ile Lys Ala Ile Arg Leu Gly Glu Lys Leu
20 25 30

Leu Pro Ala Phe Asn Thr Pro Thr Gly Ile Pro Lys Gly Val Val Ser
35 40 45

Phe Lys Ser Gly Asn Trp Gly Trp Ala Thr Ala Gly Ser Ser Ser Ile
50 55 60

Leu Ala Glu Phe Gly Ser Leu His Leu Glu Phe Leu His Leu Thr Glu
65 70 75 80

Leu Ser Gly Asn Gln Val Phe Ala Glu Lys Val Arg Asn Ile Arg Lys
85 90 95

Val Leu Arg Lys Ile Glu Lys Pro Phe Gly Leu Tyr Pro Asn Phe Leu
100 105 110

Ser Pro Val Ser Gly Asn Trp Val Gln His His Val Ser Val Gly Gly
115 120 125

Leu Gly Asp Ser Phe Tyr Glu Tyr Leu Ile Lys Ser Trp Leu Met Ser
130 135 140

Gly Lys Thr Asp Met Glu Ala Lys Asn Met Tyr Tyr Glu Ala Leu Glu
145 150 155 160

Ala Xaa Arg Asp Leu Leu Ala Glu Cys Xaa Ser Arg Gly Ala Asp Leu
165 170 175

His Cys Arg Val Ala Arg Gly Asp Ser Gly Pro Gln Asp Gly Ala Pro
180 185 190

Gly Leu Phe Leu Arg Gly His Asp Arg Pro Trp Pro Glu Asp Ala Lys
195 200 205

Glu Glu Lys Arg Ala His Tyr Arg Glu Leu Ala Ala Gln Ile Thr Lys
210 215 220

Thr Cys His Glu Ser Tyr Ala Arg Ser Asp Thr Lys Leu Gly Pro Glu
225 230 235 240

Ala Ser Gly Leu Thr Pro Ala Glu Arg Pro Trp Pro Pro Ser
245 250

<210> 1102
<211> 233
<212> PRT
<213> Homo sapiens

<400> 1102
Gly Pro Gly Trp Tyr Pro Ala Pro Leu Arg Leu Phe His Ser Asp Pro
1 5 10 15

Trp Gly His Ala Gln Pro Gly Ala Lys Arg His Arg Ile Pro Glu Pro
20 25 30

Glu Ala Ala Val Leu Phe Arg Gln Met Ala Thr Ala Leu Ala His Cys
35 40 45

His Gln His Gly Leu Val Leu Arg Asp Leu Lys Leu Cys Arg Phe Val
50 55 60

Phe Ala Asp Arg Glu Arg Lys Lys Leu Val Leu Glu Asn Leu Glu Asp
65 70 75 80

Ser Cys Val Leu Thr Gly Pro Asp Asp Ser Leu Trp Asp Lys His Ala
85 90 95

Cys Pro Ala Tyr Val Gly Pro Glu Ile Leu Ser Ser Arg Ala Ser Tyr
100 105 110

Ser Gly Lys Ala Ala Asp Val Trp Ser Leu Gly Val Ala Leu Phe Thr
115 120 125

Met Leu Ala Gly His Tyr Pro Phe Gln Asp Ser Glu Pro Val Leu Leu
130 135 140

Phe Gly Lys Ile Arg Arg Gly Ala Tyr Ala Leu Pro Ala Gly Leu Ser
145 150 155 160

Ala Pro Ala Arg Cys Leu Val Arg Cys Leu Leu Arg Arg Glu Pro Ala
165 170 175

Glu Arg Leu Thr Ala Thr Gly Ile Leu Leu His Pro Trp Leu Arg Gln
180 185 190

Asp Pro Met Pro Leu Ala Pro Thr Arg Ser His Leu Trp Glu Ala Ala
195 200 205

Gln Val Val Pro Asp Gly Leu Gly Leu Asp Glu Ala Arg Glu Glu Glu
210 215 220

Gly Asp Arg Glu Val Val Leu Tyr Gly
225 230

<210> 1103
<211> 330
<212> PRT
<213> Homo sapiens

<400> 1103
Cys Gln Leu Arg Ser Ala Ala Gly Val Pro Ser Ser Val Ser Val Ser
1 5 10 15

Pro Arg Asp Pro Ile Ala Met Glu Leu Ser Asp Ala Asn Leu Gln Thr
20 25 30

Leu Thr Glu Tyr Leu Lys Lys Thr Leu Asp Pro Asp Pro Ala Ile Arg
35 40 45

Arg Pro Ala Glu Lys Phe Leu Glu Ser Val Glu Gly Asn Gln Asn Tyr
50 55 60

Pro Leu Leu Leu Leu Thr Leu Leu Glu Lys Ser Gln Asp Asn Val Ile
65 70 75 80

Lys Val Cys Ala Ser Val Thr Phe Lys Asn Tyr Ile Lys Arg Asn Trp
85 90 95

Arg Ile Val Glu Asp Glu Pro Asn Lys Ile Cys Glu Ala Asp Arg Val

100 105 110

Ala Ile Lys Ala Asn Ile Val His Leu Met Leu Ser Ser Pro Glu Gln
115 120 125

Ile Gln Lys Gln Leu Ser Asp Ala Ile Ser Ile Ile Gly Arg Glu Asp
130 135 140

Phe Pro Gln Lys Trp Pro Asp Leu Leu Thr Glu Met Val Asn Arg Phe
145 150 155 160

Gln Ser Gly Asp Phe His Val Ile Asn Gly Val Leu Arg Thr Ala His
165 170 175

Ser Leu Phe Lys Arg Tyr Arg His Glu Phe Lys Ser Asn Glu Leu Trp
180 185 190

Thr Glu Ile Lys Leu Val Leu Asp Ala Phe Ala Leu Pro Leu Thr Asn
195 200 205

Leu Phe Lys Ala Thr Ile Glu Leu Cys Ser Thr His Ala Asn Asp Ala
210 215 220

Ser Ala Leu Arg Ile Leu Phe Ser Ser Leu Ile Leu Ile Ser Lys Leu
225 230 235 240

Phe Tyr Ser Leu Asn Phe Gln Asp Leu Pro Glu Phe Phe Glu Asp Asn
245 250 255

Met Glu Thr Trp Met Asn Asn Phe His Thr Leu Leu Thr Leu Asp Asn
260 265 270

Lys Leu Leu Gln Thr Asp Asp Glu Glu Glu Ala Gly Leu Leu Glu Leu
275 280 285

Leu Lys Ser Gln Ile Cys Asp Asn Ala Ala Leu Tyr Ala Gln Lys Tyr
290 295 300

Asp Glu Glu Phe Gln Arg Tyr Leu Pro Arg Phe Val Thr Ala Ile Trp
305 310 315 320

Glu Phe Thr Ser Tyr Asn Gly Ser Arg Gly
325 330

<210> 1104
<211> 180
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (150)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (167)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (171)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (175)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (177)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (180)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1104
Gly Thr Ser Pro Gly Arg Gly Gly Xaa Gly Val Gly Leu Arg Gly Leu
1 5 10 15

Ser Ser Leu Gln Ala Pro Gln Pro Ser Arg Val Pro Trp Pro Met Ala
20 25 30

Ala Tyr Ser Tyr Arg Pro Gly Pro Gly Ala Gly Pro Gly Pro Ala Ala
35 40 45

Gly Ala Ala Leu Pro Asp Gln Ser Phe Leu Trp Asn Val Phe Gln Arg
50 55 60

Val Asp Lys Asp Arg Ser Gly Val Ile Ser Asp Thr Glu Leu Gln Gln
65 70 75 80

Ala Leu Ser Asn Gly Thr Trp Thr Pro Phe Asn Pro Val Thr Val Arg
85 90 95

Ser Ile Ile Ser Met Phe Asp Arg Glu Asn Lys Ala Gly Val Asn Phe
100 105 110

Ser Glu Phe Thr Gly Val Trp Lys Tyr Ile Thr Asp Trp Gln Asn Val
115 120 125

Phe Arg Thr Tyr Asp Arg Asp Asn Ser Gly Met Ile Asp Lys Asn Glu
130 135 140

Leu Lys Gln Ala Leu Xaa Val Ser Ala Thr Gly Ser Leu Thr Ser Ser
145 150 155 160

Thr Thr Ser Ser Phe Glu Xaa Leu Thr Gly Xaa Gly Arg Gly Xaa Ser
165 170 175

Xaa Ser Thr Xaa
180

<210> 1105
<211> 241
<212> PRT
<213> Homo sapiens

<400> 1105
Thr Thr Arg Phe Pro Ser Gly Gln Pro Leu Lys Pro Arg Pro Thr Leu
1 5 10 15

Thr Ala Ala Gly Pro Arg Pro Gly Leu Leu Cys Phe Thr Ile Tyr Ile
20 25 30

Met Asn Pro Ser Met Lys Gln Lys Gln Glu Glu Ile Lys Glu Asn Ile
35 40 45

Lys Asn Ser Ser Val Pro Arg Arg Thr Leu Lys Met Ile Gln Pro Ser
50 55 60

Ala Ser Gly Ser Leu Val Gly Arg Glu Asn Glu Leu Ser Ala Gly Leu
65 70 75 80

Ser Lys Arg Lys His Arg Asn Asp His Leu Thr Ser Thr Thr Ser Ser
85 90 95

Pro Gly Val Ile Val Pro Glu Ser Ser Glu Asn Lys Asn Leu Gly Gly
100 105 110

Val Thr Gln Glu Ser Phe Asp Leu Met Ile Lys Glu Asn Pro Ser Ser

115 120 125

Gln Tyr Trp Lys Glu Val Ala Glu Lys Arg Arg Lys Ala Leu Tyr Glu
130 135 140

Ala Leu Lys Glu Asn Glu Lys Leu His Lys Glu Ile Glu Gln Lys Asp
145 150 155 160

Asn Glu Ile Ala Arg Leu Lys Lys Glu Asn Lys Glu Leu Ala Glu Val
165 170 175

Ala Glu His Val Gln Tyr Met Ala Glu Leu Ile Glu Arg Leu Asn Gly
180 185 190

Glu Pro Leu Asp Asn Phe Glu Ser Leu Asp Asn Gln Glu Phe Asp Ser
195 200 205

Glu Glu Glu Thr Val Glu Asp Ser Leu Val Glu Asp Ser Glu Ile Gly
210 215 220

Thr Cys Ala Glu Gly Thr Val Ser Ser Ser Thr Asp Ala Lys Pro Cys
225 230 235 240

Ile

<210> 1106
<211> 88
<212> PRT
<213> Homo sapiens

<400> 1106
Phe His Thr Glu Phe Ile Thr Ile Trp Asp Val Arg Gln Cys Ser Asn
1 5 10 15

Lys His Cys Gln His Val Asn Phe Leu Lys Ser Val Gly His Ile Ala
20 25 30

Lys Asn Leu Leu Lys His Asn Cys Ile Phe Cys Phe Arg Ala Leu Leu
35 40 45

Met Phe Cys Arg Ser Asn Val Cys Ile Phe Leu Leu Asn Lys Leu Val
50 55 60

Leu Ile Leu Glu Leu Ser Asp Asp Phe Val Leu Glu Arg Thr Thr Gln
65 70 75 80

Arg Arg Gln Cys Lys Ser Lys Ser
85

<210> 1107
<211> 124
<212> PRT
<213> Homo sapiens

<400> 1107
Leu Val Val Leu Lys Arg Arg Pro Glu Lys Ser Gln Gly His Glu His
1   5   10   15

Arg Ala Met Pro Phe Leu Asp Ile Gln Lys Arg Phe Gly Leu Asn Ile
            20   25   30

Asp Arg Trp Leu Thr Ile Gln Ser Gly Glu Gln Pro Tyr Lys Met Ala
        35   40   45

Gly Arg Cys His Ala Phe Glu Lys Glu Trp Ile Glu Cys Ala His Gly
    50   55   60

Ile Gly Tyr Thr Arg Ala Glu Lys Glu Cys Lys Ile Glu Tyr Asp Asp
65   70   75   80

Phe Val Glu Cys Leu Leu Arg Gln Lys Thr Met Arg Arg Ala Gly Thr
                85   90   95

Ile Arg Lys Gln Arg Asp Lys Leu Ile Lys Glu Gly Lys Tyr Thr Pro
            100   105   110

Pro Pro His His Ile Gly Lys Gly Glu Pro Arg Pro
        115   120

<210> 1108
<211> 299
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (32)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (186)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1108

```
His Leu Leu Cys Cys Arg Ala Gln Arg Arg Pro Gln Thr Pro Pro Ala
 1               5                  10                  15

Ala Arg Gly Leu Glu Pro Ala Gln Arg Cys Phe Glu Asp Ala Gly Xaa
            20                  25                  30

Pro Pro Leu Leu Leu Ala Ala Val Leu Leu Gly Leu Val Leu Leu Val
        35                  40                  45

Val Leu Leu Leu Leu Leu Arg His Trp Gly Trp Gly Leu Cys Leu Ile
    50                  55                  60

Gly Trp Asn Glu Phe Ile Leu Gln Pro Ile His Asn Leu Leu Met Gly
65                  70                  75                  80

Asp Thr Lys Glu Gln Arg Ile Leu Asn His Val Leu Gln His Ala Glu
                85                  90                  95

Pro Gly Asn Ala Gln Ser Val Leu Glu Ala Ile Asp Thr Tyr Cys Glu
            100                 105                 110

Gln Lys Glu Trp Ala Met Asn Val Gly Asp Lys Lys Gly Lys Ile Val
        115                 120                 125

Asp Ala Val Ile Gln Glu His Gln Pro Ser Val Leu Leu Glu Leu Gly
    130                 135                 140

Ala Tyr Cys Gly Tyr Ser Ala Val Arg Met Ala Arg Leu Leu Ser Pro
145                 150                 155                 160

Gly Ala Arg Leu Ile Thr Ile Glu Ile Asn Pro Asp Cys Ala Ala Ile
                165                 170                 175

Thr Gln Arg Met Val Asp Phe Ala Gly Xaa Lys Asp Lys Val Thr Leu
            180                 185                 190

Val Val Gly Ala Ser Gln Asp Ile Ile Pro Gln Leu Lys Lys Lys Tyr
        195                 200                 205

Asp Val Asp Thr Leu Asp Met Val Phe Leu Asp His Trp Lys Asp Arg
    210                 215                 220

Tyr Leu Pro Asp Thr Leu Leu Leu Glu Glu Cys Gly Leu Leu Arg Lys
225                 230                 235                 240

Gly Thr Val Leu Leu Ala Asp Asn Val Ile Cys Pro Gly Ala Pro Asp
                245                 250                 255

Phe Leu Ala His Val Arg Gly Ser Ser Cys Phe Glu Cys Thr His Tyr
            260                 265                 270
```

Gln Ser Phe Leu Glu Tyr Arg Glu Val Val Asp Gly Leu Glu Lys Ala
275 280 285

Ile Tyr Lys Gly Pro Gly Ser Glu Ala Gly Pro
290 295

<210> 1109
<211> 300
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (43)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1109
Trp Ile Pro Arg Ala Ala Gly Ile Arg His Glu Arg Leu Arg Asp Leu
1 5 10 15

Leu Thr Arg Arg Leu Thr Gly Ser Asn Tyr Pro Gly Leu Ser Ile Ser
20 25 30

Leu Arg Leu Thr Gly Ser Ser Ala Gln Glu Xaa Ala Ser Gly Val Ala
35 40 45

Leu Gly Glu Ala Pro Asp His Ser Tyr Glu Ser Leu Arg Val Thr Ser
50 55 60

Ala Gln Lys His Val Leu His Val Gln Leu Asn Arg Pro Asn Lys Arg
65 70 75 80

Asn Ala Met Asn Lys Val Phe Trp Arg Glu Met Val Glu Cys Phe Asn
85 90 95

Lys Ile Ser Arg Asp Ala Asp Cys Arg Ala Val Val Ile Ser Gly Ala
100 105 110

Gly Lys Met Phe Thr Ala Gly Ile Asp Leu Met Asp Met Ala Ser Asp
115 120 125

Ile Leu Gln Pro Lys Gly Asp Asp Val Ala Arg Ile Ser Trp Tyr Leu
130 135 140

Arg Asp Ile Ile Thr Arg Tyr Gln Glu Thr Phe Asn Val Ile Glu Arg
145 150 155 160

Cys Pro Lys Pro Val Ile Ala Ala Val His Gly Gly Cys Ile Gly Gly
165 170 175

```
Gly Val Asp Leu Val Thr Ala Cys Asp Ile Arg Tyr Cys Ala Gln Asp
            180                 185                 190

Ala Phe Phe Gln Val Lys Glu Val Asp Val Gly Leu Ala Ala Asp Val
        195                 200                 205

Gly Thr Leu Gln Arg Leu Pro Lys Val Ile Gly Asn Gln Ser Leu Val
    210                 215                 220

Asn Glu Leu Ala Phe Thr Ala Arg Lys Met Met Ala Asp Glu Ala Leu
225                 230                 235                 240

Gly Ser Gly Leu Val Ser Arg Val Phe Pro Asp Lys Glu Val Met Leu
                245                 250                 255

Asp Ala Ala Leu Ala Leu Ala Ala Glu Ile Ser Ser Lys Ser Pro Val
            260                 265                 270

Ala Cys Arg Ala Pro Arg Ser Thr Cys Cys Ile Pro Ala Thr Ile Arg
        275                 280                 285

Trp Pro Arg Ala Ser Thr Thr Trp Arg Pro Gly Thr
    290                 295                 300


<210> 1110
<211> 230
<212> PRT
<213> Homo sapiens

<400> 1110
Arg Ser Cys Ala Leu Val Cys Lys His Trp Tyr Arg Cys Leu His Gly
 1               5                  10                  15

Asp Glu Asn Ser Glu Val Trp Arg Ser Leu Cys Ala Arg Ser Leu Ala
            20                  25                  30

Glu Glu Ala Leu Arg Thr Asp Ile Leu Cys Asn Leu Pro Ser Tyr Lys
        35                  40                  45

Ala Lys Ile Arg Ala Phe Gln His Ala Phe Ser Thr Asn Asp Cys Ser
    50                  55                  60

Arg Asn Val Tyr Ile Lys Lys Asn Gly Phe Thr Leu His Arg Asn Pro
65                  70                  75                  80

Ile Ala Gln Ser Thr Asp Gly Ala Arg Thr Lys Ile Gly Phe Ser Glu
                85                  90                  95
```

Gly Arg His Ala Trp Glu Val Trp Trp Glu Gly Pro Leu Gly Thr Val
100 105 110

Ala Val Ile Gly Ile Ala Thr Lys Arg Ala Pro Met Gln Cys Gln Gly
115 120 125

Tyr Val Ala Leu Leu Gly Ser Asp Asp Gln Ser Trp Gly Trp Asn Leu
130 135 140

Val Asp Asn Asn Leu Leu His Asn Gly Glu Val Asn Gly Ser Phe Pro
145 150 155 160

Gln Cys Asn Asn Ala Pro Lys Tyr Gln Ile Gly Glu Arg Ile Arg Val
165 170 175

Ile Leu Asp Met Glu Asp Lys Thr Leu Ala Phe Glu Arg Gly Tyr Glu
180 185 190

Phe Leu Gly Val Ala Phe Arg Gly Leu Pro Lys Val Cys Leu Tyr Pro
195 200 205

Ala Val Ser Ala Val Tyr Gly Asn Thr Glu Val Thr Leu Val Tyr Leu
210 215 220

Gly Lys Pro Leu Asp Gly
225 230

<210> 1111
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1111
Pro Xaa Leu Thr Lys Gly Asn Lys Ser Trp Xaa Ser Thr Ala Val Xaa

```
 1               5                   10                  15

Thr Ala Leu Glu Leu Val Asp Pro Pro Gly Cys Arg Asn Ser Ala Pro
            20                  25                  30

Gln Lys Asn Leu Lys Asn Thr Val Phe Cys Ile Asp Ile Cys Thr Val
        35                  40                  45

Cys Val Cys Val Cys Glu Ile Lys Ile Arg Phe
    50                  55
```

<210> 1112
<211> 425
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (88)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (228)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1112

```
Cys Ile Xaa Gly Phe Tyr Phe Ala Val Leu Ala Pro Gln Glu Leu Leu
 1               5                   10                  15

Ile Tyr Glu Met Ala Glu Asn Gly Lys Asn Cys Asp Gln Arg Arg Val
            20                  25                  30

Ala Met Asn Lys Glu His His Asn Gly Asn Phe Thr Asp Pro Ser Ser
        35                  40                  45

Val Asn Glu Lys Lys Arg Arg Glu Arg Glu Glu Arg Gln Asn Ile Val
    50                  55                  60

Leu Trp Arg Gln Pro Leu Ile Thr Leu Gln Tyr Phe Ser Leu Glu Ile
65                  70                  75                      80

Leu Val Ile Leu Lys Glu Trp Xaa Ser Lys Leu Trp His Arg Gln Ser
                85                  90                  95
```

Ile Val Val Ser Phe Leu Leu Leu Leu Ala Val Leu Ile Ala Thr Tyr
100 105 110

Tyr Val Glu Gly Val His Gln Gln Tyr Val Gln Arg Ile Glu Lys Gln
115 120 125

Phe Leu Leu Tyr Ala Tyr Trp Ile Gly Leu Gly Ile Leu Ser Ser Val
130 135 140

Gly Leu Gly Thr Gly Leu His Thr Phe Leu Leu Tyr Leu Gly Pro His
145 150 155 160

Ile Ala Ser Val Thr Leu Ala Ala Tyr Glu Cys Asn Ser Val Asn Phe
165 170 175

Pro Glu Pro Pro Tyr Pro Asp Gln Ile Ile Cys Pro Asp Glu Glu Gly
180 185 190

Thr Glu Gly Thr Ile Ser Leu Trp Ser Ile Ile Ser Lys Val Arg Ile
195 200 205

Glu Ala Cys Met Trp Gly Ile Gly Thr Ala Ile Gly Glu Leu Pro Pro
210 215 220

Tyr Phe Met Xaa Arg Ala Ala Arg Leu Ser Gly Ala Glu Pro Asp Asp
225 230 235 240

Glu Glu Tyr Gln Glu Phe Glu Glu Met Leu Glu His Ala Glu Ser Ala
245 250 255

Gln Asp Phe Ala Ser Arg Ala Lys Leu Ala Val Gln Lys Leu Val Gln
260 265 270

Lys Val Gly Phe Phe Gly Ile Leu Ala Cys Ala Ser Ile Pro Asn Pro
275 280 285

Leu Phe Asp Leu Ala Gly Ile Thr Cys Gly His Phe Leu Val Pro Phe
290 295 300

Trp Thr Phe Phe Gly Ala Thr Leu Ile Gly Lys Ala Ile Ile Lys Met
305 310 315 320

His Ile Gln Lys Ile Phe Val Ile Ile Thr Phe Ser Lys His Ile Val
325 330 335

Glu Gln Met Val Ala Phe Ile Gly Ala Val Pro Gly Ile Gly Pro Ser
340 345 350

Leu Gln Lys Pro Phe Gln Glu Tyr Leu Glu Ala Gln Arg Gln Lys Leu
355 360 365

His His Lys Ser Glu Met Gly Thr Pro Gln Gly Glu Asn Trp Leu Ser
370 375 380

Trp Met Phe Glu Lys Leu Val Val Val Met Val Cys Tyr Phe Ile Leu
385 390 395 400

Ser Ile Ile Asn Ser Met Ala Gln Ser Tyr Ala Lys Arg Ile Gln Gln
405 410 415

Arg Leu Asn Ser Glu Glu Lys Thr Lys
420 425

<210> 1113
<211> 254
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1113
Xaa Ile Glu Ile Asn Pro His Val Lys Gly Thr Lys Ala Gly Ala Pro
1 5 10 15

Pro Arg Cys Gly Arg Ser Arg Thr Ser Gly Ser Pro Gly Leu Gln Glu
20 25 30

Phe Gly Thr Ser Ser Ser Thr Pro Ala Arg Pro Ser Ser His His Ser
35 40 45

Ala Cys Phe Leu Gly Pro Glu Ile Met Pro Leu Gly Leu Leu Trp Leu
50 55 60

Gly Leu Ala Leu Leu Gly Ala Leu His Ala Gln Ala Gln Asp Ser Thr
65 70 75 80

Ser Asp Leu Ile Pro Ala Pro Pro Leu Ser Lys Val Pro Leu Gln Gln
85 90 95

Asn Phe Gln Asp Asn Gln Phe Gln Gly Lys Trp Tyr Val Val Gly Leu
100 105 110

Ala Gly Asn Ala Ile Leu Arg Glu Asp Lys Asp Pro Gln Lys Met Tyr
115 120 125

Ala Thr Ile Tyr Glu Leu Lys Glu Asp Lys Ser Tyr Asn Val Thr Ser

130 135 140

Val Leu Phe Arg Lys Lys Lys Cys Asp Tyr Trp Ile Arg Thr Phe Val
145 150 155 160

Pro Gly Cys Gln Pro Gly Glu Phe Thr Leu Gly Asn Ile Lys Ser Tyr
165 170 175

Pro Gly Leu Thr Ser Tyr Leu Val Arg Val Val Ser Thr Asn Tyr Asn
180 185 190

Gln His Ala Met Val Phe Phe Lys Lys Val Ser Gln Asn Arg Glu Tyr
195 200 205

Phe Lys Ile Thr Leu Tyr Gly Arg Thr Lys Glu Leu Thr Ser Glu Leu
210 215 220

Lys Glu Asn Phe Ile Arg Phe Ser Lys Ser Leu Gly Leu Pro Glu Asn
225 230 235 240

His Ile Val Phe Pro Val Pro Ile Asp Gln Cys Ile Asp Gly
245 250

<210> 1114
<211> 248
<212> PRT
<213> Homo sapiens

<400> 1114
Ala Ser Glu Glu Ala Asn Pro Ala Gly Ile Arg Ala Ile Arg Thr Ala
1 5 10 15

Thr Met Thr Val Gly Lys Ser Ser Lys Met Leu Gln His Ile Asp Tyr
20 25 30

Arg Met Arg Cys Ile Leu Gln Asp Gly Arg Ile Phe Ile Gly Thr Phe
35 40 45

Lys Ala Phe Asp Lys His Met Asn Leu Ile Leu Cys Asp Cys Asp Glu
50 55 60

Phe Arg Lys Ile Lys Pro Lys Asn Ser Lys Gln Ala Glu Arg Glu Glu
65 70 75 80

Lys Arg Val Leu Gly Leu Val Leu Leu Arg Gly Glu Asn Leu Val Ser
85 90 95

Met Thr Val Glu Gly Pro Pro Pro Lys Asp Thr Gly Ile Ala Arg Val
100 105 110

Pro Leu Ala Gly Ala Ala Gly Gly Pro Gly Ile Gly Arg Ala Ala Gly
115 120 125

Arg Gly Ile Pro Ala Gly Val Pro Met Pro Gln Ala Pro Ala Gly Leu
130 135 140

Ala Gly Pro Val Arg Gly Val Gly Gly Pro Ser Gln Gln Val Met Thr
145 150 155 160

Pro Gln Gly Arg Gly Thr Val Ala Ala Ala Ala Ala Ala Ala Thr Ala
165 170 175

Ser Ile Ala Gly Ala Pro Thr Gln Tyr Pro Pro Gly Arg Gly Gly Pro
180 185 190

Pro Pro Pro Met Gly Arg Gly Ala Pro Pro Pro Gly Met Met Gly Pro
195 200 205

Pro Pro Gly Met Arg Pro Pro Met Gly Pro Pro Met Gly Ile Pro Pro
210 215 220

Gly Arg Gly Thr Pro Met Gly Met Pro Pro Pro Gly Met Arg Pro Pro
225 230 235 240

Pro Pro Gly Met Arg Gly Leu Leu
245

<210> 1115
<211> 777
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (14)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (21)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (32)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1115
```
Leu Thr Lys Gly Xaa Lys Ser Trp Xaa Ser Thr Ala Val Xaa Thr Ala
  1               5                  10                  15

Leu Glu Leu Val Xaa Pro Pro Gly Cys Arg Asn Ser Ala Arg Ala Xaa
             20                  25                  30

Pro Pro Leu Gly Ser Ser Pro Leu Gly Arg Arg Phe Arg Val Leu Ser
         35                  40                  45

Ser Leu Arg Arg Ser Pro Met Phe Glu Glu Lys Ala Ser Ser Pro Ser
     50                  55                  60

Gly Lys Met Gly Gly Glu Glu Lys Pro Ile Gly Ala Gly Glu Glu Lys
 65                  70                  75                  80

Gln Lys Glu Gly Gly Lys Lys Lys Asn Lys Glu Gly Ser Gly Asp Gly
                 85                  90                  95

Gly Arg Ala Glu Leu Asn Pro Trp Pro Glu Tyr Ile Tyr Thr Arg Leu
            100                 105                 110

Glu Met Tyr Asn Ile Leu Lys Ala Glu His Asp Ser Ile Leu Ala Glu
        115                 120                 125

Lys Ala Glu Lys Asp Ser Lys Pro Ile Lys Val Thr Leu Pro Asp Gly
    130                 135                 140

Lys Gln Val Asp Ala Glu Ser Trp Lys Thr Thr Pro Tyr Gln Ile Ala
145                 150                 155                 160

Cys Gly Ile Ser Gln Gly Leu Ala Asp Asn Thr Val Ile Ala Lys Val
                165                 170                 175

Asn Asn Val Val Trp Asp Leu Asp Arg Pro Leu Glu Glu Asp Cys Thr
            180                 185                 190

Leu Glu Leu Leu Lys Phe Glu Asp Glu Glu Ala Gln Ala Val Tyr Trp
        195                 200                 205

His Ser Ser Ala His Ile Met Gly Glu Ala Met Glu Arg Val Tyr Gly
    210                 215                 220
```

Gly Cys Leu Cys Tyr Gly Pro Pro Ile Glu Asn Gly Phe Tyr Tyr Asp
225 230 235 240

Met Tyr Leu Glu Glu Gly Gly Val Ser Ser Asn Asp Phe Ser Ser Leu
245 250 255

Glu Ala Leu Cys Lys Lys Ile Ile Lys Glu Lys Gln Ala Phe Glu Arg
260 265 270

Leu Glu Val Lys Lys Glu Thr Leu Leu Ala Met Phe Lys Tyr Asn Lys
275 280 285

Phe Lys Cys Arg Ile Leu Asn Glu Lys Val Asn Thr Pro Thr Thr Thr
290 295 300

Val Tyr Arg Cys Gly Pro Leu Ile Asp Leu Cys Arg Gly Pro His Val
305 310 315 320

Arg His Thr Gly Lys Ile Lys Ala Leu Lys Ile His Lys Asn Ser Ser
325 330 335

Thr Tyr Trp Glu Gly Lys Ala Asp Met Glu Thr Leu Gln Arg Ile Tyr
340 345 350

Gly Ile Ser Phe Pro Asp Pro Lys Met Leu Lys Glu Trp Glu Lys Phe
355 360 365

Gln Glu Glu Ala Lys Asn Arg Asp His Arg Lys Ile Gly Arg Asp Gln
370 375 380

Glu Leu Tyr Phe Phe His Glu Leu Ser Pro Gly Ser Cys Phe Phe Leu
385 390 395 400

Pro Lys Gly Ala Tyr Ile Tyr Asn Ala Leu Ile Glu Phe Ile Arg Ser
405 410 415

Glu Tyr Arg Lys Arg Gly Phe Gln Glu Val Val Thr Pro Asn Ile Phe
420 425 430

Asn Ser Arg Leu Trp Met Thr Ser Gly His Trp Gln His Tyr Ser Glu
435 440 445

Asn Met Phe Ser Phe Glu Val Glu Lys Glu Leu Phe Ala Leu Lys Pro
450 455 460

Met Asn Cys Pro Gly His Cys Leu Met Phe Asp His Arg Pro Arg Ser
465 470 475 480

Trp Arg Glu Leu Pro Leu Arg Leu Ala Asp Phe Gly Val Leu His Arg
485 490 495

```
Asn Glu Leu Ser Gly Ala Leu Thr Gly Leu Thr Arg Val Arg Arg Phe
            500                 505                 510

Gln Gln Asp Asp Ala His Ile Phe Cys Ala Met Glu Gln Ile Glu Asp
        515                 520                 525

Glu Ile Lys Gly Cys Leu Asp Phe Leu Arg Thr Val Tyr Ser Val Phe
    530                 535                 540

Gly Phe Ser Phe Lys Leu Asn Leu Ser Thr Arg Pro Glu Lys Phe Leu
545                 550                 555                 560

Gly Asp Ile Glu Val Trp Asp Gln Ala Glu Lys Gln Leu Glu Asn Ser
                565                 570                 575

Leu Asn Glu Phe Gly Glu Lys Trp Glu Leu Asn Ser Gly Asp Gly Ala
            580                 585                 590

Phe Tyr Gly Pro Lys Ile Asp Ile Gln Ile Lys Asp Ala Ile Gly Arg
        595                 600                 605

Tyr His Gln Cys Ala Thr Ile Gln Leu Asp Phe Gln Leu Pro Ile Arg
    610                 615                 620

Phe Asn Leu Thr Tyr Val Ser His Asp Gly Asp Asp Lys Lys Arg Pro
625                 630                 635                 640

Val Ile Val His Arg Ala Ile Leu Gly Ser Val Glu Arg Met Ile Ala
                645                 650                 655

Ile Leu Thr Glu Asn Tyr Gly Gly Lys Trp Pro Phe Trp Leu Ser Pro
            660                 665                 670

Arg Gln Val Met Val Val Pro Val Gly Pro Thr Cys Asp Glu Tyr Ala
        675                 680                 685

Gln Lys Val Arg Gln Gln Phe His Asp Ala Lys Phe Met Ala Asp Ile
    690                 695                 700

Asp Leu Asp Pro Gly Cys Thr Leu Asn Lys Lys Ile Arg Asn Ala Gln
705                 710                 715                 720

Leu Ala Gln Tyr Asn Phe Ile Leu Val Val Gly Glu Lys Glu Lys Ile
                725                 730                 735

Ser Gly Thr Val Asn Ile Arg Thr Arg Asp Asn Lys Val His Gly Glu
            740                 745                 750

Arg Thr Ile Ser Glu Thr Ile Glu Arg Leu Gln Gln Leu Lys Glu Phe
        755                 760                 765
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Arg Ser Lys Gln Ala Glu Glu Glu Phe
    770   775

<210> 1116
<211> 360
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (38)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1116
Thr Thr Ser Ala Xaa Arg Trp Asp Gly Thr Arg Gly Arg Thr Arg Gly
1   5   10   15

Arg Thr Xaa Gly Phe Gly Asn Leu Ser Ile Thr Gln Xaa Trp Met Met
            20   25   30

Trp Ala Met Val Ser Xaa Met Glu Ile Asp Gln Pro Ala Gly Thr Gly
        35   40   45

Thr Leu Ser Arg Thr Asn Pro Pro Thr Gln Lys Pro Pro Ser Pro Pro
    50   55   60

Met Ser Gly Arg Gly Thr Leu Gly Arg Asn Thr Pro Tyr Lys Thr Leu
65   70   75   80

Glu Pro Val Lys Pro Pro Thr Val Pro Asn Asp Tyr Met Thr Ser Pro
                85   90   95

Ala Arg Leu Gly Ser Gln His Ser Pro Gly Arg Thr Ala Ser Leu Asn

```
            100                 105                 110

Gln Arg Pro Arg Thr His Ser Gly Ser Ser Gly Gly Ser Gly Ser Arg
        115                 120                 125

Glu Asn Ser Gly Ser Ser Ser Ile Gly Ile Pro Ile Ala Val Pro Thr
    130                 135                 140

Pro Ser Pro Pro Thr Ile Gly Pro Ala Ala Pro Gly Ser Ala Pro Gly
145                 150                 155                 160

Ser Gln Tyr Gly Thr Met Thr Arg Gln Ile Ser Arg His Asn Ser Thr
                165                 170                 175

Thr Ser Ser Thr Ser Ser Gly Gly Tyr Arg Arg Thr Pro Ser Val Thr
            180                 185                 190

Ala Gln Phe Ser Ala Gln Pro His Val Asn Gly Gly Pro Leu Tyr Ser
        195                 200                 205

Gln Asn Ser Ile Ser Ile Ala Pro Pro Pro Pro Pro Met Pro Gln Leu
    210                 215                 220

Thr Pro Gln Ile Pro Leu Thr Gly Phe Val Ala Arg Val Gln Glu Asn
225                 230                 235                 240

Ile Ala Asp Ser Pro Thr Pro Pro Pro Pro Pro Pro Pro Asp Asp Ile
                245                 250                 255

Pro Met Phe Asp Asp Ser Pro Pro Pro Pro Pro Pro Pro Pro Val Asp
            260                 265                 270

Tyr Glu Asp Glu Glu Ala Ala Val Val Gln Tyr Asn Asp Pro Tyr Ala
        275                 280                 285

Asp Gly Asp Pro Ala Trp Ala Pro Lys Asn Tyr Ile Glu Lys Val Val
    290                 295                 300

Ala Ile Tyr Asp Tyr Thr Lys Asp Lys Asp Asp Glu Leu Ser Phe Met
305                 310                 315                 320

Glu Gly Ala Ile Ile Tyr Val Ile Lys Lys Asn Asp Asp Gly Trp Tyr
                325                 330                 335

Glu Gly Val Cys Asn Arg Val Thr Gly Leu Phe Pro Gly Asn Tyr Val
            340                 345                 350

Glu Ser Ile Met His Tyr Thr Asp
        355                 360
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<210> 1117
<211> 89
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (86)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1117
Pro Ala Arg Leu Gly Ile Thr Cys His Ser Pro Ala Ile Leu Ser Thr
1 5 10 15

Ala Leu Trp Gly Gly Ser Ser Pro Ile Pro Asp Ala Pro Thr Thr Gln
20 25 30

Trp Lys Val Thr Lys Pro Ala Pro Cys Pro Arg Pro Arg Arg Val Glu
35 40 45

Pro Val Cys Ser Gly Leu Gln Ala Gln Ile Leu His Cys Tyr Arg Asp
50 55 60

Arg Pro His Glu Val Leu Leu Cys Ser Asp Leu Val Lys Ala Tyr Gln
65 70 75 80

Arg Cys Val Ser Ala Xaa His Lys Gly
85

<210> 1118
<211> 347
<212> PRT
<213> Homo sapiens

<400> 1118
Arg Gly Val Val Asp Ser Glu Asp Leu Pro Leu Asn Ile Ser Arg Glu
1 5 10 15

Met Leu Gln Gln Ser Lys Ile Leu Lys Val Ile Arg Lys Asn Ile Val
20 25 30

Lys Lys Cys Leu Glu Leu Phe Ser Glu Leu Ala Glu Asp Lys Glu Asn
35 40 45

Tyr Lys Lys Phe Tyr Glu Ala Phe Ser Lys Asn Leu Lys Leu Gly Ile
50 55 60

His Glu Asp Ser Thr Asn Arg Arg Arg Leu Ser Glu Leu Leu Arg Tyr

65 70 75 80

His Thr Ser Gln Ser Gly Asp Glu Met Thr Ser Leu Ser Glu Tyr Val
85 90 95

Ser Arg Met Lys Glu Thr Gln Lys Ser Ile Tyr Tyr Ile Thr Gly Glu
100 105 110

Ser Lys Glu Gln Val Ala Asn Ser Ala Phe Val Glu Arg Val Arg Lys
115 120 125

Arg Gly Phe Glu Val Val Tyr Met Thr Glu Pro Ile Asp Glu Tyr Cys
130 135 140

Val Gln Gln Leu Lys Glu Phe Asp Gly Lys Ser Leu Val Ser Val Thr
145 150 155 160

Lys Glu Gly Leu Glu Leu Pro Glu Asp Glu Glu Glu Lys Lys Lys Met
165 170 175

Glu Glu Ser Lys Ala Lys Phe Glu Asn Leu Cys Lys Leu Met Lys Glu
180 185 190

Ile Leu Asp Lys Lys Val Glu Lys Val Thr Ile Ser Asn Arg Leu Val
195 200 205

Ser Ser Pro Cys Cys Ile Val Thr Ser Thr Tyr Gly Trp Thr Ala Asn
210 215 220

Met Glu Arg Ile Met Lys Ala Gln Ala Leu Arg Asp Asn Ser Thr Met
225 230 235 240

Gly Tyr Met Met Ala Lys Lys His Leu Glu Ile Asn Pro Asp His Pro
245 250 255

Ile Val Glu Thr Leu Arg Gln Lys Ala Glu Ala Asp Lys Asn Asp Lys
260 265 270

Ala Val Lys Asp Leu Val Val Leu Leu Phe Glu Thr Ala Leu Leu Ser
275 280 285

Ser Gly Phe Ser Leu Glu Asp Pro Gln Thr His Ser Asn Arg Ile Tyr
290 295 300

Arg Met Ile Lys Leu Gly Leu Gly Ile Asp Glu Asp Glu Val Ala Ala
305 310 315 320

Glu Glu Pro Asn Ala Ala Val Pro Asp Glu Ile Pro Pro Leu Glu Gly
325 330 335

Asp Glu Asp Ala Ser Arg Met Glu Glu Val Asp

340 345

<210> 1119
<211> 293
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (170)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1119
Pro Gly Ser Pro Asp Val Asn Arg Ala Val Val Arg Pro Pro Pro Pro
1 5 10 15

Pro Pro Pro Pro Pro Pro Ala Pro Gln Pro Thr Met Ser Arg Arg Lys
20 25 30

Gln Gly Lys Pro Gln His Leu Ser Lys Arg Glu Phe Ser Pro Glu Pro
35 40 45

Leu Glu Ala Ile Leu Thr Asp Asp Glu Pro Asp His Gly Pro Leu Gly
50 55 60

Ala Pro Glu Gly Asp His Asp Leu Leu Thr Cys Gly Gln Cys Gln Met
65 70 75 80

Asn Phe Pro Leu Gly Asp Ile Leu Ile Phe Ile Glu His Lys Arg Lys
85 90 95

Gln Cys Asn Gly Ser Leu Cys Leu Glu Lys Ala Val Asp Lys Pro Pro
100 105 110

Ser Pro Ser Pro Ile Glu Met Lys Lys Ala Ser Asn Pro Val Glu Val
115 120 125

Gly Ile Gln Val Thr Pro Glu Asp Asp Asp Cys Leu Ser Thr Ser Ser
130 135 140

Arg Gly Ile Cys Pro Lys Gln Glu His Ile Ala Asp Lys Leu Leu His
145 150 155 160

Trp Arg Gly Leu Ser Ser Pro Arg Ser Xaa Thr Trp Ser Ser Asn Pro
165 170 175

His Ala Trp Asp Glu Cys Arg Ile Cys Pro Ala Gly Ile Cys Lys Asp
180 185 190

Glu Pro Ser Ser Tyr Thr Cys Thr Thr Cys Lys Gln Pro Phe Thr Ser
195 200 205

Ala Trp Phe Leu Leu Gln His Ala Gln Asn Thr His Gly Leu Arg Ile
210 215 220

Tyr Leu Glu Ser Glu His Gly Ser Pro Leu Thr Pro Arg Val Gly Ile
225 230 235 240

Pro Ser Gly Leu Gly Ala Glu Cys Pro Ser Gln Pro Pro Leu His Gly
245 250 255

Ile His Ile Ala Asp Asn Asn Pro Phe Asn Leu Leu Arg Ile Pro Gly
260 265 270

Ser Val Ser Arg Glu Ala Ser Gly Leu Gly Arg Arg Ala Leu Ser Thr
275 280 285

His Ser Pro Pro Val
290

<210> 1120
<211> 190
<212> PRT
<213> Homo sapiens

<400> 1120
Ala Ala Ala Ala Ala Gly Asp Pro Gly Ala Met Gly Arg Ala Arg Asp
1 5 10 15

Ala Ile Leu Asp Ala Leu Glu Asn Leu Thr Ala Glu Glu Leu Lys Lys
20 25 30

Phe Lys Leu Lys Leu Leu Ser Val Pro Leu Arg Glu Gly Tyr Gly Arg
35 40 45

Ile Pro Arg Gly Ala Leu Leu Ser Met Asp Ala Leu Asp Leu Thr Asp
50 55 60

Lys Leu Val Ser Phe Tyr Leu Glu Thr Tyr Gly Ala Glu Leu Thr Ala
65 70 75 80

Asn Val Leu Arg Asp Met Gly Leu Gln Glu Met Ala Gly Gln Leu Gln
85 90 95

Ala Ala Thr His Gln Gly Ser Gly Ala Ala Pro Ala Gly Ile Gln Ala
100 105 110

Pro Pro Gln Ser Ala Ala Lys Pro Gly Leu His Phe Ile Asp Gln His

115 120 125

Arg Ala Ala Leu Ile Ala Arg Val Thr Asn Val Glu Trp Leu Leu Asp
130 135 140

Ala Leu Tyr Gly Lys Val Leu Thr Asp Glu Gln Tyr Gln Ala Val Arg
145 150 155 160

Pro Ser Pro Pro Thr Gln Ala Arg Cys Gly Ser Ser Ser Val Ser His
165 170 175

Gln Pro Gly Thr Gly Pro Ala Arg Thr Cys Ser Ser Arg Pro
180 185 190

<210> 1121
<211> 217
<212> PRT
<213> Homo sapiens

<400> 1121
Gly Arg Lys Trp Phe Cys Pro Tyr Lys Thr Trp Arg Lys Ala Phe Leu
1 5 10 15

Ser Pro Arg Lys Arg His Val Met Ser Gln Ser Cys Gly Ala Arg Ala
20 25 30

Glu Val Gln Ala Thr Gly Ser Asp Gly Ala Pro Thr Lys Ala Leu Gly
35 40 45

Leu Val Arg Val Ala Ala Val Ser Ser Asp Ser Cys Val Val Pro Met
50 55 60

Val Glu Lys Lys Thr Ser Val Arg Ser Gln Asp Pro Gly Gln Arg Arg
65 70 75 80

Val Leu Asp Arg Ala Ala Arg Gln Arg Arg Ile Asn Arg Gln Leu Glu
85 90 95

Ala Leu Glu Asn Asp Asn Phe Gln Asp Asp Pro His Ala Gly Leu Pro
100 105 110

Gln Leu Gly Lys Arg Leu Pro Gln Phe Asp Asp Asp Ala Asp Thr Gly
115 120 125

Lys Lys Lys Lys Lys Thr Arg Gly Asp His Phe Lys Leu Arg Phe Arg
130 135 140

Lys Asn Phe Gln Ala Leu Leu Glu Glu Gln Asn Leu Ser Val Ala Glu
145 150 155 160

Gly Pro Asn Tyr Leu Thr Ala Cys Ala Gly Pro Pro Ser Arg Pro Gln
165 170 175

Arg Pro Phe Cys Ala Val Cys Gly Phe Pro Ser Pro Tyr Thr Cys Val
180 185 190

Ser Cys Gly Ala Arg Tyr Cys Thr Val Arg Cys Leu Gly Thr His Gln
195 200 205

Glu Thr Arg Cys Leu Lys Trp Thr Val
210 215

<210> 1122
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1122
Gly Asn Cys Gln Lys Cys Ala Phe Gly Tyr Ser Gly Leu Asp Cys Lys
1 5 10 15

Asp Lys Phe Gln Leu Ile Leu Thr Ile Val Gly Thr Ile Ala Gly Ile
20 25 30

Val Ile Leu Ser Met Ile Ile Ala Leu Ile Val Thr Ala Arg Ser Asn
35 40 45

Asn Lys Thr Lys His Ile Glu Glu Glu Asn Leu Ile Asp Glu Asp Phe
50 55 60

Gln Asn Leu Lys Leu Arg Ser Thr Gly Phe Thr Asn Leu Gly Ala Glu
65 70 75 80

Gly Ser Val Phe Pro Lys Val Arg Ile Thr Ala Ser Arg Asp Ser Gln
85 90 95

Met Gln Asn Pro Tyr Ser Ser His Ser Ser Met Pro Arg Pro Asp Tyr
100 105 110

<210> 1123
<211> 216
<212> PRT
<213> Homo sapiens

<400> 1123
Gly Lys Leu Val Cys Gly Met Val Ser Tyr Leu Asn Asp Leu Pro Ser
1 5 10 15

Gln Arg Ile Gln Pro Gln Gln Val Ala Val Trp Pro Thr Met Val Asp
20 25 30

Ile Asn Ser Pro Glu Ser Leu Thr Glu Ala Tyr Lys Leu Arg Ala Ala
35 40 45

Arg Leu Val Glu Ile Ala Ala Lys Asn Leu Gln Lys Glu Val Ile His
50 55 60

Arg Lys Ser Lys Glu Val Ala Trp Asn Leu Thr Ser Val Asp Leu Val
65 70 75 80

Arg Ala Ser Glu Ala His Cys His Tyr Val Val Val Lys Leu Phe Ser
85 90 95

Glu Lys Leu Leu Lys Ile Gln Asp Lys Ala Ile Gln Ala Val Leu Arg
100 105 110

Ser Leu Cys Leu Leu Tyr Ser Leu Tyr Gly Ile Ser Gln Asn Ala Gly
115 120 125

Asp Phe Leu Gln Gly Ser Ile Met Thr Glu Pro Gln Ile Thr Gln Val
130 135 140

Asn Gln Arg Val Lys Glu Leu Leu Thr Leu Ile Arg Ser Asp Ala Val
145 150 155 160

Ala Leu Val Asp Ala Phe Asp Phe Gln Asp Val Thr Leu Gly Ser Val
165 170 175

Leu Gly Arg Tyr Asp Gly Asn Val Tyr Glu Asn Leu Phe Glu Trp Ala
180 185 190

Lys Asn Ser Pro Leu Asn Lys Ala Glu Val His Glu Ser Tyr Lys His
195 200 205

Leu Lys Ser Leu Gln Ser Lys Leu
210 215

<210> 1124
<211> 218
<212> PRT
<213> Homo sapiens

<400> 1124

Pro Ser Pro Arg Pro Pro Asp Pro Glu Ser Ser Gln Leu Arg Pro Gly
1   5   10   15

Gly Asp Gly Ala Glu Leu Arg Val Leu Val Asp Met Asp Gly Val Leu
            20   25   30

Ala Asp Phe Glu Ala Gly Leu Leu Arg Gly Phe Arg Arg Arg Phe Pro
        35   40   45

Glu Glu Pro His Val Pro Leu Glu Gln Arg Arg Gly Phe Leu Ala Arg
    50   55   60

Glu Gln Tyr Arg Ala Leu Arg Pro Asp Leu Ala Asp Lys Val Ala Ser
65   70   75   80

Val Tyr Glu Ala Pro Gly Phe Phe Leu Asp Leu Glu Pro Ile Pro Gly
                85   90   95

Ala Leu Asp Ala Val Arg Glu Met Asn Asp Leu Pro Asp Thr Gln Val
            100   105   110

Phe Ile Cys Thr Ser Pro Leu Leu Lys Tyr His His Cys Val Gly Glu
        115   120   125

Lys Tyr Arg Trp Val Glu Gln His Leu Gly Pro Gln Phe Val Glu Arg
    130   135   140

Ile Ile Leu Thr Arg Asp Lys Thr Val Val Leu Gly Asp Leu Leu Ile
145   150   155   160

Asp Asp Lys Asp Thr Val Arg Gly Gln Glu Glu Thr Pro Ser Trp Glu
                165   170   175

His Ile Leu Phe Thr Cys Cys His Asn Arg His Leu Val Leu Pro Pro
            180   185   190

Thr Arg Arg Arg Leu Leu Ser Trp Ser Asp Asn Trp Arg Glu Ile Leu
        195   200   205

Asp Ser Lys Arg Gly Ala Ala Gln Arg Glu
    210   215

<210> 1125
<211> 87
<212> PRT
<213> Homo sapiens

<400> 1125

Met Arg Arg Arg Val Phe Phe Leu His Arg Cys Ser Ile Leu Val Phe
1 5 10 15

Leu Phe Pro Cys Lys Cys Asn Gln Met Pro Phe Tyr Met Trp Thr Tyr
20 25 30

Leu Tyr Trp Pro Asn Ile Phe Phe Leu Leu Ser Leu Phe Phe Phe Pro
35 40 45

Phe Phe Leu Leu Pro Leu Phe Leu Tyr Ser Phe Leu Phe Leu Phe Phe
50 55 60

Phe Phe Phe Ser Phe Phe Phe Gly Ser Cys Cys Tyr Pro Arg His Phe
65 70 75 80

Thr Ser Pro Ser Leu Lys Gly
85

<210> 1126
<211> 174
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (173)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1126
Pro Pro Leu Gly Lys Lys Xaa Glu Leu His Arg Gly Gly Gly Arg Ser
1 5 10 15

Arg Leu Glu Glu Phe Gln Met Arg Ala Arg Pro Arg Pro Arg Pro Leu
20 25 30

Trp Ala Thr Val Leu Ala Leu Gly Ala Leu Ala Gly Val Gly Val Gly
35 40 45

Gly Pro Asn Ile Cys Thr Thr Arg Gly Val Ser Ser Cys Gln Gln Cys
50 55 60

Leu Ala Val Ser Pro Met Cys Ala Trp Cys Ser Asp Glu Ala Leu Pro
65 70 75 80

Leu Gly Ser Pro Arg Cys Asp Leu Lys Glu Asn Leu Leu Lys Asp Asn
85 90 95

Cys Ala Pro Glu Ser Ile Glu Phe Pro Val Ser Glu Ala Arg Val Leu
100 105 110

Glu Asp Arg Pro Leu Ser Asp Lys Gly Ser Gly Asp Ser Ser Gln Val
115 120 125

Thr Gln Val Ser Pro Gln Arg Ile Ala Leu Arg Leu Arg Pro Asp Asp
130 135 140

Ser Lys Asn Phe Ser Ile Gln Val Arg Gln Val Glu Asp Tyr Pro Val
145 150 155 160

Asp Ile Tyr Tyr Leu Met Asp Leu Ser Tyr Ser Met Xaa Gly
165 170

<210> 1127
<211> 359
<212> PRT
<213> Homo sapiens

<400> 1127
Pro Gln Pro Phe Gln Gly Ser Gly Cys Val Ile Ala Ile Leu Gly Lys
1 5 10 15

Arg Cys Ser Arg Pro Trp Arg Thr Trp Arg Gly Arg Thr Pro Ser Thr
20 25 30

Arg His Ile Cys Ser Trp Cys Thr Met Val Ser Gly Thr Ser Ala Ala
35 40 45

Val Glu Glu Tyr Ser Cys Glu Phe Gly Ser Ala Lys Tyr Tyr Ala Leu
50 55 60

Cys Gly Phe Gly Gly Val Leu Ser Cys Gly Leu Thr His Thr Ala Val
65 70 75 80

Val Pro Leu Asp Leu Val Lys Cys Arg Met Gln Val Asp Pro Gln Lys
85 90 95

Tyr Lys Gly Ile Phe Asn Gly Phe Ser Val Thr Leu Lys Glu Asp Gly
100 105 110

Val Arg Gly Leu Ala Lys Gly Trp Ala Pro Thr Phe Leu Gly Tyr Ser
115 120 125

Met Gln Gly Leu Cys Lys Phe Gly Phe Tyr Glu Val Phe Lys Val Leu

130 135 140

Tyr Ser Asn Met Leu Gly Glu Glu Asn Thr Tyr Leu Trp Arg Thr Ser
145 150 155 160

Leu Tyr Leu Ala Ala Ser Ala Ser Ala Glu Phe Phe Ala Asp Ile Ala
165 170 175

Leu Ala Pro Met Glu Ala Ala Lys Val Arg Ile Gln Thr Gln Pro Gly
180 185 190

Tyr Ala Asn Thr Leu Arg Asp Ala Ala Pro Lys Met Tyr Lys Glu Glu
195 200 205

Gly Leu Lys Ala Phe Tyr Lys Gly Val Ala Pro Leu Trp Met Arg Gln
210 215 220

Ile Pro Tyr Thr Met Met Lys Phe Ala Cys Phe Glu Arg Thr Val Glu
225 230 235 240

Ala Leu Tyr Lys Phe Val Val Pro Lys Pro Arg Ser Glu Cys Ser Lys
245 250 255

Pro Glu Gln Leu Val Val Thr Phe Val Ala Gly Tyr Ile Ala Gly Val
260 265 270

Phe Cys Ala Ile Val Ser His Pro Ala Asp Ser Val Val Ser Val Leu
275 280 285

Asn Lys Glu Lys Gly Ser Ser Ala Ser Leu Val Leu Lys Arg Leu Gly
290 295 300

Phe Lys Gly Val Trp Lys Gly Leu Phe Ala Arg Ile Ile Met Ile Gly
305 310 315 320

Thr Leu Thr Ala Leu Gln Trp Phe Ile Tyr Asp Ser Val Lys Val Tyr
325 330 335

Phe Arg Leu Pro Arg Pro Pro Pro Pro Glu Met Pro Glu Ser Leu Lys
340 345 350

Lys Lys Leu Gly Leu Thr Gln
355

<210> 1128
<211> 399
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (208)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (349)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1128
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Leu Glu Pro Pro Ala Glu Pro Leu Gln Tyr Leu Ala Cys Tyr Arg Phe
  1               5                  10                  15

His Cys Ser His Gln Leu Gly Asp Asn Met Trp Phe Leu Thr Thr Leu
             20                  25                  30

Leu Leu Trp Val Pro Val Asp Gly Gln Val Asp Thr Thr Lys Ala Val
         35                  40                  45

Ile Thr Leu Gln Pro Pro Trp Val Ser Val Phe Gln Glu Glu Thr Val
     50                  55                  60

Thr Leu His Cys Glu Val Leu His Leu Pro Gly Ser Ser Ser Thr Gln
 65                  70                  75                  80

Trp Phe Leu Asn Gly Thr Ala Thr Gln Thr Ser Thr Pro Ser Tyr Arg
                 85                  90                  95

Ile Thr Ser Ala Ser Val Asn Asp Ser Gly Glu Tyr Arg Cys Gln Arg
            100                 105                 110

Gly Leu Ser Gly Arg Ser Asp Pro Ile Gln Leu Glu Ile His Arg Gly
        115                 120                 125

Trp Leu Leu Leu Gln Val Ser Ser Arg Val Phe Thr Glu Gly Glu Pro
    130                 135                 140

Leu Ala Leu Arg Cys His Ala Trp Lys Asp Lys Leu Val Tyr Asn Val
145                 150                 155                 160

Leu Tyr Tyr Arg Asn Gly Lys Ala Phe Lys Phe Phe His Trp Asn Ser
                165                 170                 175

Asn Leu Thr Ile Leu Lys Thr Asn Ile Ser His Asn Gly Thr Tyr His
            180                 185                 190

Cys Ser Gly Met Gly Lys His Arg Tyr Thr Ser Ala Gly Ile Ser Xaa
        195                 200                 205

Thr Val Lys Glu Leu Phe Pro Ala Pro Val Leu Asn Ala Ser Val Thr
```

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    210                 215                 220

Ser Pro Leu Leu Glu Gly Asn Leu Val Thr Leu Ser Cys Glu Thr Lys
225                 230                 235                 240

Leu Leu Leu Gln Arg Pro Gly Leu Gln Leu Tyr Phe Ser Phe Tyr Met
                245                 250                 255

Gly Ser Lys Thr Leu Arg Gly Arg Asn Thr Ser Ser Glu Tyr Gln Ile
            260                 265                 270

Leu Thr Ala Arg Arg Glu Asp Ser Gly Leu Tyr Trp Cys Glu Ala Ala
        275                 280                 285

Thr Glu Asp Gly Asn Val Leu Lys Arg Ser Pro Glu Leu Glu Leu Gln
    290                 295                 300

Val Leu Gly Leu Gln Leu Pro Thr Pro Val Trp Phe His Val Leu Phe
305                 310                 315                 320

Tyr Leu Ala Val Gly Ile Met Phe Leu Val Asn Thr Val Leu Trp Val
                325                 330                 335

Thr Ile Arg Lys Glu Leu Lys Arg Lys Lys Lys Trp Xaa Leu Glu Ile
            340                 345                 350

Ser Leu Asp Ser Gly His Glu Lys Lys Val Ile Ser Ser Leu Gln Glu
        355                 360                 365

Asp Arg His Leu Glu Glu Glu Leu Lys Cys Gln Glu Gln Lys Glu Glu
    370                 375                 380

Gln Leu Gln Glu Gly Val His Arg Lys Glu Pro Gln Gly Ala Thr
385                 390                 395


<210> 1129
<211> 147
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids
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<400> 1129
Glu Ile Leu Phe Ile Phe Xaa Xaa Phe Phe Lys Gly Leu Ser Asn Ser
1 5 10 15

Ala Ala Ala Met Ala Pro Val Lys Lys Leu Val Val Lys Gly Gly Lys
20 25 30

Lys Lys Lys Gln Val Leu Lys Phe Thr Leu Asp Cys Thr His Pro Val
35 40 45

Glu Asp Gly Ile Met Asp Ala Ala Asn Phe Glu Gln Phe Leu Gln Glu
50 55 60

Arg Ile Lys Val Asn Gly Lys Ala Gly Asn Leu Gly Gly Gly Val Val
65 70 75 80

Thr Ile Glu Arg Ser Lys Ser Lys Ile Thr Val Thr Ser Glu Val Pro
85 90 95

Phe Ser Lys Arg Tyr Leu Lys Tyr Leu Thr Lys Lys Tyr Leu Lys Lys
100 105 110

Asn Asn Leu Arg Asp Trp Leu Arg Val Val Ala Asn Ser Lys Glu Ser
115 120 125

Tyr Glu Leu Arg Tyr Phe Gln Ile Asn Gln Asp Glu Glu Glu Glu Glu
130 135 140

Asp Glu Asp
145

<210> 1130
<211> 91
<212> PRT
<213> Homo sapiens

<400> 1130
Asn Cys Ser Pro Ala Phe Tyr Gly Ser Ser Leu Pro Cys Pro Gln Thr
1 5 10 15

Gln Gln Lys Arg Arg Gly Arg Ile Arg Gly Leu Ser Arg Pro Ala Pro
20 25 30

Leu Pro Thr Cys His Thr Arg Cys Glu Phe Glu His Ser Pro Glu Met
35 40 45

Glu Thr Ser His Pro Gln Leu Asn Asn Gly Pro Phe Met Pro Thr Leu
50 55 60

Pro Thr Arg Arg Gly Gln Arg Cys Thr Arg Arg Pro Ser Ser Ser Pro
65 70 75 80

Ser Ser Ala Pro Ser His Tyr Ser Trp Phe Tyr
85 90

<210> 1131
<211> 510
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (228)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (352)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1131
Thr Ser Glu Glu Ser Arg Pro Arg Leu Ser Gln Leu Ser Val Thr Asp
1 5 10 15

Val Thr Thr Ser Ser Leu Arg Leu Asn Trp Glu Ala Pro Pro Gly Ala
20 25 30

Phe Asp Ser Phe Leu Leu Arg Phe Gly Val Pro Ser Pro Ser Thr Leu
35 40 45

Glu Pro His Pro Arg Pro Leu Leu Gln Arg Glu Leu Met Val Pro Gly
50 55 60

Thr Arg His Ser Ala Val Leu Arg Asp Leu Arg Ser Gly Thr Leu Tyr
65 70 75 80

Ser Leu Thr Leu Tyr Gly Leu Arg Gly Pro His Lys Ala Asp Ser Ile
85 90 95

Gln Gly Thr Ala Arg Thr Leu Ser Pro Val Leu Glu Ser Pro Arg Asp
100 105 110

Leu Gln Phe Ser Glu Ile Arg Glu Thr Ser Ala Lys Val Asn Trp Met
115 120 125

Pro Pro Pro Ser Arg Ala Asp Ser Phe Lys Val Ser Tyr Gln Leu Ala
130 135 140

Asp Gly Gly Glu Pro Gln Ser Val Gln Val Asp Gly Gln Ala Arg Thr
145 150 155 160

Gln Lys Leu Gln Gly Leu Ile Pro Gly Ala Arg Tyr Glu Val Thr Val
165 170 175

Val Ser Val Arg Gly Phe Glu Glu Ser Glu Pro Leu Thr Gly Phe Leu
180 185 190

Thr Thr Val Pro Asp Gly Pro Thr Gln Leu Arg Ala Leu Asn Leu Thr
195 200 205

Glu Gly Phe Ala Val Leu His Trp Lys Pro Pro Gln Asn Pro Val Asp
210 215 220

Thr Tyr Asp Xaa Gln Val Thr Ala Pro Gly Ala Pro Pro Leu Gln Ala
225 230 235 240

Glu Thr Pro Gly Ser Ala Val Asp Tyr Pro Leu His Asp Leu Val Leu
245 250 255

His Thr Asn Tyr Thr Ala Thr Val Arg Gly Leu Arg Gly Pro Asn Leu
260 265 270

Thr Ser Pro Ala Ser Ile Thr Phe Thr Thr Gly Leu Glu Ala Pro Arg
275 280 285

Asp Leu Glu Ala Lys Glu Val Thr Pro Arg Thr Ala Leu Leu Thr Trp
290 295 300

Thr Glu Pro Pro Val Arg Pro Ala Gly Tyr Leu Leu Ser Phe His Thr
305 310 315 320

Pro Gly Gly Gln Thr Gln Glu Ile Leu Leu Pro Gly Gly Ile Thr Ser
325 330 335

His Gln Leu Leu Gly Leu Phe Pro Ser Thr Ser Tyr Asn Ala Arg Xaa
340 345 350

Gln Ala Met Trp Gly Gln Ser Leu Leu Pro Pro Val Ser Thr Ser Phe
355 360 365

Thr Thr Gly Gly Leu Arg Ile Pro Phe Pro Arg Asp Cys Gly Glu Glu
370 375 380

Met Gln Asn Gly Ala Gly Ala Ser Arg Thr Ser Thr Ile Phe Leu Asn
385 390 395 400

Gly Asn Arg Glu Arg Pro Leu Asn Val Phe Cys Asp Met Glu Thr Asp
405 410 415

Gly Gly Gly Trp Leu Val Phe Gln Arg Arg Met Asp Gly Gln Thr Asp
420 425 430

Phe Trp Arg Asp Trp Glu Asp Tyr Ala His Gly Phe Gly Asn Ile Ser
435 440 445

Gly Glu Phe Trp Leu Gly Asn Glu Ala Leu His Ser Leu Thr Gln Ala
450 455 460

Gly Asp Tyr Ser Met Arg Val Asp Leu Arg Ala Gly Asp Glu Ala Val
465 470 475 480

Phe Ala Gln Tyr Asp Ser Phe His Val Asp Ser Ala Ala Glu Tyr Tyr
485 490 495

Arg Leu His Leu Glu Gly Tyr His Gly Thr Ala Gly Thr Pro
500 505 510

<210> 1132
<211> 430
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (182)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (216)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (408)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (410)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (414)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (420)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (428)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1132
Arg Thr Ala Asp Gln Thr Val Thr Ala Ala Leu Thr Lys Arg Ser Trp
1 5 10 15

Asn Ser Ser Ser Ser Pro Gln Arg Arg Thr Glu Gln Thr Ala Glu Thr
20 25 30

Met Glu Ser Pro Ser Ala Pro Pro His Arg Trp Cys Ile Pro Trp Gln
35 40 45

Arg Leu Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn Pro Pro Thr
50 55 60

Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val Ala Glu Gly
65 70 75 80

Lys Glu Val Leu Leu Leu Val His Asn Leu Pro Gln His Leu Phe Gly
85 90 95

Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Arg Gln Ile Ile
100 105 110

Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro Ala Tyr Ser
115 120 125

Gly Arg Glu Ile Ile Tyr Pro Asn Ala Ser Leu Leu Ile Gln Asn Ile
130 135 140

Ile Gln Asn Asp Thr Gly Phe Tyr Thr Leu His Val Ile Lys Ser Asp
145 150 155 160

Leu Val Asn Glu Glu Ala Thr Gly Gln Phe Arg Val Tyr Pro Glu Leu
165 170 175

Pro Lys Pro Ser Ile Xaa Ser Asn Asn Ser Lys Pro Val Glu Asp Lys
180 185 190

Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Thr Gln Asp Ala Thr Tyr
195 200 205

Leu Trp Trp Val Asn Asn Gln Xaa Leu Pro Val Ser Pro Arg Leu Gln

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    210                 215                 220

Leu Ser Asn Gly Asn Arg Thr Leu Thr Leu Phe Asn Val Thr Arg Asn
225                 230                 235                 240

Asp Thr Ala Ser Tyr Lys Cys Glu Thr Gln Asn Pro Val Ser Ala Arg
                245                 250                 255

Arg Ser Asp Ser Val Ile Leu Asn Val Leu Tyr Gly Pro Asp Ala Pro
            260                 265                 270

Thr Ile Ser Pro Leu Asn Thr Ser Tyr Arg Ser Gly Glu Asn Leu Asn
        275                 280                 285

Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr Ser Trp Phe
    290                 295                 300

Val Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe Ile Pro Asn
305                 310                 315                 320

Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala His Asn Ser
                325                 330                 335

Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr Val Tyr Ala
            340                 345                 350

Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn Pro Val Glu
        355                 360                 365

Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile Gln Asn Thr
    370                 375                 380

Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val Ser Pro Arg
385                 390                 395                 400

Leu His Leu Pro Met Thr Thr Xaa Pro Xaa Leu Tyr Ser Xaa Ala Gln
                405                 410                 415

Gly Met Met Xaa Asp Pro Met Asn Val Glu Ser Xaa Thr Asn
            420                 425                 430
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<210> 1133
<211> 737
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (140)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (186)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (194)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (308)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (534)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (535)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1133
Xaa His Ala Ser Ala Ala Xaa Pro Thr Val Thr Ala Ala Leu Thr Arg
1 5 10 15

Ala Phe Leu Glu Leu Lys Leu Ser Thr Lys Arg Trp Thr Glu Lys Thr
20 25 30

Ala Glu Thr Met Gly Pro Pro Ser Ala Pro Pro Cys Arg Leu His Val
35 40 45

Pro Trp Lys Glu Val Leu Leu Thr Ala Ser Leu Leu Thr Phe Trp Asn
50 55 60

Pro Pro Thr Thr Ala Lys Leu Thr Ile Glu Ser Thr Pro Phe Asn Val

65 70 75 80

Ala Glu Gly Lys Glu Val Leu Leu Leu Ala His Asn Leu Pro Gln Asn
85 90 95

Arg Ile Gly Tyr Ser Trp Tyr Lys Gly Glu Arg Val Asp Gly Asn Ser
100 105 110

Leu Ile Val Gly Tyr Val Ile Gly Thr Gln Gln Ala Thr Pro Gly Pro
115 120 125

Ala Tyr Ser Gly Arg Glu Thr Ile Tyr Pro Asn Xaa Ser Leu Leu Ile
130 135 140

Gln Asn Val Thr Gln Asn Asp Thr Gly Phe Tyr Thr Leu Gln Val Ile
145 150 155 160

Lys Ser Asp Leu Val Asn Glu Glu Ala Thr Gly Gln Phe His Val Tyr
165 170 175

Pro Glu Leu Pro Lys Pro Ser Ile Ser Xaa Asn Asn Ser Asn Pro Val
180 185 190

Glu Xaa Lys Asp Ala Val Ala Phe Thr Cys Glu Pro Glu Val Gln Asn
195 200 205

Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu Pro Val Ser Pro
210 215 220

Arg Leu Gln Leu Ser Asn Gly Asn Met Thr Leu Thr Leu Leu Ser Val
225 230 235 240

Lys Arg Asn Asp Ala Gly Ser Tyr Glu Cys Glu Ile Gln Asn Pro Ala
245 250 255

Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asn Val Leu Tyr Gly Pro
260 265 270

Asp Gly Pro Thr Ile Ser Pro Ser Lys Ala Asn Tyr Arg Pro Gly Glu
275 280 285

Asn Leu Asn Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala Gln Tyr
290 295 300

Ser Trp Phe Xaa Asn Gly Thr Phe Gln Gln Ser Thr Gln Glu Leu Phe
305 310 315 320

Ile Pro Asn Ile Thr Val Asn Asn Ser Gly Ser Tyr Thr Cys Gln Ala
325 330 335

His Asn Ser Asp Thr Gly Leu Asn Arg Thr Thr Val Thr Thr Ile Thr

340 345 350

Val Tyr Ala Glu Pro Pro Lys Pro Phe Ile Thr Ser Asn Asn Ser Asn
355 360 365

Pro Val Glu Asp Glu Asp Ala Val Ala Leu Thr Cys Glu Pro Glu Ile
370 375 380

Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Asn Gln Ser Leu Pro Val
385 390 395 400

Ser Pro Arg Leu Gln Leu Ser Asn Asp Asn Arg Thr Leu Thr Leu Leu
405 410 415

Ser Val Thr Arg Asn Asp Val Gly Pro Tyr Glu Cys Gly Ile Gln Asn
420 425 430

Glu Leu Ser Val Asp His Ser Asp Pro Val Ile Leu Asn Val Leu Tyr
435 440 445

Gly Pro Asp Asp Pro Thr Ile Ser Pro Ser Tyr Thr Tyr Tyr Arg Pro
450 455 460

Gly Val Asn Leu Ser Leu Ser Cys His Ala Ala Ser Asn Pro Pro Ala
465 470 475 480

Gln Tyr Ser Trp Leu Ile Asp Gly Asn Ile Gln Gln His Thr Gln Glu
485 490 495

Leu Phe Ile Ser Asn Ile Thr Glu Lys Asn Ser Gly Leu Tyr Thr Cys
500 505 510

Gln Ala Asn Asn Ser Ala Ser Gly His Ser Arg Thr Thr Val Lys Thr
515 520 525

Ile Thr Val Ser Ala Xaa Xaa Pro Lys Pro Ser Ile Ser Ser Asn Asn
530 535 540

Ser Lys Pro Val Glu Asp Lys Asp Ala Val Ala Phe Thr Cys Glu Pro
545 550 555 560

Glu Ala Gln Asn Thr Thr Tyr Leu Trp Trp Val Asn Gly Gln Ser Leu
565 570 575

Pro Val Ser Pro Arg Leu Gln Leu Ser Asn Gly Asn Arg Thr Leu Thr
580 585 590

Leu Phe Asn Val Thr Arg Asn Asp Ala Arg Ala Tyr Val Cys Gly Ile
595 600 605

Gln Asn Ser Val Ser Ala Asn Arg Ser Asp Pro Val Thr Leu Asp Val

```
    610                 615                 620

Leu Tyr Gly Pro Asp Thr Pro Ile Ile Ser Pro Pro Asp Ser Ser Tyr
625                 630                 635                 640

Leu Ser Gly Ala Asn Leu Asn Leu Ser Cys His Ser Ala Ser Asn Pro
                645                 650                 655

Ser Pro Gln Tyr Ser Trp Arg Ile Asn Gly Ile Pro Gln Gln His Thr
            660                 665                 670

Gln Val Leu Phe Ile Ala Lys Ile Thr Pro Asn Asn Asn Gly Thr Tyr
        675                 680                 685

Ala Cys Phe Val Ser Asn Leu Ala Thr Gly Arg Asn Asn Ser Ile Val
    690                 695                 700

Lys Ser Ile Thr Val Ser Ala Ser Gly Thr Ser Pro Gly Leu Ser Ala
705                 710                 715                 720

Gly Ala Thr Val Gly Ile Met Ile Gly Val Leu Val Gly Val Ala Leu
                725                 730                 735

Ile



<210> 1134
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1134
Phe Gly Thr Xaa Arg Ser Val Val Leu Leu Leu Val Ala Val Arg Leu
  1               5                  10                  15

His Thr Leu Leu Ser Cys Pro Leu Glu Gln Pro Ala Gly Thr Glu Trp
             20                  25                  30

Ile Leu Glu Glu Gly Val Thr Thr Gly Pro Pro Arg Lys Pro Arg Ala
         35                  40                  45

Asp Ile Tyr Asn Leu Arg Ser Pro Asp Glu Phe Ile Val Gly Gln Asn
     50                  55                  60
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Gln Ala Leu Ile Glu Pro Gly
65 70

<210> 1135
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (101)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1135
Gly Leu Arg Arg Leu Asp Ser Ala Ser Gly Thr Val Tyr Thr Ala Met
1 5 10 15

Asp Val Ala Thr Gly Gln Glu Val Ala Ile Lys Gln Met Asn Leu Gln
20 25 30

Gln Gln Pro Lys Lys Glu Leu Ile Ile Asn Glu Ile Leu Val Met Arg
35 40 45

Glu Asn Lys Asn Pro Asn Ile Val Asn Tyr Leu Asp Ser Tyr Leu Val
50 55 60

Gly Asp Glu Leu Trp Val Val Met Glu Tyr Leu Ala Gly Gly Ser Leu
65 70 75 80

Thr Asp Val Val Thr Glu Thr Cys Met Asp Glu Gly Gln Ile Ala Ala
85 90 95

Val Cys Arg Glu Xaa Leu Gln Ala Leu Glu Phe Leu His Ser Asn Gln
100 105 110

Ile Thr Pro Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr Pro Tyr
115 120 125

Trp Met Ala Pro Glu Val Val Thr Arg Lys Ala Tyr Gly Pro Lys Val
130 135 140

Asp Ile Trp Ser Leu Gly Ile Met Ala Ile Glu Met Ile Glu Gly Glu
145 150 155 160

Pro Pro Tyr Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu Ile Ala
165 170 175

Thr Asn Gly Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser Ala Ile
180 185 190

Phe Arg Asp Phe Leu Asn Arg Cys Leu Glu Met Asp Val Glu Lys Arg
195 200 205

Gly Ser Ala Lys Glu Leu Leu Gln His Gln Phe Leu Lys Ile Ala Lys
210 215 220

Pro Leu Ser Ser Leu Thr Pro Leu Ile Ala Ala Ala Lys Glu Ala Thr
225 230 235 240

Lys Asn Asn His

<210> 1136
<211> 166
<212> PRT
<213> Homo sapiens

<400> 1136
Arg Ala Glu Phe Gly Thr Ser Pro Arg Ala Arg Arg His Glu Cys Cys
1 5 10 15

Arg Phe Leu Asp Asp Asn Gln Ile Ile Thr Ser Ser Gly Asp Thr Thr
20 25 30

Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln Thr Val Gly Phe Ala
35 40 45

Gly His Ser Gly Asp Val Met Ser Leu Ser Leu Ala Pro Asp Gly Arg
50 55 60

Thr Phe Val Ser Gly Ala Cys Asp Ala Ser Ile Lys Leu Trp Asp Val
65 70 75 80

Arg Asp Ser Met Cys Arg Gln Thr Phe Ile Gly His Glu Ser Asp Ile
85 90 95

Asn Ala Val Ala Phe Phe Pro Asn Gly Tyr Ala Phe Thr Thr Gly Ser
100 105 110

Asp Asp Ala Thr Cys Arg Leu Phe Asp Leu Arg Ala Asp Gln Glu Leu
115 120 125

Leu Met Tyr Ser His Asp Asn Ile Ile Cys Gly Ile Thr Ser Val Ala
130 135 140

Phe Ser Arg Ser Asp Gly Cys Cys Ser Leu Ala Thr Thr Thr Ser Thr
145 150 155 160

Ala Thr Ser Gly Met Pro
165

<210> 1137
<211> 79
<212> PRT
<213> Homo sapiens

<400> 1137
Thr Asn Asn Lys Ser Leu Val Gln Leu Lys His Ile Ser Asn Asp Phe
1 5 10 15

Ser Lys Phe Lys Val Asp His Asp Arg Ile Ile Lys Asp Arg Lys Asp
20 25 30

Leu Ser Asn Leu Val Met Thr Ile Ile Ser Ile Phe Ala Glu Leu Lys
35 40 45

Ile Phe Asn Phe Ile Asn Met Leu Leu Gln Leu Pro Asp Leu Lys Lys
50 55 60

Lys Ser Phe Pro His Ser Gln Leu Lys Val Arg Thr Leu His Phe
65 70 75

<210> 1138
<211> 397
<212> PRT
<213> Homo sapiens

<400> 1138
Pro Thr Arg Pro Ser Ser Val Ser Arg Arg Asp Lys Ser Lys Gln Val
1 5 10 15

Trp Glu Ala Val Leu Leu Pro Leu Ser Leu Leu Ser Met Met Asp Leu
20 25 30

Arg Asn Thr Pro Ala Lys Ser Leu Asp Lys Phe Ile Glu Asp Tyr Leu
35 40 45

Leu Pro Asp Thr Cys Phe Arg Met Gln Ile Asn His Ala Ile Asp Ile
50 55 60

Ile Cys Gly Phe Leu Lys Glu Arg Cys Phe Arg Gly Ser Ser Tyr Pro
65 70 75 80

Val Cys Val Ser Lys Val Val Lys Gly Gly Ser Ser Gly Lys Gly Thr
85 90 95

```
Thr Leu Arg Gly Arg Ser Asp Ala Asp Leu Val Val Phe Leu Ser Pro
            100                 105                 110

Leu Thr Thr Phe Gln Asp Gln Leu Asn Arg Arg Gly Glu Phe Ile Gln
        115                 120                 125

Glu Ile Arg Arg Gln Leu Glu Ala Cys Gln Arg Glu Arg Ala Phe Ser
    130                 135                 140

Val Lys Phe Glu Val Gln Ala Pro Arg Trp Gly Asn Pro Arg Ala Leu
145                 150                 155                 160

Ser Phe Val Leu Ser Ser Leu Gln Leu Gly Glu Gly Val Glu Phe Asp
                165                 170                 175

Val Leu Pro Ala Phe Asp Ala Leu Asp Phe Ala Arg Thr Gly Gln Leu
            180                 185                 190

Thr Gly Gly Tyr Lys Pro Asn Pro Gln Ile Tyr Val Lys Leu Ile Glu
        195                 200                 205

Glu Cys Thr Asp Leu Gln Lys Glu Gly Glu Phe Ser Thr Cys Phe Thr
    210                 215                 220

Glu Leu Gln Arg Asp Phe Leu Lys Gln Arg Pro Thr Lys Leu Lys Ser
225                 230                 235                 240

Leu Ile Arg Leu Val Lys His Trp Tyr Gln Asn Cys Lys Lys Lys Leu
                245                 250                 255

Gly Lys Leu Pro Pro Gln Tyr Ala Leu Glu Leu Leu Thr Val Tyr Ala
            260                 265                 270

Trp Glu Arg Gly Ser Met Lys Thr His Phe Asn Thr Ala Gln Gly Phe
        275                 280                 285

Arg Thr Val Leu Glu Leu Val Ile Asn Tyr Gln Gln Leu Cys Ile Tyr
    290                 295                 300

Trp Thr Lys Tyr Tyr Asp Phe Lys Asn Pro Ile Ile Glu Lys Tyr Leu
305                 310                 315                 320

Arg Arg Gln Leu Thr Lys Pro Arg Pro Val Ile Leu Asp Pro Ala Asp
                325                 330                 335

Pro Thr Gly Asn Leu Gly Gly Gly Asp Pro Lys Gly Trp Arg Gln Leu
            340                 345                 350

Ala Gln Glu Ala Glu Ala Trp Leu Asn Tyr Pro Cys Phe Lys Asn Trp
        355                 360                 365
```

Asp Gly Ser Pro Val Ser Ser Trp Ile Leu Leu Val Arg Pro Pro Ala
370 375 380

Ser Ser Leu Pro Phe Ile Pro Ala Pro Leu His Glu Ala
385 390 395

<210> 1139
<211> 180
<212> PRT
<213> Homo sapiens

<400> 1139
Phe Leu Leu Ser Asn Ala Arg Trp Ser Asn Arg Pro Asp Thr Ala Thr
1 5 10 15

Ala Leu Ala Gly Gly Ala Val Met Pro Glu Leu Ile Leu Ser Pro Ala
20 25 30

Thr Ala Pro His Pro Leu Lys Met Phe Ala Cys Ser Lys Phe Val Ser
35 40 45

Thr Pro Ser Leu Val Lys Ser Thr Ser Gln Leu Leu Ser Arg Pro Leu
50 55 60

Ser Ala Val Val Leu Lys Arg Pro Glu Ile Leu Thr Asp Glu Ser Leu
65 70 75 80

Ser Ser Leu Ala Val Ser Cys Pro Leu Thr Ser Leu Val Ser Ser Arg
85 90 95

Ser Phe Gln Thr Ser Ala Ile Ser Arg Asp Ile Asp Thr Ala Ala Lys
100 105 110

Phe Ile Gly Ala Gly Ala Ala Thr Val Gly Val Ala Gly Ser Gly Ala
115 120 125

Gly Ile Gly Thr Val Phe Gly Ser Leu Ile Ile Gly Tyr Ala Arg Asn
130 135 140

Pro Ser Leu Lys Gln Gln Leu Phe Ser Tyr Ala Ile Leu Gly Phe Ala
145 150 155 160

Leu Ser Glu Ala Met Gly Leu Phe Cys Leu Met Val Ala Phe Leu Ile
165 170 175

Leu Phe Ala Met
180

<210> 1140
<211> 484
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (25)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1140
Trp Leu Leu Arg Ser Pro Gly Lys Leu Thr Ala Arg Glu Arg Ile Ser
1 5 10 15

Leu Leu Leu Asp Pro Gly Ser Phe Xaa Glu Ser Asp Met Phe Val Glu
20 25 30

His Arg Cys Ala Asp Phe Gly Met Ala Ala Asp Lys Asn Lys Phe Pro
35 40 45

Gly Asp Ser Val Val Thr Gly Arg Gly Arg Ile Asn Gly Arg Leu Val
50 55 60

Tyr Val Phe Ser Gln Asp Phe Thr Val Phe Gly Gly Ser Leu Ser Gly
65 70 75 80

Ala His Ala Gln Lys Ile Cys Lys Ile Met Asp Gln Ala Ile Thr Val
85 90 95

Gly Ala Pro Val Ile Gly Leu Asn Asp Ser Gly Gly Ala Arg Ile Gln
100 105 110

Glu Gly Val Glu Ser Leu Ala Gly Tyr Ala Asp Ile Phe Leu Arg Asn
115 120 125

Val Thr Ala Ser Gly Val Ile Pro Gln Ile Ser Leu Ile Met Gly Pro
130 135 140

Cys Ala Gly Gly Ala Val Tyr Ser Pro Ala Leu Thr Asp Phe Thr Phe
145 150 155 160

Met Val Lys Asp Thr Ser Tyr Leu Phe Ile Thr Gly Pro Asp Val Val
165 170 175

Lys Ser Val Thr Asn Glu Asp Val Thr Gln Glu Glu Leu Gly Gly Ala
180 185 190

Lys Thr His Thr Thr Met Ser Gly Val Ala His Arg Ala Phe Glu Asn
195 200 205

```
Asp Val Asp Ala Leu Cys Asn Leu Arg Asp Phe Phe Asn Tyr Leu Pro
    210                 215                 220

Leu Ser Ser Gln Asp Pro Ala Pro Val Arg Glu Cys His Asp Pro Ser
225                 230                 235                 240

Asp Arg Leu Val Pro Glu Leu Asp Thr Ile Val Pro Leu Glu Ser Thr
                245                 250                 255

Lys Ala Tyr Asn Met Val Asp Ile Ile His Ser Val Val Asp Glu Arg
            260                 265                 270

Glu Phe Phe Glu Ile Met Pro Asn Tyr Ala Lys Asn Ile Ile Val Gly
        275                 280                 285

Phe Ala Arg Met Asn Gly Arg Thr Val Gly Ile Val Gly Asn Gln Pro
    290                 295                 300

Lys Val Ala Ser Gly Cys Leu Asp Ile Asn Ser Ser Val Lys Gly Ala
305                 310                 315                 320

Arg Phe Val Arg Phe Cys Asp Ala Phe Asn Ile Pro Leu Ile Thr Phe
                325                 330                 335

Val Asp Val Pro Gly Phe Leu Pro Gly Thr Ala Gln Glu Tyr Gly Gly
            340                 345                 350

Ile Ile Arg His Gly Ala Lys Leu Leu Tyr Ala Phe Ala Glu Ala Thr
        355                 360                 365

Val Pro Lys Val Thr Val Ile Thr Arg Lys Ala Tyr Gly Gly Ala Tyr
    370                 375                 380

Asp Val Met Ser Ser Lys His Leu Cys Gly Asp Thr Asn Tyr Ala Trp
385                 390                 395                 400

Pro Thr Ala Glu Ile Ala Val Met Gly Ala Lys Gly Ala Val Glu Ile
                405                 410                 415

Ile Phe Lys Gly His Glu Asn Val Glu Ala Ala Gln Ala Glu Tyr Ile
            420                 425                 430

Glu Lys Phe Ala Asn Pro Phe Pro Ala Ala Val Arg Gly Phe Val Asp
        435                 440                 445

Asp Ile Ile Gln Pro Ser Ser Thr Arg Ala Arg Ile Cys Cys Asp Leu
    450                 455                 460

Asp Val Leu Ala Ser Lys Lys Val Gln Arg Pro Trp Arg Lys His Ala
465                 470                 475                 480
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Asn Ile Pro Leu

<210> 1141
<211> 59
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (53)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (54)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1141
Leu Xaa Glu Leu Glu Arg Tyr Val Thr Ser Cys Leu Arg Lys Lys Arg
1 5 10 15

Lys Pro Gln Ala Glu Lys Val Asp Val Ile Ala Gly Ser Ser Lys Met
20 25 30

Lys Gly Phe Ser Ser Ser Glu Ser Glu Ser Ser Ser Glu Ser Ser Ser
35 40 45

Ser Asp Ser Glu Xaa Xaa Glu Thr Gly Pro Ala
50 55

<210> 1142
<211> 199
<212> PRT
<213> Homo sapiens

<400> 1142
Ser Gly Tyr Lys Thr Ile Ser Ala Met Gln Thr Ile Lys Cys Val Val
1 5 10 15

Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Ile Ser Tyr Thr

```
             20                  25                  30

Thr Asn Lys Phe Pro Ser Glu Tyr Val Pro Thr Val Phe Asp Asn Tyr
        35                  40                  45

Ala Val Thr Val Met Ile Gly Gly Glu Pro Tyr Thr Leu Gly Leu Phe
    50                  55                  60

Asp Thr Ala Gly Gln Glu Asp Tyr Asp Arg Leu Arg Pro Leu Ser Tyr
65                  70                  75                  80

Pro Gln Thr Asp Val Phe Leu Val Cys Phe Ser Val Val Ser Pro Ser
                85                  90                  95

Ser Phe Glu Asn Val Lys Glu Lys Trp Val Pro Glu Ile Thr His His
            100                 105                 110

Cys Pro Lys Thr Pro Phe Leu Leu Val Gly Thr Gln Ile Asp Leu Arg
        115                 120                 125

Asp Asp Pro Ser Thr Ile Glu Lys Leu Ala Lys Asn Lys Gln Lys Pro
    130                 135                 140

Ile Thr Pro Glu Thr Ala Glu Lys Leu Ala Arg Asp Leu Lys Ala Val
145                 150                 155                 160

Lys Tyr Val Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys Asn Val
                165                 170                 175

Phe Asp Glu Ala Ile Leu Ala Ala Leu Glu Pro Pro Glu Pro Lys Lys
            180                 185                 190

Ser Arg Arg Cys Val Leu Leu
        195


<210> 1143
<211> 171
<212> PRT
<213> Homo sapiens

<400> 1143
Gly Asp Leu Asp Cys Pro Asp Trp Val Leu Ala Glu Ile Ser Thr Leu
1               5                   10                  15

Ala Lys Met Tyr Glu Lys Ile Leu Lys Leu Thr Ala Asp Ala Lys Phe
            20                  25                  30

Glu Ser Gly Asp Val Lys Ala Thr Val Ala Val Leu Ser Phe Ile Leu
        35                  40                  45
```

Ser Ser Ala Ala Lys His Ser Val Asp Gly Glu Ser Leu Ser Ser Glu
    50   55   60

Leu Gln Gln Leu Gly Leu Pro Lys Glu His Ala Ala Ser Leu Cys Arg
65   70   75   80

Cys Tyr Glu Glu Lys Gln Ser Pro Leu Gln Lys His Leu Arg Val Cys
                85   90   95

Ser Leu Arg Met Asn Arg Leu Ala Gly Val Gly Trp Arg Val Asp Tyr
            100   105   110

Thr Leu Ser Ser Ser Leu Leu Gln Ser Val Glu Glu Pro Met Val His
        115   120   125

Leu Arg Leu Glu Val Ala Ala Ala Pro Gly Thr Pro Ala Gln Pro Val
    130   135   140

Ala Met Ser Leu Ser Ala Asp Lys Phe Gln Val Leu Leu Ala Glu Leu
145   150   155   160

Lys Gln Ala Gln Thr Leu Met Ser Ser Leu Gly
                165   170

<210> 1144
<211> 151
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (38)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (40)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1144
Gln Trp Arg Gln Gly Val Gln Gly Arg Ser Ala Ser Gly Thr Ser Thr
1   5   10   15

Cys Arg Val Ala Arg Xaa Gly Gln Asp Trp Pro Ala Ala Ser Pro Gly
20 25 30

Val Asn Leu Arg Asn Xaa Phe Xaa Pro Pro Leu Leu Leu Ala Pro Val
35 40 45

Pro Thr Pro Val Ala Pro Ser Leu Gly Ser Pro Leu Leu Leu Ser His
50 55 60

Pro Glu Arg Gln Ser Gly Pro Val Thr Gly Gly Ala Gly Glu Gly His
65 70 75 80

Arg Cys Ala Ser Pro Gln Thr Val Cys Gln Val Ser Glu Leu Val Thr
85 90 95

Arg Pro Ala Ala Gln Pro Ser Ala Ala Ala Gln Pro Ala Ala Pro Ala
100 105 110

Gly Gly Arg Thr Pro Gly Arg Ala Gly Pro His Leu Pro Ile Tyr Lys
115 120 125

Ile Gly Gln Gly Asn Met Lys Ala Asp Leu Gln Ala Ala Ala Thr Ala
130 135 140

Lys Pro Gly Lys Ser Gln Gln
145 150

<210> 1145
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1145
Ala Asp Ile Ala Gly Val Leu Ala Ile Arg Pro Asp Glu Leu Arg Phe
1 5 10 15

Arg Tyr Ser Met Val Ala Tyr Trp Arg Gln Ala Gly Leu Ser Tyr Ile
20 25 30

Arg Tyr Ser Gln Ile Cys Ala Lys Ala Val Arg Asp Ala Leu Lys Thr
35 40 45

Glu Phe Lys Ala Asn Ala Glu Lys Thr Ser Gly Ser Asn Val Lys Ile
50 55 60

Val Lys Val Lys Lys Glu
65 70

<210> 1146
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1146
Leu His Ala Asn Gln Val Ile His Arg Asp Ile Lys Ser Asp Asn Val
1 5 10 15

Leu Leu Gly Met Glu Gly Ser Val Lys Leu Thr Asp Phe Gly Phe Cys
20 25 30

Ala Gln Ile Thr Pro Glu Gln Ser Lys Arg Ser Thr Met Val Gly Thr
35 40 45

Pro Tyr Trp Met Ala Pro Glu Xaa Val Thr Arg Lys Ala Tyr Gly Pro
50 55 60

Lys Val Asp Ile Trp Ser Leu Gly Ile Met Ala Ile Glu Met Val Glu
65 70 75 80

Gly Glu Pro Pro Tyr Leu Asn Glu Asn Pro Leu Arg Ala Leu Tyr Leu
85 90 95

Ile Ala Thr Asn Gly Thr Pro Glu Leu Gln Asn Pro Glu Lys Leu Ser
100 105 110

Pro Ile Phe Arg Asp Phe Leu Asn Arg Cys Leu Glu Met Asp Val Glu
115 120 125

Lys Arg Gly Ser Ala Lys Glu Leu Leu Gln His Pro Phe Leu Lys Leu
130 135 140

Ala Lys Pro Leu Ser Ser Leu Thr Pro Leu Ile Met Ala Ala Lys Glu
145 150 155 160

Ala Met Lys Ser Asn Arg
165

<210> 1147
<211> 420
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (203)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1147
Cys Pro Pro Phe Ser Val Arg Val Pro Pro Trp Ala Gly Leu Ala Leu
1   5   10   15

Leu Pro Ser Pro Ser Leu Met Ala Leu Leu Arg Arg Pro Thr Val Ser
            20   25   30

Ser Asp Leu Glu Asn Ile Asp Thr Gly Val Asn Ser Lys Val Lys Ser
        35   40   45

His Val Thr Ile Arg Arg Thr Val Leu Glu Glu Ile Gly Asn Arg Val
    50   55   60

Thr Thr Arg Ala Ala Gln Val Ala Lys Lys Ala Gln Asn Thr Lys Val
65   70   75   80

Pro Val Gln Pro Thr Lys Thr Thr Asn Val Asn Lys Gln Leu Lys Pro
                85   90   95

Thr Ala Ser Val Lys Pro Val Gln Met Glu Lys Leu Ala Pro Lys Gly
            100   105   110

Pro Ser Pro Thr Pro Glu Asp Val Ser Met Lys Glu Glu Asn Leu Cys
        115   120   125

Gln Ala Phe Ser Asp Ala Leu Leu Cys Lys Ile Glu Asp Ile Asp Asn
    130   135   140

Glu Asp Trp Glu Asn Pro Gln Leu Cys Ser Asp Tyr Val Lys Asp Ile
145   150   155   160

Tyr Gln Tyr Leu Arg Gln Leu Glu Val Leu Gln Ser Ile Asn Pro His
                165   170   175

Phe Leu Asp Gly Arg Asp Ile Asn Gly Arg Met Arg Ala Ile Leu Val
            180   185   190

Asp Trp Leu Val Gln Val His Ser Lys Phe Xaa Leu Leu Gln Glu Thr
        195   200   205

Leu Tyr Met Cys Val Gly Ile Met Asp Arg Phe Leu Gln Val Gln Pro
    210   215   220

Val Ser Arg Lys Lys Leu Gln Leu Val Gly Ile Thr Ala Leu Leu Leu
225   230   235   240

Ala Ser Lys Tyr Glu Glu Met Phe Ser Pro Asn Ile Glu Asp Phe Val
245 250 255

Tyr Ile Thr Asp Asn Ala Tyr Thr Ser Ser Gln Ile Arg Glu Met Glu
260 265 270

Thr Leu Ile Leu Lys Glu Leu Lys Phe Glu Leu Gly Arg Pro Leu Pro
275 280 285

Leu His Phe Leu Arg Arg Ala Ser Lys Ala Gly Glu Val Asp Val Glu
290 295 300

Gln His Thr Leu Ala Lys Tyr Leu Met Glu Leu Thr Leu Ile Asp Tyr
305 310 315 320

Asp Met Val His Tyr His Pro Ser Lys Val Ala Ala Ala Ala Ser Cys
325 330 335

Leu Ser Gln Lys Val Leu Gly Gln Gly Lys Trp Asn Leu Lys Gln Gln
340 345 350

Tyr Tyr Thr Gly Tyr Thr Glu Asn Glu Val Leu Glu Val Met Gln His
355 360 365

Met Ala Lys Asn Val Val Lys Val Asn Glu Asn Leu Thr Lys Phe Ile
370 375 380

Ala Ile Lys Asn Lys Tyr Ala Ser Ser Lys Leu Leu Lys Ile Ser Met
385 390 395 400

Ile Pro Gln Leu Asn Ser Lys Ala Val Lys Asp Leu Ala Ser Pro Leu
405 410 415

Ile Gly Arg Ser
420

<210> 1148
<211> 249
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (244)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1148
Gln Ser Asn Ala Val Trp Leu Leu Gly His Leu His Leu Ser Thr Leu

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1               5                   10                  15
Ser Ser Ser Gln Ser Arg Ala Ser Val Pro Thr Asp Tyr Ser Tyr Leu
            20                  25                  30
Pro Glu Ser Ser Phe Ile Gly Ala Ala Ile Gly Phe Phe Ile Thr Gly
        35                  40                  45
Gly Lys Lys Gly Pro Glu Ser Val Pro Pro Ser Leu Leu Lys Val Val
    50                  55                  60
Met Lys Pro Ile Ala Thr Val Gly Glu Ser Tyr Gln Tyr Pro Pro Val
65                  70                  75                  80
Asn Trp Ala Ala Leu Leu Ser Pro Leu Met Arg Leu Asn Phe Gly Glu
                85                  90                  95
Glu Ile Gln Gln Leu Cys Leu Glu Ile Met Val Thr Gln Ala Gln Ser
            100                 105                 110
Ser Gln Asn Ala Ala Ala Leu Leu Gly Leu Trp Val Thr Pro Pro Leu
        115                 120                 125
Ile His Ser Leu Ser Leu Asn Thr Lys Arg Tyr Leu Leu Ile Ser Ala
    130                 135                 140
Pro Leu Trp Ile Lys His Ile Ser Asp Glu Gln Ile Leu Gly Phe Val
145                 150                 155                 160
Glu Asn Leu Met Val Ala Val Phe Lys Ala Ala Ser Pro Leu Gly Ser
                165                 170                 175
Pro Glu Leu Cys Pro Ser Ala Leu His Gly Leu Ser Gln Ala Met Lys
            180                 185                 190
Leu Pro Ser Pro Ala His His Leu Trp Ser Leu Leu Ser Glu Ala Thr
        195                 200                 205
Gly Lys Ile Phe Asp Leu Leu Pro Asn Lys Ile Arg Arg Lys Asp Leu
    210                 215                 220
Glu Leu Tyr Ile Ser Ile Ala Lys Cys Leu Leu Glu Met Thr Asp Asp
225                 230                 235                 240
Asp Ala Asn Xaa Asp Arg Pro Gly Tyr
                245
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<210> 1149
<211> 239

<212> PRT
<213> Homo sapiens

<400> 1149
Arg Asp Pro Pro Arg Pro Val Gln Ser Gly Leu Gly Ala Ala Gly Thr
1 5 10 15

Leu Ser Trp Leu Pro Pro Pro Glu Gln Pro Val Leu Val Pro Arg Leu
20 25 30

Pro Ala Pro Arg Pro Val Met Thr Leu Arg Pro Ser Leu Leu Pro Leu
35 40 45

His Leu Leu Leu Leu Leu Leu Leu Ser Ala Ala Val Cys Arg Ala Glu
50 55 60

Ala Gly Leu Glu Thr Glu Ser Pro Val Arg Thr Leu Gln Val Glu Thr
65 70 75 80

Leu Val Glu Pro Pro Glu Pro Cys Ala Glu Pro Ala Ala Phe Gly Asp
85 90 95

Thr Leu His Ile His Tyr Thr Gly Ser Leu Val Asp Gly Arg Ile Ile
100 105 110

Asp Thr Ser Leu Thr Arg Asp Pro Leu Val Ile Glu Leu Gly Gln Lys
115 120 125

Gln Val Ile Pro Gly Leu Glu Gln Ser Leu Leu Asp Met Cys Val Gly
130 135 140

Glu Lys Arg Arg Ala Ile Ile Pro Ser His Leu Ala Tyr Gly Lys Arg
145 150 155 160

Gly Phe Pro Pro Ser Val Pro Ala Asp Ala Val Val Gln Tyr Asp Val
165 170 175

Glu Leu Ile Ala Leu Ile Arg Ala Asn Tyr Trp Leu Lys Leu Val Lys
180 185 190

Gly Ile Leu Pro Leu Val Gly Met Ala Met Val Pro Ala Leu Leu Gly
195 200 205

Leu Ile Gly Tyr His Leu Tyr Arg Lys Ala Asn Arg Pro Lys Val Ser
210 215 220

Lys Lys Lys Leu Lys Glu Glu Lys Arg Asn Lys Ser Lys Lys Lys
225 230 235

<210> 1150
<211> 394
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1150
Ala Glu Xaa Gly Lys Thr Glu Trp Leu Phe Gly Met Asp Glu Gly Arg
1   5   10   15

Lys Gln Leu Ala Ala Ser Ala Gly Phe Arg Arg Leu Ile Thr Val Ala
            20   25   30

Leu His Arg Gly Gln Gln Tyr Glu Ser Met Asp His Ile Gln Ala Glu
        35   40   45

Leu Ser Ala Arg Val Met Glu Leu Ala Pro Ala Gly Met Pro Thr Gln
    50   55   60

Gln Gln Val Pro Phe Leu Ser Val Gly Gly Asp Ile Gly Val Arg Thr
65   70   75   80

Val Gln His Gln Asp Cys Ser Pro Leu Ser Gly Asp Tyr Val Ile Glu
                85   90   95

Asp Val Gln Gly Asp Asp Lys Arg Tyr Phe Arg Arg Leu Ile Phe Leu
            100   105   110

Ser Asn Arg Asn Val Val Gln Ser Glu Ala Arg Leu Leu Lys Asp Val
        115   120   125

Ser His Lys Ala Gln Lys Lys Arg Lys Lys Asp Arg Lys Lys Gln Arg
    130   135   140

Pro Ala Asp Ala Glu Asp Leu Pro Ala Ala Pro Gly Gln Ser Ile Asp
145   150   155   160

Lys Ser Tyr Leu Cys Cys Glu His His Lys Ala Met Ile Ala Gly Leu
                165   170   175

Ala Leu Leu Arg Asn Pro Glu Leu Leu Leu Glu Ile Pro Leu Ala Leu
            180   185   190

Leu Val Val Gly Leu Gly Gly Gly Ser Leu Pro Leu Phe Val His Asp
        195   200   205

His Phe Pro Lys Ser Cys Ile Asp Ala Val Glu Ile Asp Pro Ser Met

210 215 220

Leu Glu Val Ala Thr Gln Trp Phe Gly Phe Ser Gln Ser Asp Arg Met
225 230 235 240

Lys Val His Ile Ala Asp Gly Leu Asp Tyr Ile Ala Ser Leu Ala Gly
245 250 255

Gly Gly Glu Ala Arg Pro Cys Tyr Asp Val Ile Met Phe Asp Val Asp
260 265 270

Ser Lys Asp Pro Thr Leu Gly Met Ser Cys Pro Pro Pro Ala Phe Val
275 280 285

Glu Gln Ser Phe Leu Gln Lys Val Lys Ser Ile Leu Thr Pro Glu Gly
290 295 300

Val Phe Ile Leu Asn Leu Val Cys Arg Asp Leu Gly Leu Lys Asp Ser
305 310 315 320

Val Leu Ala Gly Leu Lys Ala Val Phe Pro Leu Leu Tyr Val Arg Arg
325 330 335

Ile Glu Gly Glu Val Asn Glu Ile Leu Phe Cys Gln Leu His Pro Glu
340 345 350

Gln Lys Leu Ala Thr Pro Glu Leu Leu Glu Thr Ala Gln Ala Leu Glu
355 360 365

Arg Thr Leu Arg Lys Pro Gly Arg Gly Trp Asp Asp Thr Tyr Val Leu
370 375 380

Ser Asp Met Leu Lys Thr Val Lys Ile Val
385 390

<210> 1151
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1151
Val Asn Val Asn Asn Pro Ser Leu Cys His Ser Ser His Leu Val Asp
1 5 10 15

Leu Gly Ser Gly Ser Val Glu Phe Cys Ala Trp Glu Trp Ser Trp Arg
20 25 30

Glu Trp Gly Leu Cys Thr Ala Ala Thr Ser Pro Arg Ser Ser His Leu
35 40 45

Pro Ala Pro Arg Pro Gly Cys Met Ala Ala Pro Val Cys Val Gln Arg
50 55 60

Ser Val Ser His Pro Leu His Leu Leu Ser Gly Gly Leu Gly Ser Pro
65 70 75 80

Thr Cys Cys Gln Asp Leu Gly Ala Ile Lys Tyr Ser Gly Phe Val Lys
85 90 95

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
100 105 110

<210> 1152
<211> 172
<212> PRT
<213> Homo sapiens

<400> 1152
Leu Gly Asp Thr Ile Glu Gly Arg Leu Gln Val Pro Val Arg Asn Ser
1 5 10 15

Arg Val Asp Pro Arg Val Arg Ala Arg Gly Ala Asp Arg Met Gly Lys
20 25 30

Cys Arg Gly Leu Arg Thr Ala Arg Lys Leu Arg Ser His Arg Arg Asp
35 40 45

Gln Lys Trp His Asp Lys Gln Tyr Lys Lys Ala His Leu Gly Thr Ala
50 55 60

Leu Lys Ala Asn Pro Phe Gly Gly Ala Ser His Ala Lys Gly Ile Val
65 70 75 80

Leu Glu Lys Val Gly Val Glu Ala Lys Gln Pro Asn Ser Ala Ile Arg
85 90 95

Lys Cys Val Arg Val Gln Leu Ile Lys Asn Gly Lys Lys Ile Thr Ala
100 105 110

Phe Val Pro Asn Asp Gly Cys Leu Asn Phe Ile Glu Glu Asn Asp Glu
115 120 125

Val Leu Val Ala Gly Phe Gly Arg Lys Gly His Ala Val Gly Asp Ile
130 135 140

Pro Gly Val Arg Phe Lys Val Val Lys Val Ala Asn Val Ser Leu Leu
145 150 155 160

Ala Leu Tyr Lys Gly Lys Lys Glu Arg Pro Arg Ser
165 170

<210> 1153
<211> 197
<212> PRT
<213> Homo sapiens

<400> 1153
Tyr Trp Cys Glu Gln Cys Asp Val Gln Phe Ser Ser Ser Ser Glu Leu
1 5 10 15

Tyr Leu His Phe Gln Glu His Ser Cys Asp Glu Gln Tyr Leu Cys Gln
20 25 30

Phe Cys Glu His Glu Thr Asn Asp Pro Glu Asp Leu His Ser His Val
35 40 45

Val Asn Glu His Ala Cys Lys Leu Ile Glu Leu Ser Asp Lys Tyr Asn
50 55 60

Asn Gly Glu His Gly Gln Tyr Ser Leu Leu Ser Lys Ile Thr Phe Asp
65 70 75 80

Lys Cys Lys Asn Phe Phe Val Cys Gln Val Cys Gly Phe Arg Ser Arg
85 90 95

Leu His Thr Asn Val Asn Arg His Val Ala Ile Glu His Thr Lys Ile
100 105 110

Phe Pro His Val Cys Asp Asp Cys Gly Lys Gly Phe Ser Ser Met Leu
115 120 125

Glu Tyr Cys Lys His Leu Asn Ser His Leu Ser Glu Gly Ile Tyr Leu
130 135 140

Cys Gln Tyr Cys Glu Tyr Ser Thr Gly Gln Ile Glu Asp Leu Lys Ile
145 150 155 160

His Leu Asp Phe Lys His Ser Ala Asp Leu Pro His Lys Cys Ser Asp
165 170 175

Cys Leu Met Arg Phe Gly Asn Glu Arg Glu Leu Ile Ser His Leu Pro
180 185 190

Val His Glu Thr Thr
195

<210> 1154
<211> 156
<212> PRT
<213> Homo sapiens

<400> 1154
Pro Ala Lys Glu Arg Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
1 5 10 15

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Gly
20 25 30

Ser Ser Ser Ser Asp Ser Glu Gly Ser Ser Leu Pro Val Gln Pro Glu
35 40 45

Val Ala Leu Lys Arg Val Pro Ser Pro Thr Pro Ala Pro Lys Glu Ala
50 55 60

Val Arg Glu Gly Arg Pro Pro Glu Pro Thr Pro Ala Lys Arg Lys Arg
65 70 75 80

Arg Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
85 90 95

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
100 105 110

Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Pro Ser Pro Ala Lys
115 120 125

Pro Gly Pro Gln Ala Cys Pro Asn Leu Gln Ala Pro Arg Ser His Pro
130 135 140

Leu Ala Ser Gly Gly Pro Ala Ala Pro Gly Ser Gln
145 150 155

<210> 1155
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (73)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (105)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (122)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1155
Pro Glu Ala Pro Arg Gly Val Val Thr Cys Leu Arg Ala Leu Leu Ser
1 5 10 15

His Gln His Gln Thr Arg Pro His Arg Val Pro Gly Thr Met Phe Gly
20 25 30

Lys Arg Lys Lys Arg Val Glu Ile Ser Ala Pro Ser Asn Phe Glu His
35 40 45

Arg Val His Thr Gly Phe Asp Gln His Glu Gln Lys Phe Thr Gly Leu
50 55 60

Pro Arg Gln Trp Gln Ser Leu Ile Xaa Glu Ser Ala Arg Arg Pro Lys
65 70 75 80

Pro Leu Val Asp Pro Ala Cys Ile Thr Ser Ile Gln Pro Gly Ala Pro
85 90 95

Lys Thr Ile Val Arg Gly Ser Lys Xaa Ala Lys Asp Gly Ala Leu Thr
100 105 110

Leu Leu Leu Asp Glu Phe Glu Asn Met Xaa Val Thr Arg
115 120 125

<210> 1156
<211> 202
<212> PRT
<213> Homo sapiens

<400> 1156
Arg Pro Thr Arg Pro Gln Pro Ser Pro Asp Glu Ala Arg Pro Leu Gln
1 5 10 15

Ala Leu Leu Asp Gly Arg Gly Leu Cys Val Asn Ala Ser Ala Val Ser
20 25 30

Arg Leu Arg Ala Tyr Leu Leu Pro Ala Pro Pro Ala Pro Gly Asn Ala
35 40 45

Ser Glu Ser Glu Glu Asp Arg Ser Ala Gly Ser Val Glu Ser Pro Ser

50 55 60

Val Ser Ser Thr His Arg Val Ser Asp Pro Lys Phe His Pro Leu His
65 70 75 80

Ser Lys Ile Ile Ile Ile Lys Lys Gly His Ala Lys Asp Ser Gln Arg
85 90 95

Tyr Lys Val Asp Tyr Glu Ser Gln Ser Thr Asp Thr Gln Asn Phe Ser
100 105 110

Ser Glu Ser Lys Arg Glu Thr Glu Tyr Gly Pro Cys Arg Arg Glu Met
115 120 125

Glu Asp Thr Leu Asn His Leu Lys Phe Leu Asn Val Leu Ser Pro Arg
130 135 140

Gly Val His Ile Pro Asn Cys Asp Lys Lys Gly Phe Tyr Lys Lys Lys
145 150 155 160

Gln Cys Arg Pro Ser Lys Gly Arg Lys Arg Gly Phe Cys Trp Cys Val
165 170 175

Asp Lys Tyr Gly Gln Pro Leu Pro Gly Tyr Thr Thr Lys Gly Lys Glu
180 185 190

Asp Val His Cys Tyr Ser Met Gln Ser Lys
195 200

<210> 1157
<211> 269
<212> PRT
<213> Homo sapiens

<400> 1157
Arg Arg Cys Cys His Ser Ala Thr Met Phe Glu Ala Arg Leu Val Gln
1 5 10 15

Gly Ser Ile Leu Lys Lys Val Leu Glu Ala Leu Lys Asp Leu Ile Asn
20 25 30

Glu Ala Cys Trp Asp Ile Ser Ser Ser Gly Val Asn Leu Gln Ser Met
35 40 45

Asp Ser Ser His Val Ser Leu Val Gln Leu Thr Leu Arg Ser Glu Gly
50 55 60

Phe Asp Thr Tyr Arg Cys Asp Arg Asn Leu Ala Met Gly Val Asn Leu
65 70 75 80

Thr Ser Met Ser Lys Ile Leu Lys Cys Ala Gly Asn Glu Asp Ile Ile
85 90 95

Thr Leu Arg Ala Glu Asp Asn Ala Asp Thr Leu Ala Leu Val Phe Glu
100 105 110

Ala Pro Asn Gln Glu Lys Val Ser Asp Tyr Glu Met Lys Leu Met Asp
115 120 125

Leu Asp Val Glu Gln Leu Gly Ile Pro Glu Gln Glu Tyr Ser Cys Val
130 135 140

Val Lys Met Pro Ser Gly Glu Phe Ala Arg Ile Cys Arg Asp Leu Ser
145 150 155 160

His Ile Gly Asp Ala Val Val Ile Ser Cys Ala Lys Asp Gly Val Lys
165 170 175

Phe Ser Ala Ser Gly Glu Leu Gly Asn Gly Asn Ile Lys Leu Ser Gln
180 185 190

Thr Ser Asn Val Asp Lys Glu Glu Glu Ala Val Thr Ile Glu Met Asn
195 200 205

Glu Pro Val Gln Leu Thr Phe Ala Leu Arg Tyr Leu Asn Phe Phe Thr
210 215 220

Lys Ala Thr Pro Leu Ser Ser Thr Val Thr Leu Ser Met Ser Ala Asp
225 230 235 240

Val Pro Leu Val Val Glu Tyr Lys Ile Ala Asp Met Gly His Leu Lys
245 250 255

Tyr Tyr Leu Ala Pro Lys Ile Glu Asp Glu Glu Gly Ser
260 265

<210> 1158
<211> 639
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (129)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (150)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1158
Met Asp Glu Met Ala Thr Thr Gln Ile Ser Lys Asp Glu Leu Asp Glu
1 5 10 15

Leu Lys Glu Ala Phe Ala Lys Val Asp Leu Asn Ser Asn Gly Phe Ile
20 25 30

Cys Asp Tyr Glu Leu His Glu Leu Phe Lys Glu Ala Asn Met Pro Leu
35 40 45

Pro Gly Tyr Lys Val Arg Glu Ile Ile Gln Lys Leu Met Leu Asp Gly
50 55 60

Asp Arg Asn Lys Asp Gly Lys Ile Ser Phe Asp Glu Phe Val Tyr Ile
65 70 75 80

Phe Gln Glu Val Lys Ser Ser Asp Ile Ala Lys Thr Phe Arg Lys Ala
85 90 95

Ile Asn Arg Lys Glu Gly Ile Cys Ala Leu Gly Gly Thr Ser Glu Leu
100 105 110

Ser Ser Glu Gly Thr Gln His Ser Tyr Ser Glu Glu Glu Lys Tyr Ala
115 120 125

Xaa Val Asn Trp Ile Asn Lys Ala Leu Glu Asn Asp Pro Asp Cys Arg
130 135 140

His Val Ile Pro Met Xaa Pro Asn Thr Asp Asp Leu Phe Lys Ala Val
145 150 155 160

Gly Asp Gly Ile Val Leu Cys Lys Met Ile Asn Leu Ser Val Pro Asp
165 170 175

Thr Ile Asp Glu Arg Ala Ile Asn Lys Lys Lys Leu Thr Pro Phe Ile
180 185 190

Ile Gln Glu Asn Leu Asn Leu Ala Leu Asn Ser Ala Ser Ala Ile Gly
195 200 205

Cys His Val Val Asn Ile Gly Ala Glu Asp Leu Arg Ala Gly Lys Pro
210 215 220

His Leu Val Leu Gly Leu Leu Trp Gln Ile Ile Lys Ile Gly Leu Phe
225 230 235 240

Ala Asp Ile Glu Leu Ser Arg Asn Glu Ala Leu Ala Ala Leu Leu Arg
245 250 255

Asp Gly Glu Thr Leu Glu Glu Leu Met Lys Leu Ser Pro Glu Glu Leu
260 265 270

Leu Leu Arg Trp Ala Asn Phe His Leu Glu Asn Ser Gly Trp Gln Lys
275 280 285

Ile Asn Asn Phe Ser Ala Asp Ile Lys Leu Ile Asp Phe Ser Asn Ser
290 295 300

Val Lys Asp Ser Lys Ala Tyr Phe His Leu Leu Asn Gln Ile Ala Pro
305 310 315 320

Lys Gly Gln Lys Glu Gly Glu Pro Arg Ile Asp Ile Asn Met Ser Gly
325 330 335

Phe Asn Glu Thr Asp Asp Leu Lys Arg Ala Glu Ser Met Leu Gln Gln
340 345 350

Ala Asp Lys Leu Gly Cys Arg Gln Phe Val Thr Pro Ala Asp Val Val
355 360 365

Ser Gly Asn Pro Lys Leu Asn Leu Ala Phe Val Ala Asn Leu Phe Asn
370 375 380

Lys Tyr Pro Ala Leu Thr Lys Pro Glu Asn Gln Asp Ile Asp Trp Thr
385 390 395 400

Leu Leu Glu Gly Glu Thr Arg Glu Glu Arg Thr Phe Arg Asn Trp Met
405 410 415

Asn Ser Leu Gly Val Asn Pro His Val Asn His Leu Tyr Ala Asp Leu
420 425 430

Gln Asp Ala Leu Val Ile Leu Gln Leu Tyr Glu Arg Ile Lys Val Pro
435 440 445

Val Asp Trp Ser Lys Val Asn Lys Pro Pro Tyr Pro Lys Leu Gly Ala
450 455 460

Asn Met Lys Lys Leu Glu Asn Cys Asn Tyr Ala Val Glu Leu Gly Lys
465 470 475 480

His Pro Ala Lys Phe Ser Leu Val Gly Ile Gly Gly Gln Asp Leu Asn
485 490 495

Asp Gly Asn Gln Thr Leu Thr Leu Ala Leu Val Trp Gln Leu Met Arg
500 505 510

Arg Tyr Thr Leu Asn Val Leu Glu Asp Leu Gly Asp Gly Gln Lys Ala
515 520 525

Asn Asp Asp Ile Ile Val Asn Trp Val Asn Arg Thr Leu Ser Glu Ala
530 535 540

Gly Lys Ser Thr Ser Ile Gln Ser Phe Lys Asp Lys Thr Ile Ser Ser
545 550 555 560

Ser Leu Ala Val Val Asp Leu Ile Asp Ala Ile Gln Pro Gly Cys Ile
565 570 575

Asn Tyr Asp Leu Val Lys Ser Gly Asn Leu Thr Glu Asp Asp Lys His
580 585 590

Asn Asn Ala Lys Tyr Ala Val Ser Met Ala Arg Arg Ile Gly Ala Arg
595 600 605

Val Tyr Ala Leu Pro Glu Asp Leu Val Glu Val Lys Pro Lys Met Val
610 615 620

Met Thr Val Phe Ala Cys Leu Met Gly Arg Gly Met Lys Arg Val
625 630 635

<210> 1159
<211> 63
<212> PRT
<213> Homo sapiens

<400> 1159
Thr Ile Trp Pro Leu Asn Phe His Arg Lys Asn Asp Pro Thr Phe Leu
1 5 10 15

Ser Met Ser Tyr Leu Ile Ser Arg Ser Trp Asp Gly Leu Thr Ile Leu
20 25 30

Val Tyr Ile Leu Asp Thr Glu Arg Cys Tyr Ala Ser Val Ile Ile Pro
35 40 45

Arg Leu Glu Ile Gly Arg Ala Lys Lys Val Leu Leu Phe Phe Leu
50 55 60

<210> 1160
<211> 207
<212> PRT
<213> Homo sapiens

<400> 1160
Glu Val Tyr Gly Gly Ser Leu Asp Lys Glu Phe Asp Glu Ser Ser Pro

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1               5                   10                  15
Lys Gln Pro Thr Asn Pro Tyr Ala Ser Ser Lys Ala Ala Ala Glu Cys
            20                  25                  30
Phe Val Gln Ser Tyr Trp Glu Gln Tyr Lys Phe Pro Val Val Ile Thr
        35                  40                  45
Arg Ser Ser Asn Val Tyr Gly Pro His Gln Tyr Pro Glu Lys Val Ile
    50                  55                  60
Pro Lys Phe Ile Ser Leu Leu Gln His Asn Arg Lys Cys Cys Ile His
65                  70                  75                  80
Gly Ser Gly Leu Gln Thr Arg Asn Phe Leu Tyr Ala Thr Asp Val Val
                85                  90                  95
Glu Ala Phe Leu Thr Val Leu Lys Lys Gly Lys Pro Gly Glu Ile Tyr
            100                 105                 110
Asn Ile Gly Thr Asn Phe Glu Met Ser Val Val Gln Leu Ala Lys Glu
        115                 120                 125
Leu Ile Gln Leu Ile Lys Glu Thr Asn Ser Glu Ser Glu Met Glu Asn
    130                 135                 140
Trp Val Asp Tyr Val Asn Asp Arg Pro Thr Asn Asp Met Arg Tyr Pro
145                 150                 155                 160
Met Lys Ser Glu Lys Ile His Gly Leu Gly Trp Arg Pro Lys Val Pro
                165                 170                 175
Trp Lys Glu Gly Ile Lys Lys Thr Ile Glu Trp Tyr Arg Glu Asn Phe
            180                 185                 190
His Asn Trp Lys Asn Val Glu Lys Ala Leu Glu Pro Phe Pro Val
        195                 200                 205
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<210> 1161
<211> 848
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (815)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<221> SITE
<222> (844)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1161
Ala Leu Gly Leu Gly Val Thr Met Ala Thr Glu Glu Phe Ile Ile Arg
1   5   10   15

Ile Pro Pro Tyr His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val
            20   25   30

Ser Arg Val Glu Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu
        35   40   45

Arg Val Leu Phe Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His
    50   55   60

Tyr Cys Thr Val Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val
65   70   75   80

Leu Phe Asp Val Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu
                85   90   95

Ile Arg Leu Ala Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu
            100   105   110

Glu Lys Asp Ile Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu
        115   120   125

His Leu Lys Ala Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val
    130   135   140

Val Ala Gly Asp Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro
145   150   155   160

Arg Lys Glu Val Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg
                165   170   175

Gln Asn Gln Ala Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg
            180   185   190

Asp Gly Lys Glu Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val
        195   200   205

Gly Ala Tyr Leu Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp
    210   215   220

Ala Val Ile Leu Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg
225   230   235   240

Asn Phe Arg Asp Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp

245 250 255

Leu Val Thr Val Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu
260 265 270

Glu Val Leu Gly Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr
275 280 285

Cys Val Ile Leu Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly
290 295 300

Gln Lys Arg Val Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly
305 310 315 320

Glu Gln Leu Glu Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln
325 330 335

Gln Gly Leu Leu Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp
340 345 350

Glu Glu Lys Val Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly
355 360 365

Pro Leu Glu Tyr Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg
370 375 380

Gln Ala Ile Pro Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val
385 390 395 400

Lys Thr Gly Lys Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr
405 410 415

Gln Asp Glu Val Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu
420 425 430

Leu Leu Asn Lys Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp
435 440 445

Thr Ala Lys Ser Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val
450 455 460

Val Ser Tyr Arg Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr
465 470 475 480

Arg Glu Lys Arg Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu
485 490 495

Gly Pro Glu Glu Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro
500 505 510

Lys Arg Pro His Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp

515 520 525

Phe Phe Thr Asp Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu
530 535 540

Gln Leu Gln Leu Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys
545 550 555 560

Asp Pro Gln Glu Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly
565 570 575

Asp Ala Cys Lys Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser
580 585 590

Val Thr Phe Asp Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr
595 600 605

Ala Val Phe Gly Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met
610 615 620

Ala Leu Pro Arg Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu
625 630 635 640

Val Val Ser Ser Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg
645 650 655

Thr Arg Asp Ala Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr
660 665 670

Thr Asn Ser Gln Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu
675 680 685

Gln Glu Ala Arg Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser
690 695 700

Glu Ala Glu Lys Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser
705 710 715 720

Met Ala Val Glu Ser Thr Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg
725 730 735

Ala Glu Ala Ala Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys
740 745 750

Leu Lys Ala Gln Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg
755 760 765

Val Gln Lys Val Arg Glu Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu
770 775 780

Glu Leu Glu Val Ser Lys Ala Gln Gln Leu Ala Glu Val Glu Val Lys

785 790 795 800

Lys Phe Lys Gln Met Thr Glu Ala Ile Gly Pro Ser Thr Ile Xaa Asp
805 810 815

Leu Ala Val Ala Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu
820 825 830

Gly Leu Lys Ser Thr Leu Ile Thr Asp Gly Phe Xaa Ser Ile Asn Phe
835 840 845

<210> 1162
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (28)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1162
Phe Xaa Val Gly Ile Val Asn Phe Ser Gln Pro Pro His Ala Ala Gly
1 5 10 15

Glu Cys Gly Cys Ser Ser Ser Glu Met Leu Thr Xaa Lys Arg Glu Val
20 25 30

Lys Gln Ser Arg Tyr Val Gln Pro Cys Leu Gln Asn Pro Ser Leu Ser
35 40 45

Ser Leu Ile Arg Ser Phe Leu Val Phe Tyr
50 55

<210> 1163
<211> 565
<212> PRT
<213> Homo sapiens

<400> 1163

Ile Pro Gly Ser Thr His Ala Ser Ala Gly Asn Leu Asp Ser Pro Glu
1   5   10   15

Gly Gly Phe Asp Ala Ile Met Gln Val Ala Val Cys Gly Ser Leu Ile
            20   25   30

Gly Trp Arg Asn Val Thr Arg Leu Leu Val Phe Ser Thr Asp Ala Gly
        35   40   45

Phe His Phe Ala Gly Asp Gly Lys Leu Gly Gly Ile Val Leu Pro Asn
    50   55   60

Asp Gly Gln Cys His Leu Glu Asn Asn Met Tyr Thr Met Ser His Tyr
65   70   75   80

Tyr Asp Tyr Pro Ser Ile Ala His Leu Val Gln Lys Leu Ser Glu Asn
                85   90   95

Asn Ile Gln Thr Ile Phe Ala Val Thr Glu Glu Phe Gln Pro Val Tyr
            100   105   110

Lys Glu Leu Lys Asn Leu Ile Pro Lys Ser Ala Val Gly Thr Leu Ser
        115   120   125

Ala Asn Ser Ser Asn Val Ile Gln Leu Ile Ile Asp Ala Tyr Asn Ser
    130   135   140

Leu Ser Ser Glu Val Ile Leu Glu Asn Gly Lys Leu Ser Glu Gly Val
145   150   155   160

Thr Ile Ser Tyr Lys Ser Tyr Cys Lys Asn Gly Val Asn Gly Thr Gly
                165   170   175

Glu Asn Gly Arg Lys Cys Ser Asn Ile Ser Ile Gly Asp Glu Val Gln
            180   185   190

Phe Glu Ile Ser Ile Thr Ser Asn Lys Cys Pro Lys Lys Asp Ser Asp
        195   200   205

Ser Phe Lys Ile Arg Pro Leu Gly Phe Thr Glu Glu Val Glu Val Ile
    210   215   220

Leu Gln Tyr Ile Cys Glu Cys Glu Cys Gln Ser Glu Gly Ile Pro Glu
225   230   235   240

Ser Pro Lys Cys His Glu Gly Asn Gly Thr Phe Glu Cys Gly Ala Cys
                245   250   255

Arg Cys Asn Glu Gly Arg Val Gly Arg His Cys Glu Cys Ser Thr Asp
            260   265   270

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Glu Val Asn Ser Glu Asp Met Asp Ala Tyr Cys Arg Lys Glu Asn Ser
        275                 280                 285

Ser Glu Ile Cys Ser Asn Asn Gly Glu Cys Val Cys Gly Gln Cys Val
    290                 295                 300

Cys Arg Lys Arg Asp Asn Thr Asn Glu Ile Tyr Ser Gly Lys Phe Cys
305                 310                 315                 320

Glu Cys Asp Asn Phe Asn Cys Asp Arg Ser Asn Gly Leu Ile Cys Gly
                325                 330                 335

Gly Asn Gly Val Cys Lys Cys Arg Val Cys Glu Cys Asn Pro Asn Tyr
            340                 345                 350

Thr Gly Ser Ala Cys Asp Cys Ser Leu Asp Thr Ser Thr Cys Glu Ala
        355                 360                 365

Ser Asn Gly Gln Ile Cys Asn Gly Arg Gly Ile Cys Glu Cys Gly Val
    370                 375                 380

Cys Lys Cys Thr Asp Pro Lys Phe Gln Gly Gln Thr Cys Glu Met Cys
385                 390                 395                 400

Gln Thr Cys Leu Gly Val Cys Ala Glu His Lys Glu Cys Val Gln Cys
                405                 410                 415

Arg Ala Phe Asn Lys Gly Glu Lys Lys Asp Thr Cys Thr Gln Glu Cys
            420                 425                 430

Ser Tyr Phe Asn Ile Thr Lys Val Glu Ser Arg Asp Lys Leu Pro Gln
        435                 440                 445

Pro Val Gln Pro Asp Pro Val Ser His Cys Lys Glu Lys Asp Val Asp
    450                 455                 460

Asp Cys Trp Phe Tyr Phe Thr Tyr Ser Val Asn Gly Asn Asn Glu Val
465                 470                 475                 480

Met Val His Val Val Glu Asn Pro Glu Cys Pro Thr Gly Pro Asp Ile
                485                 490                 495

Ile Pro Ile Val Ala Gly Val Val Ala Gly Ile Val Leu Ile Gly Leu
            500                 505                 510

Ala Leu Leu Leu Ile Trp Lys Leu Leu Met Ile Ile His Asp Arg Arg
        515                 520                 525

Glu Phe Ala Lys Phe Glu Lys Glu Lys Met Asn Ala Lys Trp Asp Thr
    530                 535                 540
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Gly Glu Asn Pro Ile Tyr Lys Ser Ala Val Thr Thr Val Val Asn Pro
545 550 555 560

Lys Tyr Glu Gly Lys
565

<210> 1164
<211> 138
<212> PRT
<213> Homo sapiens

<400> 1164
Gly Thr Ala Gly Gly Ala Gly Gly Gln Arg Glu Val Arg Gly Cys Ser
1 5 10 15

Ala Gln Glu Thr Met Ser Gly Gly Ser Ser Cys Ser Gln Thr Pro Ser
20 25 30

Arg Ala Ile Pro Ala Thr Arg Arg Val Val Leu Gly Asp Gly Val Gln
35 40 45

Leu Pro Pro Gly Asp Tyr Ser Thr Thr Pro Gly Gly Thr Leu Phe Ser
50 55 60

Thr Thr Pro Gly Gly Thr Arg Ile Ile Tyr Asp Arg Lys Phe Leu Met
65 70 75 80

Glu Cys Arg Asn Ser Pro Val Thr Lys Thr Pro Pro Arg Asp Leu Pro
85 90 95

Thr Ile Pro Gly Val Thr Ser Pro Ser Ser Asp Glu Pro Pro Met Glu
100 105 110

Ala Ser Gln Ser His Leu Arg Asn Ser Pro Glu Asp Lys Arg Ala Gly
115 120 125

Gly Glu Glu Ser Gln Phe Glu Met Asp Ile
130 135

<210> 1165
<211> 407
<212> PRT
<213> Homo sapiens

<400> 1165
Ala Ala Cys Gln Pro Arg Cys Cys Cys Ser Ser Cys Cys Gly Thr Ala

1   5   10   15

Asp Arg Ala Ala Ala Pro Leu Ser Pro Leu Gln Ala Pro Ile Trp Ala
            20   25   30

Pro Ala Thr Ser Met Asp Ala Arg Arg Val Pro Gln Lys Asp Leu Arg
        35   40   45

Val Lys Lys Asn Leu Lys Lys Phe Arg Tyr Val Lys Leu Ile Ser Met
    50   55   60

Glu Thr Ser Ser Ser Ser Asp Asp Ser Cys Asp Ser Phe Ala Ser Asp
65   70   75   80

Asn Phe Ala Asn Thr Arg Leu Gln Ser Val Arg Glu Gly Cys Arg Thr
                85   90   95

Arg Ser Gln Cys Arg His Ser Gly Pro Leu Arg Val Ala Met Lys Phe
            100   105   110

Pro Ala Arg Ser Thr Arg Gly Ala Thr Asn Lys Lys Ala Glu Ser Arg
        115   120   125

Gln Pro Ser Glu Asn Ser Val Thr Asp Ser Asn Ser Asp Ser Glu Asp
    130   135   140

Glu Ser Gly Met Asn Phe Leu Glu Lys Arg Ala Leu Asn Ile Lys Gln
145   150   155   160

Asn Lys Ala Met Leu Ala Lys Leu Met Ser Glu Leu Glu Ser Phe Pro
                165   170   175

Gly Ser Phe Arg Gly Arg His Pro Leu Pro Gly Ser Asp Ser Gln Ser
            180   185   190

Arg Arg Pro Arg Arg Arg Thr Phe Pro Gly Val Ala Ser Arg Arg Asn
        195   200   205

Pro Glu Arg Arg Ala Arg Pro Leu Thr Arg Ser Arg Ser Arg Ile Leu
    210   215   220

Gly Ser Leu Asp Ala Leu Pro Met Glu Glu Glu Glu Glu Glu Asp Lys
225   230   235   240

Tyr Met Leu Val Arg Lys Arg Lys Thr Val Asp Gly Tyr Met Asn Glu
                245   250   255

Asp Asp Leu Pro Arg Ser Arg Arg Ser Arg Ser Ser Val Thr Leu Pro
            260   265   270

His Ile Ile Arg Pro Val Glu Glu Ile Thr Glu Glu Glu Leu Glu Asn

275 280 285

Val Cys Ser Asn Ser Arg Glu Lys Ile Tyr Asn Arg Ser Leu Gly Ser
290 295 300

Thr Cys His Gln Cys Arg Gln Lys Thr Ile Asp Thr Lys Thr Asn Cys
305 310 315 320

Arg Asn Pro Asp Cys Trp Gly Val Arg Gly Gln Phe Cys Gly Pro Cys
325 330 335

Leu Arg Asn Arg Tyr Gly Glu Glu Val Arg Asp Ala Leu Leu Asp Pro
340 345 350

Asn Trp His Cys Pro Pro Cys Arg Gly Ile Cys Asn Cys Ser Phe Cys
355 360 365

Arg Gln Arg Asp Gly Arg Cys Ala Thr Gly Val Leu Val Tyr Leu Ala
370 375 380

Lys Tyr His Gly Phe Gly Asn Val His Ala Tyr Leu Lys Ser Leu Lys
385 390 395 400

Gln Glu Phe Glu Met Gln Ala
405

<210> 1166
<211> 240
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (197)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (201)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (202)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (219)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1166

Pro Asp Gly Arg Pro Thr Gly Asp Ala Phe Val Leu Phe Ala Cys Glu
1 5 10 15

Glu Tyr Ala Gln Asn Ala Leu Arg Lys His Lys Asp Leu Leu Gly Lys
20 25 30

Arg Tyr Ile Glu Leu Phe Arg Ser Thr Ala Ala Glu Val Gln Gln Val
35 40 45

Leu Asn Arg Phe Ser Ser Ala Pro Leu Ile Pro Leu Pro Thr Pro Pro
50 55 60

Ile Ile Pro Val Leu Pro Gln Gln Phe Val Pro Pro Thr Asn Val Arg
65 70 75 80

Asp Cys Ile Arg Leu Arg Gly Leu Pro Tyr Ala Ala Thr Ile Glu Asp
85 90 95

Ile Leu Asp Phe Leu Gly Glu Phe Ala Thr Asp Ile Arg Thr His Gly
100 105 110

Val His Met Val Leu Asn His Gln Gly Arg Pro Ser Gly Asp Ala Phe
115 120 125

Ile Gln Met Lys Ser Ala Asp Arg Ala Phe Met Ala Ala Gln Lys Cys
130 135 140

His Lys Lys Asn Met Lys Asp Arg Tyr Val Glu Val Phe Gln Cys Ser
145 150 155 160

Ala Glu Glu Met Asn Phe Val Leu Met Gly Gly Thr Leu Asn Arg Asn
165 170 175

Gly Leu Ser Pro Pro Pro Cys Leu Ser Pro Pro Ser Tyr Thr Phe Pro
180 185 190

Ala Pro Ala Ala Xaa Ile Pro Thr Xaa Xaa Ala Ile Tyr Gln Pro Ser
195 200 205

Val Ile Leu Asn Pro Arg Ala Leu Gln Pro Xaa Thr Ala Tyr Tyr Pro
210 215 220

Ala Gly Thr Gln Leu Phe Met Asn Tyr Thr Ala Tyr Tyr Pro Ser Val
225 230 235 240

<210> 1167
<211> 106
<212> PRT
<213> Homo sapiens

<400> 1167
Gly Gly Tyr Ser Val Asp Ser Pro Thr Leu Thr Arg Phe Phe Thr Phe
1   5   10   15

His Phe Ile Leu Pro Phe Ile Ile Ala Ala Leu Ala Ala Leu His Leu
            20   25   30

Leu Phe Leu His Glu Thr Gly Ser Asn Asn Pro Leu Gly Ile Thr Ser
        35   40   45

His Ser Asp Lys Ile Thr Phe His Pro Tyr Tyr Thr Ile Lys Asp Ala
    50   55   60

Leu Gly Leu Leu Leu Phe Leu Leu Ser Leu Met Thr Leu Thr Leu Phe
65   70   75   80

Ser Pro Asp Leu Leu Gly Asp Pro Asp Asn Tyr Thr Leu Ala Asn Pro
                85   90   95

Leu Asn Thr Pro Pro His Ile Lys Pro Glu
            100   105

<210> 1168
<211> 210
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (53)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1168
Gln His Val Gln Arg Glu Trp Ser Gly His Gly Glu Asp Arg Gly Asp
1   5   10   15

Gly Glu Asp Ala Glu Arg Gly Ser Cys Arg Glu Glu Pro Ala His Gly
            20   25   30

Val Glu Gly Ala Gly Asp Gly Ala Ala Ala Ala Gly Pro Gly Gly Gly
        35   40   45

Ala Ala Glu Ala Xaa Gln Val Glu Arg Arg Leu Gln Ser Glu Ser Ala
    50   55   60

Arg Arg Gln Gln Leu Val Glu Lys Glu Val Lys Met Arg Glu Lys Gln
65   70   75   80

Phe Ser Gln Ala Arg Pro Leu Thr Arg Tyr Leu Pro Ile Arg Lys Glu
                85   90   95

Asp Phe Asp Leu Lys Thr His Ile Glu Ser Ser Gly His Gly Val Asp
            100   105   110

Thr Cys Leu His Val Val Leu Ser Ser Lys Val Cys Arg Gly Tyr Leu
        115   120   125

Val Lys Met Gly Gly Lys Ile Lys Ser Trp Lys Lys Arg Trp Phe Val
    130   135   140

Phe Asp Arg Leu Lys Arg Thr Leu Ser Tyr Tyr Val Asp Lys His Glu
145   150   155   160

Thr Lys Leu Lys Gly Val Ile Tyr Phe Gln Ala Ile Glu Gly Ser Val
                165   170   175

Leu Arg Pro Pro Ala Pro Val Gln Pro Arg Arg Gly Phe Ser Ala Ser
            180   185   190

Thr Met Val Thr Glu Lys Pro Glu Pro Ser Pro His Leu Leu Arg Lys
        195   200   205

Asp Pro
    210

<210> 1169
<211> 181
<212> PRT
<213> Homo sapiens

<400> 1169
Thr Ser Lys Met Arg Ser Leu Glu Thr Leu Gly Arg Pro Lys Pro Glu
1   5   10   15

Cys Glu Gly Tyr Asp Pro Asn Ala Leu Tyr Cys Ile Cys Arg Gln Pro
            20   25   30

His Asn Asn Arg Phe Met Ile Cys Cys Asp Arg Cys Glu Glu Trp Phe
        35   40   45

His Gly Asp Cys Val Gly Ile Ser Glu Ala Arg Gly Arg Leu Leu Glu

50 55 60

Arg Asn Gly Glu Asp Tyr Ile Cys Pro Asn Cys Thr Ile Leu Gln Val
65 70 75 80

Gln Asp Glu Thr His Ser Glu Thr Ala Asp Gln Gln Glu Ala Lys Trp
85 90 95

Arg Pro Gly Asp Ala Asp Gly Thr Asp Cys Thr Ser Ile Gly Thr Ile
100 105 110

Glu Gln Lys Ser Ser Glu Asp Gln Gly Ile Lys Gly Arg Ile Glu Lys
115 120 125

Ala Ala Asn Pro Ser Gly Lys Lys Lys Leu Lys Ile Phe Gln Pro Val
130 135 140

Ile Glu Ala Pro Gly Ala Ser Lys Cys Ile Gly Pro Gly Cys Cys His
145 150 155 160

Val Ala His Pro Thr Arg Cys Thr Ala Val Met Thr Val Ser Ser Asn
165 170 175

Thr Pro Gln Arg Gln
180

<210> 1170
<211> 166
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (18)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (131)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1170
Ala Gln Xaa Leu Ser Ser Pro Val Arg Gly Ile Ser Gly Glu Gln Ser
1 5 10 15

Thr Xaa Gly Ser Phe Pro Leu Arg Tyr Val Gln Asp Gln Val Ala Ala
20 25 30

Pro Phe Gln Leu Ser Asn His Thr Gly Arg Ile Lys Val Val Phe Thr
35 40 45

Pro Ser Ile Cys Lys Val Thr Cys Thr Lys Gly Ser Cys Gln Asn Ser
50 55 60

Cys Glu Lys Gly Asn Thr Thr Thr Leu Ile Ser Glu Asn Gly His Ala
65 70 75 80

Ala Asp Thr Leu Thr Ala Thr Asn Phe Arg Val Val Ile Cys His Leu
85 90 95

Pro Cys Met Asn Gly Gly Gln Cys Ser Ser Arg Asp Lys Cys Gln Cys
100 105 110

Pro Pro Asn Phe Thr Gly Lys Leu Cys Gln Ile Pro Val His Gly Ala
115 120 125

Ser Val Xaa Lys Leu Tyr Gln His Ser Gln Gln Pro Gly Lys Ala Leu
130 135 140

Gly Thr His Val Ile His Ser Thr His Thr Leu Pro Leu Thr Val Thr
145 150 155 160

Ser Gln Gln Glu Ser Lys
165

<210> 1171
<211> 37
<212> PRT
<213> Homo sapiens

<400> 1171
Asp Leu Ser Val Asn Phe Trp Glu Pro Asn Gly Phe Gly His Asp Phe
1 5 10 15

Pro Ala His Tyr Ile Leu Thr Gln Asn Phe Phe Arg Met Ala Phe Thr
20 25 30

Ser Thr Pro Glu Ile
35

<210> 1172

<211> 169
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (70)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (115)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (116)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (163)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (167)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1172
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Arg Gly Ala Met Val Ser Cys Arg Pro Gly Cys Cys Cys Pro Trp Thr
  1               5                  10                  15

Pro Ala Val Leu Arg Xaa Ser Val Arg Gly Thr Phe Tyr Ser Pro Pro
             20                  25                  30

Glu Ser Phe Ala Gly Ser Asp Asn Glu Ser Asp Glu Glu Val Ala Gly
         35                  40                  45

Lys Lys Ser Phe Ser Ala Gln Glu Arg Glu Tyr Ile Arg Gln Gly Lys
     50                  55                  60

Glu Ala Thr Ala Val Xaa Asp Gln Ile Leu Ala Gln Glu Glu Asn Trp
 65                  70                  75                  80

Lys Phe Glu Lys Asn Asn Glu Tyr Gly Asp Thr Val Tyr Thr Ile Glu
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                85                  90                  95

Val Pro Phe His Gly Lys Thr Phe Ile Leu Lys Thr Phe Leu Pro Cys
            100                 105                 110

Pro Ala Xaa Xaa Val Tyr Gln Glu Val Ile Leu Gln Pro Glu Arg Met
        115                 120                 125

Val Leu Trp Asn Lys Thr Val Thr Ala Cys Gln Ile Leu Gln Arg Val
    130                 135                 140

Glu Asp Asn Thr Leu Ile Ser Tyr Asp Val Ser Ala Arg Gly Cys Gly
145                 150                 155                 160

Arg Arg Xaa Leu Pro Gln Xaa Thr Ser
                165



<210> 1173
<211> 180
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (171)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1173
Glu Tyr Gly Asp Thr Val Tyr Thr Ile Glu Val Pro Phe His Gly Lys
  1               5                  10                  15

Thr Phe Ile Leu Lys Thr Phe Leu Pro Cys Pro Ala Glu Leu Val Tyr
             20                  25                  30

Gln Glu Val Ile Leu Gln Pro Glu Arg Met Val Leu Trp Asn Lys Thr
         35                  40                  45

Val Thr Ala Cys Gln Ile Leu Gln Arg Val Glu Asp Asn Thr Leu Ile
     50                  55                  60

Ser Tyr Asp Val Ser Ala Gly Ala Ala Gly Gly Val Val Ser Pro Arg
 65                  70                  75                  80

Asp Phe Val Asn Val Arg Arg Ile Glu Arg Arg Arg Asp Arg Tyr Leu
                 85                  90                  95

Ser Ser Gly Ile Ala Thr Ser His Ser Ala Lys Pro Pro Thr His Lys
            100                 105                 110
```

Tyr Val Arg Gly Glu Asn Gly Pro Gly Gly Phe Ile Val Leu Lys Ser
        115   120   125

Ala Ser Asn Pro Arg Val Cys Thr Phe Val Trp Ile Leu Asn Thr Asp
    130   135   140

Leu Lys Gly Arg Leu Pro Arg Tyr Leu Ile His Gln Ser Leu Ala Ala
145   150   155   160

Thr Met Phe Glu Phe Ala Phe His Leu Arg Xaa Arg Ile Ser Glu Leu
                165   170   175

Gly Ala Arg Ala
            180

<210> 1174
<211> 436
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (14)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (426)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1174
Arg His Gln Arg Arg Arg Ser Val Trp Arg Ser Arg Gly Xaa Cys Cys
  1   5   10   15

Arg Cys Cys Cys Thr Asn Arg Arg Ser Pro Gln Pro Cys Ala Ser Ser
             20   25   30

Leu Pro Pro Arg Thr Gly Glu Lys Gln Pro Arg Asn Phe Met Asn Lys
         35   40   45

His Gln Lys Pro Val Leu Thr Gly Gln Arg Phe Lys Thr Arg Lys Arg
     50   55   60

Asp Glu Lys Glu Lys Phe Glu Pro Thr Val Phe Arg Asp Thr Leu Val
 65   70   75   80

Gln Gly Leu Asn Glu Ala Gly Asp Asp Leu Glu Ala Val Ala Lys Phe
                 85   90   95

Leu Asp Ser Thr Gly Ser Arg Leu Asp Tyr Arg Arg Tyr Ala Asp Thr
100 105 110

Leu Phe Asp Ile Leu Val Ala Gly Ser Met Leu Ala Pro Gly Gly Thr
115 120 125

Arg Ile Asp Asp Gly Asp Lys Thr Lys Met Thr Asn His Cys Val Phe
130 135 140

Ser Ala Asn Glu Asp His Glu Thr Ile Arg Asn Tyr Ala Gln Val Phe
145 150 155 160

Asn Lys Leu Ile Arg Arg Tyr Lys Tyr Leu Glu Lys Ala Phe Glu Asp
165 170 175

Glu Met Lys Lys Leu Leu Leu Phe Leu Lys Ala Phe Ser Glu Thr Glu
180 185 190

Gln Thr Lys Leu Ala Met Leu Ser Gly Ile Leu Leu Gly Asn Gly Thr
195 200 205

Leu Pro Ala Thr Ile Leu Thr Ser Leu Phe Thr Asp Ser Leu Val Lys
210 215 220

Glu Gly Ile Ala Ala Ser Phe Ala Val Lys Leu Phe Lys Ala Trp Met
225 230 235 240

Ala Glu Lys Asp Ala Asn Ser Val Thr Ser Ser Leu Arg Lys Ala Asn
245 250 255

Leu Asp Lys Arg Leu Leu Glu Leu Phe Pro Val Asn Arg Gln Ser Val
260 265 270

Asp His Phe Ala Lys Tyr Phe Thr Asp Ala Gly Leu Lys Glu Leu Ser
275 280 285

Asp Phe Leu Arg Val Gln Gln Ser Leu Gly Thr Arg Lys Glu Leu Gln
290 295 300

Lys Glu Leu Gln Glu Arg Leu Ser Gln Glu Cys Pro Ile Lys Glu Val
305 310 315 320

Val Leu Tyr Val Lys Glu Glu Met Lys Arg Asn Asp Leu Pro Glu Thr
325 330 335

Ala Val Ile Gly Leu Leu Trp Thr Cys Ile Met Asn Ala Val Glu Trp
340 345 350

Asn Lys Lys Glu Glu Leu Val Ala Glu Gln Ala Leu Lys His Leu Lys
355 360 365

Gln Tyr Ala Pro Leu Leu Ala Val Phe Ser Ser Gln Gly Gln Ser Glu
370 375 380

Leu Ile Leu Leu Gln Lys Val Gln Glu Tyr Cys Tyr Asp Asn Ile His
385 390 395 400

Phe Met Lys Ala Phe Gln Lys Ile Val Leu Pro Tyr Thr Ile Ser Val
405 410 415

Leu Leu Leu Arg Ser Glu His Gln Leu Xaa Ser Cys Arg Phe Gly Thr
420 425 430

Ser Gly Thr Ser
435

<210> 1175
<211> 366
<212> PRT
<213> Homo sapiens

<400> 1175
Thr Glu Pro Val Gly Tyr Thr Lys Ala Glu Glu Pro Ile Ala Met Arg
1 5 10 15

Ser Leu Gly Ala Leu Leu Leu Leu Leu Ser Ala Cys Leu Ala Val Ser
20 25 30

Ala Gly Pro Val Pro Thr Pro Pro Asp Asn Ile Gln Val Gln Glu Asn
35 40 45

Phe Asn Ile Ser Arg Ile Tyr Gly Lys Trp Tyr Asn Leu Ala Ile Gly
50 55 60

Ser Thr Cys Pro Trp Leu Lys Lys Ile Met Asp Arg Met Thr Val Ser
65 70 75 80

Thr Leu Val Leu Gly Glu Gly Ala Thr Glu Ala Glu Ile Ser Met Thr
85 90 95

Ser Thr Arg Trp Arg Lys Gly Val Cys Glu Glu Thr Ser Gly Ala Tyr
100 105 110

Glu Lys Thr Asp Thr Asp Gly Lys Phe Leu Tyr His Lys Ser Lys Trp
115 120 125

Asn Ile Thr Met Glu Ser Tyr Val Val His Thr Asn Tyr Asp Glu Tyr
130 135 140

Ala Ile Phe Leu Thr Lys Lys Phe Ser Arg His His Gly Pro Thr Ile

145 150 155 160

Thr Ala Lys Leu Tyr Gly Arg Ala Pro Gln Leu Arg Glu Thr Leu Leu
165 170 175

Gln Asp Phe Arg Val Val Ala Gln Gly Val Gly Ile Pro Glu Asp Ser
180 185 190

Ile Phe Thr Met Ala Asp Arg Gly Glu Cys Val Pro Gly Glu Gln Glu
195 200 205

Pro Glu Pro Ile Leu Ile Pro Arg Val Arg Arg Ala Val Leu Pro Gln
210 215 220

Glu Glu Glu Gly Ser Gly Gly Gly Gln Leu Val Thr Glu Val Thr Lys
225 230 235 240

Lys Glu Asp Ser Cys Gln Leu Gly Tyr Ser Ala Gly Pro Cys Met Gly
245 250 255

Met Thr Ser Arg Tyr Phe Tyr Asn Gly Thr Ser Met Ala Cys Glu Thr
260 265 270

Phe Gln Tyr Gly Gly Cys Met Gly Asn Gly Asn Asn Phe Val Thr Glu
275 280 285

Lys Glu Cys Leu Gln Thr Cys Arg Thr Val Ala Ala Cys Asn Leu Pro
290 295 300

Ile Val Arg Gly Pro Cys Arg Ala Phe Ile Gln Leu Trp Ala Phe Asp
305 310 315 320

Ala Val Lys Gly Lys Cys Val Leu Phe Pro Tyr Gly Gly Cys Gln Gly
325 330 335

Asn Gly Asn Lys Phe Tyr Ser Glu Lys Glu Cys Arg Glu Tyr Cys Gly
340 345 350

Val Pro Gly Asp Gly Asp Glu Glu Leu Leu Arg Phe Ser Asn
355 360 365

<210> 1176
<211> 133
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (105)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (120)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (126)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1176
Met Pro Arg Ser Ser His His Pro Pro Arg Arg His Tyr His His His
1 5 10 15

His Tyr His Gln Pro Pro Pro Ser Pro Cys Pro Ser Pro Pro Leu Thr
20 25 30

Ser Pro Ser Pro Leu Ser Trp Ile Leu Trp Thr Cys Trp Pro Ser Thr
35 40 45

Ala Ala Thr Arg Pro Gly Arg Arg Lys Trp Gly Cys Arg Leu Cys Pro
50 55 60

Arg His Ser Ser Pro Leu Leu Leu Leu His Leu Asn Leu Leu Ala Trp
65 70 75 80

Ala Pro Tyr Pro His Pro Ala Thr Thr Arg Gly Asp Arg Lys Gln Lys
85 90 95

Lys Arg Asp Gln Asn Lys Ser Ala Xaa Leu Arg Tyr Arg Gln Arg Lys
100 105 110

Gly Ala Gly Gly Val Glu Gly Xaa Gly Lys Gly Lys Leu Xaa Gly Gly
115 120 125

Trp Glu Gly Lys Gly
130

<210> 1177
<211> 583
<212> PRT
<213> Homo sapiens

<400> 1177
Thr Ala Gln Arg Pro Arg Ser Pro Glu Asn Cys Arg Pro Ser Thr Met
1 5 10 15

Trp Leu Arg Ala Phe Ile Leu Ala Thr Leu Ser Ala Ser Ala Ala Trp
20 25 30

Ala Gly His Pro Ser Ser Pro Pro Val Val Asp Thr Val His Gly Lys
35 40 45

Val Leu Gly Lys Phe Val Ser Leu Glu Gly Phe Ala Gln Pro Val Ala
50 55 60

Ile Phe Leu Gly Ile Pro Phe Ala Lys Pro Pro Leu Gly Pro Leu Arg
65 70 75 80

Phe Thr Pro Pro Gln Pro Ala Glu Pro Trp Ser Phe Val Lys Asn Ala
85 90 95

Thr Ser Tyr Pro Pro Met Cys Thr Gln Asp Pro Lys Ala Gly Gln Leu
100 105 110

Leu Ser Glu Leu Phe Thr Asn Arg Lys Glu Asn Ile Pro Leu Lys Leu
115 120 125

Ser Glu Asp Cys Leu Tyr Leu Asn Ile Tyr Thr Pro Ala Asp Leu Thr
130 135 140

Lys Lys Asn Arg Leu Pro Val Met Val Trp Ile His Gly Gly Gly Leu
145 150 155 160

Met Val Gly Ala Ala Ser Thr Tyr Asp Gly Leu Ala Leu Ala Ala His
165 170 175

Glu Asn Val Val Val Val Thr Ile Gln Tyr Arg Leu Gly Ile Trp Gly
180 185 190

Phe Phe Ser Thr Gly Asp Glu His Ser Arg Gly Asn Trp Gly His Leu
195 200 205

Asp Gln Val Ala Ala Leu Arg Trp Val Gln Asp Asn Ile Ala Ser Phe
210 215 220

Gly Gly Asn Pro Gly Ser Val Thr Ile Phe Gly Glu Ser Ala Gly Gly
225 230 235 240

Glu Ser Val Ser Val Leu Val Leu Ser Pro Leu Ala Lys Asn Leu Phe
245 250 255

His Arg Ala Ile Ser Glu Ser Gly Val Ala Leu Thr Ser Val Leu Val
260 265 270

Lys Lys Gly Asp Val Lys Pro Leu Ala Glu Gln Ile Ala Ile Thr Ala
275 280 285

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Gly Cys Lys Thr Thr Thr Ser Ala Val Met Val His Cys Leu Arg Gln
    290                 295                 300

Lys Thr Glu Glu Glu Leu Leu Glu Thr Thr Leu Lys Met Lys Phe Leu
305                 310                 315                 320

Ser Leu Asp Leu Gln Gly Asp Pro Arg Glu Ser Gln Pro Leu Leu Gly
                325                 330                 335

Thr Val Ile Asp Gly Met Leu Leu Leu Lys Thr Pro Glu Glu Leu Gln
            340                 345                 350

Ala Glu Arg Asn Phe His Thr Val Pro Tyr Met Val Gly Ile Asn Lys
        355                 360                 365

Gln Glu Phe Gly Trp Leu Ile Pro Met Gln Leu Met Ser Tyr Pro Leu
    370                 375                 380

Ser Glu Gly Gln Leu Asp Gln Lys Thr Ala Met Ser Leu Leu Trp Lys
385                 390                 395                 400

Ser Tyr Pro Leu Val Cys Ile Ala Lys Glu Leu Ile Pro Glu Ala Thr
                405                 410                 415

Glu Lys Tyr Leu Gly Gly Thr Asp Asp Thr Val Lys Lys Lys Asp Leu
            420                 425                 430

Phe Leu Asp Leu Ile Ala Asp Val Met Phe Gly Val Pro Ser Val Ile
        435                 440                 445

Val Ala Arg Asn His Arg Asp Ala Gly Ala Pro Thr Tyr Met Tyr Glu
    450                 455                 460

Phe Gln Tyr Arg Pro Ser Phe Ser Ser Asp Met Lys Pro Lys Thr Val
465                 470                 475                 480

Ile Gly Asp His Gly Asp Glu Leu Phe Ser Val Phe Gly Ala Pro Phe
                485                 490                 495

Leu Lys Glu Gly Ala Ser Glu Glu Glu Ile Arg Leu Ser Lys Met Val
            500                 505                 510

Met Lys Phe Trp Ala Asn Phe Ala Arg Asn Gly Asn Pro Asn Gly Glu
        515                 520                 525

Gly Leu Pro His Trp Pro Glu Tyr Asn Gln Lys Glu Gly Tyr Leu Gln
    530                 535                 540

Ile Gly Ala Asn Thr Gln Ala Ala Gln Lys Leu Lys Asp Lys Glu Val
545                 550                 555                 560
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Ala Phe Trp Thr Asn Leu Phe Ala Lys Lys Ala Val Glu Lys Pro Pro
                565                 570                 575

Gln Thr Glu His Ile Glu Leu
            580



<210> 1178
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1178
Pro Gly Arg Xaa Gln Leu Arg Ala Lys Phe Ser Cys Pro Pro Ala Asp
  1               5                  10                  15

Arg Val Asn Val Thr Val Arg Pro Gly Leu Ala Met Ala Leu Ser Gly
             20                  25                  30

Ser Thr Glu Pro Cys Ala Gln Leu Ser Ile Ser Ser Ile Gly Val Val
         35                  40                  45

Gly Thr Ala Glu Asp Asn Arg Ser His Ser Ala His Phe Phe Glu Phe
     50                  55                  60

Leu Thr Lys Glu Leu Ala Leu Gly Gln Asp Arg Ile Leu Ile Arg Phe
 65                  70                  75                  80

Phe Pro Leu Glu Ser Trp Gln Ile Gly Lys Ile Gly Thr Val Met Thr
                 85                  90                  95

Phe Leu



<210> 1179
<211> 127
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids
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<220>
<221> SITE
<222> (50)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1179
Phe Arg Pro Ala Val Ser Xaa Gly Ser Leu Cys Leu Pro Ala Arg Thr
1 5 10 15

Ala His Ser Pro Ala Ser Ser Ala Ala Cys Arg Thr Met Ala Gln Gly
20 25 30

Gln Arg Lys Phe Gln Ala His Lys Pro Ala Lys Ser Lys Thr Ala Ala
35 40 45

Ala Xaa Ser Glu Lys Asn Arg Gly Pro Arg Lys Gly Gly Arg Val Ile
50 55 60

Ala Pro Xaa Lys Ala Arg Val Val Gln Gln Gln Lys Leu Lys Lys Asn
65 70 75 80

Leu Glu Val Gly Ile Arg Lys Lys Ile Glu His Asp Val Val Met Lys
85 90 95

Ala Ser Ser Ser Leu Pro Lys Lys Leu Ala Leu Leu Lys Ala Pro Ala
100 105 110

Lys Lys Lys Gly Ala Ala Ala Ala Thr Ser Ser Lys Thr Pro Ser
115 120 125

<210> 1180
<211> 94
<212> PRT
<213> Homo sapiens

<400> 1180
Ser Ser Tyr Arg Ser Lys Ala Tyr Thr His Thr Lys Ile Thr Val Pro
1 5 10 15

Arg Glu Arg Val Cys Val Ser Val Arg Val Ser Val Cys Ala Arg Ala
20 25 30

Arg Ser Trp Pro Asn Val Arg Thr Leu His Lys Gly Gly Arg Ser Ser

```
        35                  40                  45

Tyr Arg Leu Phe Asn Val Arg Glu Thr Ile Phe Leu Leu Phe Gln Leu
    50                  55                  60

Tyr Gln Ile Leu Val Pro Gln His Arg Asn Asp Ser Glu Ser Gln Thr
65                  70                  75                  80

Lys Cys Ile Ile Cys Ser Ile Leu Ile Leu Leu Leu His Ser
                85                  90
```

<210> 1181
<211> 353
<212> PRT
<213> Homo sapiens

<400> 1181

```
Gly Ser Leu Asp Leu Trp Arg Gly Ala Glu Leu Ser Pro Gly His Ser
1               5                   10                  15

Thr Leu Phe Thr Leu Cys Ala Cys Ala Lys Gly Ala Met Ala Ala Ser
            20                  25                  30

Cys Val Leu Leu His Thr Gly Gln Lys Met Pro Leu Ile Gly Leu Gly
        35                  40                  45

Thr Trp Lys Ser Glu Pro Gly Gln Val Lys Ala Ala Val Lys Tyr Ala
    50                  55                  60

Leu Ser Val Gly Tyr Arg His Ile Asp Cys Ala Ala Ile Tyr Gly Asn
65                  70                  75                  80

Glu Pro Glu Ile Gly Glu Ala Leu Lys Glu Asp Val Gly Pro Gly Lys
                85                  90                  95

Ala Val Pro Arg Glu Glu Leu Phe Val Thr Ser Lys Leu Trp Asn Thr
            100                 105                 110

Lys His His Pro Glu Asp Val Glu Pro Ala Leu Arg Lys Thr Leu Ala
        115                 120                 125

Asp Leu Gln Leu Glu Tyr Leu Asp Leu Tyr Leu Met His Trp Pro Tyr
    130                 135                 140

Ala Phe Glu Arg Gly Asp Asn Pro Phe Pro Lys Asn Ala Asp Gly Thr
145                 150                 155                 160

Ile Cys Tyr Asp Ser Thr His Tyr Lys Glu Thr Trp Lys Ala Leu Glu
                165                 170                 175
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Ala Leu Val Ala Lys Gly Leu Val Gln Ala Leu Gly Leu Ser Asn Phe
180 185 190

Asn Ser Arg Gln Ile Asp Asp Ile Leu Ser Val Ala Ser Val Arg Pro
195 200 205

Ala Val Leu Gln Val Glu Cys His Pro Tyr Leu Ala Gln Asn Glu Leu
210 215 220

Ile Ala His Cys Gln Ala Arg Gly Leu Glu Val Thr Ala Tyr Ser Pro
225 230 235 240

Leu Gly Ser Ser Asp Arg Ala Trp Arg Asp Pro Asp Glu Pro Val Leu
245 250 255

Leu Glu Glu Pro Val Val Leu Ala Leu Ala Glu Lys Tyr Gly Arg Ser
260 265 270

Pro Ala Gln Ile Leu Leu Arg Trp Gln Val Gln Arg Lys Val Ile Cys
275 280 285

Ile Pro Lys Ser Ile Thr Pro Ser Arg Ile Leu Gln Asn Ile Lys Val
290 295 300

Phe Asp Phe Thr Phe Ser Pro Glu Glu Met Lys Gln Leu Asn Ala Leu
305 310 315 320

Asn Lys Asn Trp Arg Tyr Ile Val Pro Met Leu Thr Val Asp Gly Lys
325 330 335

Arg Val Pro Arg Asp Ala Gly His Pro Leu Tyr Pro Phe Asn Asp Pro
340 345 350

Tyr

<210> 1182
<211> 174
<212> PRT
<213> Homo sapiens

<400> 1182
Ala Arg Asp Ser Leu Gln Leu Ser Met Ala Gln Thr Ser Ser Tyr Phe
1 5 10 15

Met Leu Ile Ser Cys Leu Met Phe Leu Ser Gln Ser Gln Gly Gln Glu
20 25 30

```
Ala Gln Thr Glu Leu Pro Gln Ala Arg Ile Ser Cys Pro Glu Gly Thr
        35                  40                  45

Asn Ala Tyr Arg Ser Tyr Cys Tyr Tyr Phe Asn Glu Asp Arg Glu Thr
    50                  55                  60

Trp Val Asp Ala Asp Leu Tyr Cys Gln Asn Met Asn Ser Gly Asn Leu
65                  70                  75                  80

Val Ser Val Leu Thr Gln Ala Glu Gly Ala Phe Val Ala Ser Leu Ile
                85                  90                  95

Lys Glu Ser Gly Thr Asp Asp Phe Asn Val Trp Ile Gly Leu His Asp
            100                 105                 110

Pro Lys Lys Asn Arg Arg Trp His Trp Ser Ser Gly Ser Leu Val Ser
        115                 120                 125

Tyr Lys Ser Trp Gly Ile Gly Ala Pro Ser Ser Val Asn Pro Gly Tyr
    130                 135                 140

Cys Val Ser Leu Thr Ser Ser Thr Gly Phe Gln Lys Trp Lys Asp Val
145                 150                 155                 160

Pro Cys Glu Asp Lys Phe Ser Phe Val Cys Lys Phe Lys Asn
                165                 170
```

<210> 1183
<211> 342
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (169)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (171)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (187)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (302)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (308)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1183

```
Ser Ile Phe Ser Tyr Ile Arg Leu Glu Leu Pro Ser Met Trp Leu Leu
1               5                   10                  15

Val Ser Val Ile Leu Ile Ser Arg Ile Ser Ser Val Gly Gly Glu Ala
            20                  25                  30

Thr Phe Cys Asp Phe Pro Lys Ile Asn His Gly Ile Leu Tyr Asp Glu
        35                  40                  45

Glu Lys Tyr Lys Pro Phe Ser Gln Val Pro Thr Gly Glu Val Phe Tyr
    50                  55                  60

Tyr Ser Cys Glu Tyr Asn Phe Val Ser Pro Ser Lys Ser Phe Trp Thr
65                  70                  75                  80

Arg Ile Thr Cys Thr Glu Glu Gly Trp Ser Pro Thr Pro Lys Cys Leu
                85                  90                  95

Arg Leu Cys Phe Phe Pro Phe Val Glu Asn Gly His Ser Glu Ser Ser
            100                 105                 110

Gly Gln Thr His Leu Glu Gly Asp Thr Val Gln Ile Ile Cys Asn Thr
        115                 120                 125

Gly Tyr Arg Leu Gln Asn Asn Glu Asn Asn Ile Ser Cys Val Glu Arg
    130                 135                 140

Gly Trp Ser Thr Pro Pro Lys Cys Arg Ser Thr Asp Thr Ser Cys Val
145                 150                 155                 160

Asn Pro Pro Thr Val Gln Asn Ala Xaa Ile Xaa Ser Arg Gln Met Ser
                165                 170                 175

Lys Tyr Pro Ser Gly Glu Arg Val Arg Tyr Xaa Cys Arg Ser Pro Tyr
            180                 185                 190

Glu Met Phe Gly Asp Glu Glu Val Met Cys Leu Asn Gly Asn Trp Thr
        195                 200                 205

Glu Pro Pro Gln Cys Lys Asp Ser Thr Gly Lys Cys Gly Pro Pro Pro
    210                 215                 220
```

Pro Ile Asp Asn Gly Asp Ile Thr Ser Phe Pro Leu Ser Val Tyr Ala
225 230 235 240

Pro Ala Ser Ser Val Glu Tyr Gln Cys Gln Asn Leu Tyr Gln Leu Glu
245 250 255

Gly Asn Lys Arg Ile Thr Cys Arg Asn Gly Gln Trp Ser Glu Pro Pro
260 265 270

Lys Cys Leu His Pro Cys Val Ile Ser Arg Glu Ile Met Glu Asn Tyr
275 280 285

Asn Ile Ala Leu Arg Trp Thr Ala Lys Gln Lys Leu Tyr Xaa Arg Thr
290 295 300

Gly Glu Ser Xaa Glu Phe Val Cys Lys Arg Gly Tyr Arg Leu Ser Ser
305 310 315 320

Arg Ser His Thr Leu Arg Thr Thr Cys Trp Asp Gly Lys Leu Glu Tyr
325 330 335

Pro Thr Cys Ala Lys Arg
340

<210> 1184
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (161)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1184
Pro Xaa Arg Pro Arg Gly Ala Ala Ala Ala Ala Ala Ala Ala Gly Ala
1 5 10 15

Ala Met Pro Lys Gly Gly Arg Lys Gly Gly His Lys Gly Arg Ala Arg
20 25 30

Gln Tyr Thr Ser Pro Glu Glu Ile Asp Ala Gln Leu Gln Ala Glu Lys
35 40 45

Gln Lys Ala Arg Glu Glu Glu Glu Gln Lys Glu Gly Gly Asp Gly Ala
50 55 60

Ala Gly Asp Pro Lys Lys Glu Lys Lys Ser Leu Asp Ser Asp Glu Ser
65 70 75 80

Glu Asp Glu Glu Asp Asp Tyr Gln Gln Lys Arg Lys Gly Val Glu Gly
85 90 95

Leu Ile Asp Ile Glu Asn Pro Asn Arg Val Ala Gln Thr Thr Lys Lys
100 105 110

Val Thr Gln Leu Asp Leu Asp Gly Pro Lys Glu Leu Ser Arg Arg Glu
115 120 125

Arg Glu Glu Ile Glu Lys Gln Lys Ala Lys Glu Arg Tyr Met Lys Met
130 135 140

His Leu Ala Gly Lys Thr Glu Gln Ala Lys Ala Asp Leu Ala Arg Leu
145 150 155 160

Xaa Ile Ile Arg Lys Gln Arg Glu Glu Ala Ala Arg Lys Lys Glu Glu
165 170 175

Glu Arg Lys Ala Lys Asp Asp Ala Thr Leu Ser Gly Lys Arg Met Gln
180 185 190

Ser Leu Ser Leu Asn Lys
195

<210> 1185
<211> 210
<212> PRT
<213> Homo sapiens

<400> 1185
Ala His Ala Ser Ala His Ala Ser Gly Met Asp Leu Ser Leu Leu Trp
1 5 10 15

Val Leu Leu Pro Leu Val Thr Met Ala Trp Gly Gln Tyr Gly Asp Tyr
20 25 30

Gly Tyr Pro Tyr Gln Gln Tyr His Asp Tyr Ser Asp Asp Gly Trp Val
35 40 45

Asn Leu Asn Arg Gln Gly Phe Ser Tyr Gln Cys Pro Gln Gly Gln Val
50 55 60

Ile Val Ala Val Arg Ser Ile Phe Ser Lys Lys Glu Gly Ser Asp Arg

65 70 75 80

Gln Trp Asn Tyr Ala Cys Met Pro Thr Pro Gln Ser Leu Gly Glu Pro
85 90 95

Thr Glu Cys Trp Trp Glu Glu Ile Asn Arg Ala Gly Met Glu Trp Tyr
100 105 110

Gln Thr Cys Ser Asn Asn Gly Leu Val Ala Gly Phe Gln Ser Arg Tyr
115 120 125

Phe Glu Ser Val Leu Asp Arg Glu Trp Gln Phe Tyr Cys Cys Arg Tyr
130 135 140

Ser Lys Arg Cys Pro Tyr Ser Cys Trp Leu Thr Thr Glu Tyr Pro Gly
145 150 155 160

His Tyr Gly Glu Glu Met Asp Met Ile Ser Tyr Asn Tyr Asp Tyr Tyr
165 170 175

Ile Arg Gly Ala Thr Thr Thr Phe Ser Ala Val Glu Arg Asp Arg Gln
180 185 190

Trp Lys Phe Ile Met Cys Arg Met Thr Glu Tyr Asp Cys Glu Phe Ala
195 200 205

Asn Val
210

<210> 1186
<211> 141
<212> PRT
<213> Homo sapiens

<400> 1186
Arg Ala Ile Tyr Phe Leu Arg Val His Arg Leu Trp Ser Ser Ile Ser
1 5 10 15

Leu Leu Phe Phe Pro Ser Ala Lys Met Ala Leu Glu Thr Val Pro Lys
20 25 30

Asp Leu Arg His Leu Arg Ala Cys Leu Leu Cys Ser Leu Val Lys Thr
35 40 45

Ile Asp Gln Phe Glu Tyr Asp Gly Cys Asp Asn Cys Asp Ala Tyr Leu
50 55 60

Gln Met Lys Gly Asn Arg Glu Met Val Tyr Asp Cys Thr Ser Ser Ser
65 70 75 80

Phe Asp Gly Ile Ile Ala Met Met Ser Pro Glu Asp Ser Trp Val Ser
85 90 95

Lys Trp Gln Arg Val Ser Asn Phe Lys Pro Gly Val Tyr Ala Val Ser
100 105 110

Val Thr Gly Arg Leu Pro Gln Gly Ile Val Arg Glu Leu Lys Ser Arg
115 120 125

Gly Val Ala Tyr Lys Ser Arg Asp Thr Ala Ile Lys Thr
130 135 140

<210> 1187
<211> 76
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (66)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1187
Leu Leu Gly Ser Cys Leu Gln Glu Ala Met Thr Leu Asn Ser Glu Pro
1 5 10 15

Tyr Ser Val Leu Thr Ser Gly Ser His Val Phe Leu Cys Gln Val Ile
20 25 30

Lys Tyr Leu Val Leu Val Phe Cys Leu Xaa Pro Lys Leu Pro Leu Trp
35 40 45

Val His Arg Arg Leu Gly Ser Ile Val Arg Met Ala Ile Arg Glu Tyr
50 55 60

Lys Xaa Gly Phe Ser Lys Gly Leu Gly Xaa Asp Ser
65 70 75

<210> 1188
<211> 516
<212> PRT
<213> Homo sapiens

<400> 1188
Ile Arg Ile Ala Ala Leu Asp Asp Phe Arg Thr Ser Leu Thr Met Ser
1   5   10   15

Ser Thr Arg Ser Gln Asn Pro His Gly Leu Lys Gln Ile Gly Leu Asp
            20   25   30

Gln Ile Trp Asp Asp Leu Arg Ala Gly Ile Gln Gln Val Tyr Thr Arg
        35   40   45

Gln Ser Met Ala Lys Ser Arg Tyr Met Glu Leu Tyr Thr His Val Tyr
    50   55   60

Asn Tyr Cys Thr Ser Val His Gln Ser Asn Gln Ala Arg Gly Ala Gly
65   70   75   80

Val Pro Pro Ser Lys Ser Lys Lys Gly Gln Thr Pro Gly Gly Ala Gln
                85   90   95

Phe Val Gly Leu Glu Leu Tyr Lys Arg Leu Lys Glu Phe Leu Lys Asn
            100   105   110

Tyr Leu Thr Asn Leu Leu Lys Asp Gly Glu Asp Leu Met Asp Glu Ser
        115   120   125

Val Leu Lys Phe Tyr Thr Gln Gln Trp Glu Asp Tyr Arg Phe Ser Ser
    130   135   140

Lys Val Leu Asn Gly Ile Cys Ala Tyr Leu Asn Arg His Trp Val Arg
145   150   155   160

Arg Glu Cys Asp Glu Gly Arg Lys Gly Ile Tyr Glu Ile Tyr Ser Leu
                165   170   175

Ala Leu Val Thr Trp Arg Asp Cys Leu Phe Arg Pro Leu Asn Lys Gln
            180   185   190

Val Thr Asn Ala Val Leu Lys Leu Ile Glu Lys Glu Arg Asn Gly Glu
        195   200   205

Thr Ile Asn Thr Arg Leu Ile Ser Gly Val Val Gln Ser Tyr Val Glu
    210   215   220

Leu Gly Leu Asn Glu Asp Asp Ala Phe Ala Lys Gly Pro Thr Leu Thr

225 230 235 240

Val Tyr Lys Glu Ser Phe Glu Ser Gln Phe Leu Ala Asp Thr Glu Arg
245 250 255

Phe Tyr Thr Arg Glu Ser Thr Glu Phe Leu Gln Gln Asn Pro Val Thr
260 265 270

Glu Tyr Met Lys Lys Ala Glu Ala Arg Leu Leu Glu Glu Gln Arg Arg
275 280 285

Val Gln Val Tyr Leu His Glu Ser Thr Gln Asp Glu Leu Ala Arg Lys
290 295 300

Cys Glu Gln Val Leu Ile Glu Lys His Leu Glu Ile Phe His Thr Glu
305 310 315 320

Phe Gln Asn Leu Leu Asp Ala Asp Lys Asn Glu Asp Leu Gly Arg Met
325 330 335

Tyr Asn Leu Val Ser Arg Ile Gln Asp Gly Leu Gly Glu Leu Lys Lys
340 345 350

Leu Leu Glu Thr His Ile His Asn Gln Gly Leu Ala Ala Ile Glu Lys
355 360 365

Cys Gly Glu Ala Ala Leu Asn Asp Pro Lys Met Tyr Val Gln Thr Val
370 375 380

Leu Asp Val His Lys Lys Tyr Asn Ala Leu Val Met Ser Ala Phe Asn
385 390 395 400

Asn Asp Ala Gly Phe Val Ala Ala Leu Asp Lys Ala Cys Gly Arg Phe
405 410 415

Ile Asn Asn Asn Ala Val Thr Lys Met Ala Gln Ser Ser Ser Lys Ser
420 425 430

Pro Glu Leu Leu Ala Arg Tyr Cys Asp Ser Leu Leu Lys Lys Ser Ser
435 440 445

Lys Asn Pro Glu Glu Ala Glu Leu Glu Asp Thr Leu Asn Gln Val Met
450 455 460

Val Val Phe Lys Tyr Ile Glu Asp Lys Asp Val Phe Gln Lys Phe Tyr
465 470 475 480

Ala Lys Met Leu Ala Lys Arg Leu Val His Gln Asn Ser Ala Ser Asp
485 490 495

Asp Ala Glu Ala Ser Met Ile Ser Lys Leu Lys Gln Ala Cys Gly Phe

500 505 510

Glu Tyr Thr Ser
515

<210> 1189
<211> 287
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (20)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (24)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (172)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (254)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (271)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (274)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (275)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (280)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1189
Met Ser Tyr Cys Asp Glu Ser Arg Leu Ser Asn Leu Leu Arg Arg Ile
1 5 10 15

Thr Arg Glu Xaa Asp Arg Asp Xaa Arg Leu Xaa Thr Val Lys Gln Leu
20 25 30

Lys Glu Phe Ile Gln Gln Pro Glu Asn Lys Leu Val Leu Val Lys Gln
35 40 45

Leu Asp Ile Leu Ala Ala Xaa His Asp Val Leu Asn Glu Ser Ser Lys
50 55 60

Leu Leu Gln Glu Leu Arg Gln Glu Gly Ala Cys Cys Leu Gly Leu Leu
65 70 75 80

Cys Ala Ser Leu Ser Tyr Glu Ala Glu Lys Ile Phe Lys Trp Ile Phe
85 90 95

Ser Lys Phe Ser Ser Ser Ala Lys Asp Glu Val Lys Leu Leu Tyr Leu
100 105 110

Cys Ala Thr Tyr Lys Ala Leu Glu Thr Val Gly Glu Lys Lys Ala Phe
115 120 125

Ser Ser Val Met Gln Leu Val Met Thr Ser Leu Gln Ser Ile Leu Glu
130 135 140

Asn Val Asp Thr Pro Glu Leu Leu Cys Lys Cys Val Lys Cys Ile Leu
145 150 155 160

Leu Val Ala Arg Cys Tyr Pro His Ile Phe Ser Xaa Asn Phe Arg Asp
165 170 175

Thr Val Asp Ile Leu Val Gly Trp His Arg Asp His Thr Gln Lys Pro
180 185 190

Ser Leu Thr Gln Gln Val Ser Gly Trp Leu Gln Ser Leu Glu Pro Phe
195 200 205

Trp Val Ala Asp Leu Ala Phe Pro Thr Thr Leu Leu Gly Gln Phe Leu
    210   215   220

Glu Asp Met Glu Ala Tyr Ala Glu Asp Leu Ser His Val Ala Ser Gly
225   230   235   240

Glu Ser Val Asp Glu Asp Val Pro Pro Pro Ser Val Ser Xaa Pro Lys
                245   250   255

Leu Ala Ala Leu Leu Arg Val Phe Ser Thr Val Val Arg Ser Xaa Gly
            260   265   270

Glu Xaa Xaa Ser Pro Ile Arg Xaa Leu Gln Leu Leu Arg His Thr
        275   280   285

<210> 1190
<211> 100
<212> PRT
<213> Homo sapiens

<400> 1190
Arg Pro Pro Ser Arg Trp Ser Trp Trp Gln Gly Lys Pro Thr Gly Gly
  1   5   10   15

Val Cys Val Ala Ala Ala Arg Ser Ser Pro Ser Val Thr Ala Pro Thr
            20   25   30

Ser Ser Asn Ala Leu Ala Tyr Leu His Ser Ser Ser Arg Pro Lys Arg
        35   40   45

Pro Ala Trp Trp His Ser Val Pro Ala Arg Pro Leu Arg Gly Pro Arg
    50   55   60

Thr Ala Met Ala Pro Thr Gly Val Ser Ala Cys Arg Arg Gln Lys Trp
65   70   75   80

Ala Pro His Ser Glu Gly Ala Ala Ala Val Gln Pro Gln Val Ala Leu
                85   90   95

Ala Pro Gly Leu
            100

<210> 1191
<211> 115
<212> PRT
<213> Homo sapiens

<400> 1191
Asn Asp Val Ile His Gln Tyr Val Tyr Met Tyr Phe Tyr Ile Asp Leu
1   5   10   15

Glu Asn Thr Ala Lys Thr Phe Met Thr Ser Cys Ile Thr Ala Phe Val
            20   25   30

Tyr Ile Phe Leu Thr Val Ile Ile Pro Thr Gly Thr Leu Thr Val Ala
        35   40   45

Leu Leu Asn Val Gln Asn Leu Tyr Phe Arg Asn Asn Lys Lys Lys Asp
    50   55   60

Thr Tyr Met Phe Pro Lys Gln Trp Cys Gly Glu Cys Val Arg Lys Thr
65   70   75   80

Asn Leu Ile Gly Ser Thr Asn Thr Lys Cys Ile Thr Asn Ala Pro Val
                85   90   95

His Val Phe Val Leu Lys Arg Val Asn Glu Asp Leu Tyr Ile Ser Ile
            100   105   110

Asn Asp Ile
        115

<210> 1192
<211> 415
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1192
Arg Ile Pro Pro Glu Ser Leu Ala Arg Glu Xaa Arg Xaa Thr Lys Ser
1   5   10   15

Phe Ser Asn Pro Arg Arg Pro Asp Arg Gly Thr Trp Ser Leu Ser Glu
            20   25   30

Lys Phe Asn Leu Arg Asp Lys Met Gln Trp Thr Ser Leu Leu Leu Leu
        35   40   45

Ala Gly Leu Phe Ser Leu Ser Gln Ala Gln Tyr Glu Asp Asp Pro His
    50   55   60

Trp Trp Phe His Tyr Leu Arg Ser Gln Gln Ser Thr Tyr Tyr Asp Pro
65   70   75   80

Tyr Asp Pro Tyr Pro Tyr Glu Thr Tyr Glu Pro Tyr Pro Tyr Gly Val
                85   90   95

Asp Glu Gly Pro Ala Tyr Thr Tyr Gly Ser Pro Ser Pro Pro Asp Pro
            100   105   110

Arg Asp Cys Pro Gln Glu Cys Asp Cys Pro Pro Asn Phe Pro Thr Ala
        115   120   125

Met Tyr Cys Asp Asn Arg Asn Leu Lys Tyr Leu Pro Phe Val Pro Ser
    130   135   140

Arg Met Lys Tyr Val Tyr Phe Gln Asn Asn Gln Ile Thr Ser Ile Gln
145   150   155   160

Glu Gly Val Phe Asp Asn Ala Thr Gly Leu Leu Trp Ile Ala Leu His
                165   170   175

Gly Asn Gln Ile Thr Ser Asp Lys Val Gly Arg Lys Val Phe Ser Lys
            180   185   190

Leu Arg His Leu Glu Arg Leu Tyr Leu Asp His Asn Asn Leu Thr Arg
        195   200   205

Met Pro Gly Pro Leu Pro Arg Ser Leu Arg Glu Leu His Leu Asp His
    210   215   220

Asn Gln Ile Ser Arg Val Pro Asn Asn Ala Leu Glu Gly Leu Glu Asn
225   230   235   240

Leu Thr Ala Leu Tyr Leu Gln His Asn Glu Ile Gln Glu Val Gly Ser
                245   250   255

Ser Met Arg Gly Leu Arg Ser Leu Ile Leu Leu Asp Leu Ser Tyr Asn
            260   265   270

His Leu Arg Lys Val Pro Asp Gly Leu Pro Ser Ala Leu Glu Gln Leu
        275   280   285

Tyr Met Glu His Asn Asn Val Tyr Thr Val Pro Asp Ser Tyr Phe Arg
    290   295   300

Gly Ala Pro Lys Leu Leu Tyr Val Arg Leu Ser His Asn Ser Leu Thr
305   310   315   320

Asn Asn Gly Leu Ala Ser Asn Thr Phe Asn Ser Ser Ser Leu Leu Glu
                325   330   335

Leu Asp Leu Ser Tyr Asn Gln Leu Gln Lys Ile Pro Pro Val Asn Thr
            340   345   350

Asn Leu Glu Asn Leu Tyr Leu Gln Gly Asn Arg Ile Asn Glu Phe Ser
        355   360   365

Ile Ser Ser Phe Cys Thr Val Val Asp Val Val Asn Phe Ser Lys Leu
    370   375   380

Gln Val Leu Arg Leu Asp Gly Asn Glu Ile Lys Arg Ser Ala Met Pro
385   390   395   400

Ala Asp Ala Pro Leu Cys Leu Arg Leu Ala Ser Leu Ile Glu Ile
                405   410   415

<210> 1193
<211> 620
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (375)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (501)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (532)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (546)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1193
Ser Ala Val Thr Ala Phe Ser Glu Gly Ser Val Ile Ala Tyr Tyr Trp
  1   5   10   15

Ser Glu Phe Ser Ile Pro Gln His Leu Val Glu Glu Ala Glu Arg Val

```
                20                  25                  30

Met Ala Glu Glu Arg Val Val Met Leu Pro Pro Arg Ala Arg Ser Leu
            35                  40                  45

Lys Ser Phe Val Val Thr Ser Val Val Ala Phe Pro Thr Asp Ser Lys
    50                  55                  60

Thr Val Gln Arg Thr Gln Asp Asn Ser Cys Ser Phe Gly Leu His Ala
65                  70                  75                  80

Arg Gly Val Glu Leu Met Arg Phe Thr Thr Pro Gly Phe Pro Asp Ser
                85                  90                  95

Pro Tyr Pro Ala His Ala Arg Cys Gln Trp Ala Leu Arg Gly Asp Ala
            100                 105                 110

Asp Ser Val Leu Ser Leu Thr Phe Arg Ser Phe Asp Leu Ala Ser Cys
        115                 120                 125

Asp Glu Arg Gly Ser Asp Leu Val Thr Val Tyr Asn Thr Leu Ser Pro
    130                 135                 140

Met Glu Pro His Ala Leu Val Gln Leu Cys Gly Thr Tyr Pro Pro Ser
145                 150                 155                 160

Tyr Asn Leu Thr Phe His Ser Ser Gln Asn Val Leu Leu Ile Thr Leu
                165                 170                 175

Ile Thr Asn Thr Glu Arg Arg His Pro Gly Phe Glu Ala Thr Phe Phe
            180                 185                 190

Gln Leu Pro Arg Met Ser Ser Cys Gly Gly Arg Leu Arg Lys Ala Gln
        195                 200                 205

Gly Thr Phe Asn Ser Pro Tyr Tyr Pro Gly His Tyr Pro Pro Asn Ile
    210                 215                 220

Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val Lys Val
225                 230                 235                 240

Arg Phe Lys Phe Phe Tyr Leu Leu Glu Pro Gly Val Pro Ala Gly Thr
                245                 250                 255

Cys Pro Lys Asp Tyr Val Glu Ile Asn Gly Glu Lys Tyr Cys Gly Glu
            260                 265                 270

Arg Ser Gln Phe Val Val Thr Ser Asn Ser Asn Lys Ile Thr Val Arg
        275                 280                 285

Phe His Ser Asp Gln Ser Tyr Thr Asp Thr Gly Phe Leu Ala Glu Tyr
```

290 295 300

Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr Cys Arg
305 310 315 320

Thr Gly Arg Cys Ile Arg Lys Glu Leu Arg Cys Asp Gly Trp Ala Asp
325 330 335

Cys Thr Asp His Ser Asp Glu Leu Asn Cys Ser Cys Asp Ala Gly His
340 345 350

Gln Phe Thr Cys Lys Asn Lys Phe Cys Lys Pro Leu Phe Trp Val Cys
355 360 365

Asp Ser Val Asn Asp Cys Xaa Asp Asn Ser Asp Glu Gln Gly Cys Ser
370 375 380

Cys Pro Ala Gln Thr Phe Arg Cys Ser Asn Gly Lys Cys Leu Ser Lys
385 390 395 400

Ser Gln Gln Cys Asn Gly Lys Asp Asp Cys Gly Asp Gly Ser Asp Glu
405 410 415

Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His Thr Tyr
420 425 430

Arg Cys Leu Asn Gly Leu Cys Leu Ser Lys Gly Asn Pro Glu Cys Asp
435 440 445

Gly Lys Glu Asp Cys Ser Asp Gly Ser Asp Glu Lys Asp Cys Asp Cys
450 455 460

Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly Thr Asp
465 470 475 480

Ala Asp Glu Gly Glu Trp Pro Trp Gln Val Ser Leu His Ala Leu Gly
485 490 495

Gln Gly Thr Ser Xaa Gly Ala Ser Leu Ile Ser Pro Asn Trp Leu Val
500 505 510

Ser Ala Ala His Cys Tyr Ile Asp Asp Arg Gly Phe Arg Tyr Ser Asp
515 520 525

Pro Thr Gln Xaa Thr Ala Phe Leu Gly Leu His Asp Gln Ser Gln Arg
530 535 540

Ser Xaa Leu Gly Cys Arg Ser Ala Gly Ser Ser Ala Ser Ser Pro Thr
545 550 555 560

Pro Ser Ser Met Thr Ser Pro Ser Thr Met Thr Ser Arg Cys Trp Ser

565 570 575

Trp Arg Asn Arg Gln Ser Thr Ala Pro Trp Cys Gly Pro Ser Ala Cys
580 585 590

Arg Thr Pro Pro Met Ser Ser Leu Pro Ala Arg Pro Ser Gly Ser Arg
595 600 605

Ala Gly Asp Thr Pro Ser Met Glu Ala Leu Ala Arg
610 615 620

<210> 1194
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1194
Arg Thr Leu Cys His Leu Thr Thr Leu Asp Glu Leu Ser Cys Gln Arg
1 5 10 15

Glu Asn Leu Met Phe Lys Glu His Phe Pro Leu Ala Asp Val Thr Ala
20 25 30

Gly Phe Val Phe His Met Cys Phe Ser Tyr Thr His Leu Asn Ala Phe
35 40 45

Lys His Leu
50

<210> 1195
<211> 269
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (245)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (246)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (257)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (266)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1195
Pro Ala Glu Asp Ala Ala Ser Leu Thr Trp Gly Val Ala Ile Arg Ala
1 5 10 15

Gly Arg Ser Trp Phe Ser Gly Pro Ala Ala Pro Ala Ala Ala Met Ser
20 25 30

Phe Phe Pro Glu Leu Tyr Phe Asn Val Asp Asn Gly Tyr Leu Glu Gly
35 40 45

Leu Val Arg Gly Leu Lys Ala Gly Val Leu Ser Gln Ala Asp Tyr Leu
50 55 60

Asn Leu Val Gln Cys Glu Thr Leu Glu Asp Leu Lys Leu His Leu Gln
65 70 75 80

Ser Thr Asp Tyr Gly Asn Phe Leu Ala Asn Glu Ala Ser Pro Leu Thr
85 90 95

Val Ser Val Ile Asp Asp Arg Leu Lys Glu Lys Met Val Val Glu Phe
100 105 110

Arg His Met Arg Asn His Ala Tyr Glu Pro Leu Ala Ser Phe Leu Asp
115 120 125

Phe Ile Thr Tyr Ser Tyr Met Ile Asp Asn Val Ile Leu Leu Ile Thr
130 135 140

Gly Thr Leu His Gln Arg Ser Ile Ala Glu Leu Val Pro Lys Cys His
145 150 155 160

Pro Leu Gly Ser Phe Glu Gln Met Glu Ala Val Asn Ile Ala Gln Thr
165 170 175

Pro Ala Glu Leu Tyr Asn Ala Ile Leu Val Asp Thr Pro Leu Ala Ala
180 185 190

Phe Phe Gln Asp Cys Ile Ser Glu Gln Asp Leu Asp Glu Met Asn Ile
195 200 205

Glu Ile Ile Arg Asn Thr Leu Tyr Lys Ala Tyr Leu Glu Ser Phe Tyr
210 215 220

Lys Phe Cys Thr Leu Leu Gly Gly Thr Thr Ala Asp Ala Met Cys Pro

225 230 235 240

Ile Leu Glu Phe Xaa Xaa Gln Thr Val Pro Ser Ser Phe His Thr Val
245 250 255

Xaa Gly Ser Thr Leu Arg Ala Trp Arg Xaa Gly Ser Gly
260 265

<210> 1196
<211> 301
<212> PRT
<213> Homo sapiens

<400> 1196
Arg His Glu Pro Ala Pro Arg Glu Ala Pro Gly Ser Arg Ala Ser Ala
1 5 10 15

Phe Leu Leu Pro Ser Phe Leu Pro Gly Pro Arg Leu Val Pro Ala Gly
20 25 30

His Pro Thr Ala Thr Met Phe Val Pro Cys Gly Glu Ser Ala Pro Asp
35 40 45

Leu Ala Gly Phe Thr Leu Leu Met Pro Ala Val Ser Val Gly Asn Val
50 55 60

Gly Gln Leu Ala Met Asp Leu Ile Ile Ser Thr Leu Asn Met Ser Lys
65 70 75 80

Ile Gly Tyr Phe Tyr Thr Asp Cys Leu Val Pro Met Val Gly Asn Asn
85 90 95

Pro Tyr Ala Thr Thr Glu Gly Asn Ser Thr Glu Leu Ser Ile Asn Ala
100 105 110

Glu Val Tyr Ser Leu Pro Ser Arg Lys Leu Val Ala Leu Gln Leu Arg
115 120 125

Ser Ile Phe Ile Lys Tyr Lys Ser Lys Pro Phe Cys Glu Lys Leu Leu
130 135 140

Ser Trp Val Lys Ser Ser Gly Cys Ala Arg Val Ile Val Leu Ser Ser
145 150 155 160

Ser His Ser Tyr Gln Arg Asn Asp Leu Gln Leu Arg Ser Thr Pro Phe
165 170 175

Arg Tyr Leu Leu Thr Pro Ser Met Gln Lys Ser Val Gln Asn Lys Ile
180 185 190

Lys Ser Leu Asn Trp Glu Glu Met Glu Lys Ser Arg Cys Ile Pro Glu
195 200 205

Ile Asp Asp Ser Glu Phe Cys Ile Arg Ile Pro Gly Gly Gly Ile Thr
210 215 220

Lys Thr Leu Tyr Asp Glu Ser Cys Ser Lys Glu Ile Gln Met Ala Val
225 230 235 240

Leu Leu Lys Phe Val Ser Glu Gly Asp Asn Ile Pro Asp Ala Leu Gly
245 250 255

Leu Val Glu Tyr Leu Asn Glu Trp Leu Gln Ile Leu Lys Pro Leu Ser
260 265 270

Asp Asp Pro Thr Val Ser Ala Ser Arg Trp Lys Ile Pro Ser Ser Trp
275 280 285

Arg Leu Leu Phe Gly Ser Gly Leu Pro Pro Ala Leu Phe
290 295 300

<210> 1197
<211> 246
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (65)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (230)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1197
Gly Thr Arg Asp Leu Leu Leu Ala Ala Ala Ala Ala Thr Gly Lys Leu
1 5 10 15

Lys Ser Phe Ala Arg Lys Phe Ile Asn Leu Asn Glu Phe Thr Thr Tyr
20 25 30

Gly Ser Glu Glu Ser Thr Lys Pro Ala Ser Val Arg Ala Leu Leu Phe
35 40 45

Xaa Ile Ser Phe Leu Met Leu Cys His Val Ala Gln Thr Tyr Gly Ser
50 55 60

Xaa Val Ile Leu Ser Glu Ser Arg Thr Gly Ala Glu Val Pro Phe Phe
65 70 75 80

Glu Thr Trp Met Gln Thr Cys Met Pro Glu Glu Gly Lys Ile Leu Asn
85 90 95

Pro Asp His Pro Cys Phe Arg Pro Asp Ser Thr Lys Val Glu Ser Leu
100 105 110

Val Ala Leu Leu Asn Asn Ser Ser Glu Met Lys Leu Val Gln Met Lys
115 120 125

Trp His Glu Ala Cys Leu Ser Ile Ser Ala Ala Ile Leu Glu Ile Leu
130 135 140

Asn Ala Trp Glu Asn Gly Val Leu Ala Phe Glu Ser Ile Gln Lys Ile
145 150 155 160

Thr Asp Asn Ile Lys Gly Lys Val Cys Ser Leu Ala Val Cys Ala Val
165 170 175

Ala Trp Leu Val Ala His Val Arg Met Leu Gly Leu Asp Glu Arg Glu
180 185 190

Lys Ser Leu Gln Met Ile Arg Gln Leu Ala Gly Pro Leu Phe Ser Glu
195 200 205

Asn Thr Leu Gln Phe Tyr Asn Glu Arg Val Val Ile Met Asn Ser Ile
210 215 220

Leu Gly Ala His Val Xaa Arg Arg Ala Ala Ala Asp Ser His Ala Gly
225 230 235 240

Phe Lys Phe Pro Ser Asn
245

<210> 1198
<211> 465
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (203)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (460)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (461)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1198
Lys Asn Met Glu Thr Glu Gln Pro Glu Glu Thr Phe Pro Asn Thr Glu
1 5 10 15

Thr Asn Gly Glu Phe Gly Lys Arg Pro Ala Glu Asp Met Glu Glu Glu
20 25 30

Gln Ala Phe Lys Arg Ser Arg Asn Thr Asp Glu Met Val Glu Leu Arg
35 40 45

Ile Leu Leu Gln Ser Lys Asn Ala Gly Ala Val Ile Gly Lys Gly Gly
50 55 60

Lys Asn Ile Lys Ala Leu Arg Thr Asp Tyr Asn Ala Ser Val Ser Val
65 70 75 80

Pro Asp Ser Ser Gly Pro Glu Arg Ile Leu Ser Ile Ser Ala Asp Ile
85 90 95

Glu Thr Ile Gly Glu Ile Leu Lys Lys Ile Ile Pro Thr Leu Glu Glu
100 105 110

Gly Leu Gln Leu Pro Ser Pro Thr Ala Thr Ser Gln Leu Pro Leu Glu
115 120 125

Ser Asp Ala Val Glu Cys Leu Asn Tyr Gln His Tyr Lys Gly Ser Asp
130 135 140

Phe Asp Cys Glu Leu Arg Leu Leu Ile His Gln Ser Leu Ala Gly Gly
145 150 155 160

Ile Ile Gly Val Lys Gly Ala Lys Ile Lys Glu Leu Arg Glu Asn Thr
165 170 175

Gln Thr Thr Ile Lys Leu Phe Gln Glu Cys Cys Pro His Ser Thr Asp
180 185 190

Arg Val Val Leu Ile Gly Gly Lys Pro Asp Xaa Val Val Glu Cys Ile

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        195                 200                 205

Lys Ile Ile Leu Asp Leu Ile Ser Glu Ser Pro Ile Lys Gly Arg Ala
    210                 215                 220

Gln Pro Tyr Asp Pro Asn Phe Tyr Asp Glu Thr Tyr Asp Tyr Gly Gly
225                 230                 235                 240

Phe Thr Met Met Phe Asp Asp Arg Arg Gly Arg Pro Val Gly Phe Pro
                245                 250                 255

Met Arg Gly Arg Gly Gly Phe Asp Arg Met Pro Pro Gly Arg Gly Gly
            260                 265                 270

Arg Pro Met Pro Pro Ser Arg Arg Asp Tyr Asp Asp Met Ser Pro Arg
        275                 280                 285

Arg Gly Pro Pro Pro Pro Pro Pro Gly Arg Gly Gly Arg Gly Gly Ser
    290                 295                 300

Arg Ala Arg Asn Leu Pro Leu Pro Pro Pro Pro Pro Pro Arg Gly Gly
305                 310                 315                 320

Asp Leu Met Ala Tyr Asp Arg Arg Gly Arg Pro Gly Asp Arg Tyr Asp
                325                 330                 335

Gly Met Val Gly Phe Ser Ala Asp Glu Thr Trp Asp Ser Ala Ile Asp
            340                 345                 350

Thr Trp Ser Pro Ser Glu Trp Gln Met Ala Tyr Glu Pro Gln Gly Gly
        355                 360                 365

Ser Gly Tyr Asp Tyr Ser Tyr Ala Gly Gly Arg Gly Ser Tyr Gly Asp
    370                 375                 380

Leu Gly Gly Pro Ile Ile Thr Thr Gln Val Thr Ile Pro Lys Asp Leu
385                 390                 395                 400

Ala Gly Ser Ile Ile Gly Lys Gly Gly Gln Arg Ile Lys Gln Ile Arg
                405                 410                 415

His Glu Ser Gly Ala Ser Ile Lys Ile Asp Glu Pro Leu Glu Gly Ser
            420                 425                 430

Glu Asp Arg Ile Ile Thr Ile Thr Gly Thr Gln Asp Gln Ile Gln Asn
        435                 440                 445

Ala Gln Tyr Leu Leu Gln Asn Ser Val Ser Ser Xaa Xaa Leu Ala Leu
    450                 455                 460

Cys
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465

<210> 1199
<211> 446
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (87)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (88)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1199
Tyr Pro Ala Ala Cys Xaa Thr Gly Pro Glu Phe Pro Gly Arg Pro Thr
1 5 10 15

Arg Pro His Glu Met Asp Gln Tyr Trp Gly Ile Gly Ser Leu Ala Ser
20 25 30

Gly Ile Asn Leu Phe Thr Asn Ser Phe Glu Gly Pro Val Leu Asp His
35 40 45

Arg Tyr Tyr Ala Gly Gly Cys Ser Pro His Tyr Ile Leu Asn Thr Arg
50 55 60

Phe Arg Lys Pro Tyr Asn Val Glu Ser Tyr Thr Pro Gln Thr Gln Gly
65 70 75 80

Lys Tyr Glu Phe Ile Leu Xaa Xaa Tyr Glu Ser Tyr Ser Asp Phe Glu
85 90 95

Arg Asn Val Thr Glu Lys Met Ala Ser Lys Ser Gly Phe Ser Phe Gly
100 105 110

Phe Lys Ile Pro Gly Ile Phe Glu Leu Gly Ile Ser Ser Gln Ser Asp
115 120 125

Arg Gly Lys His Tyr Ile Arg Arg Thr Lys Arg Phe Ser His Thr Lys
130 135 140

```
Ser Val Phe Leu His Ala Arg Ser Asp Leu Glu Val Ala His Tyr Lys
145                 150                 155                 160

Leu Lys Pro Arg Ser Leu Met Leu His Tyr Glu Phe Leu Gln Arg Val
                165                 170                 175

Lys Arg Leu Pro Leu Glu Tyr Ser Tyr Gly Glu Tyr Arg Asp Leu Phe
            180                 185                 190

Arg Asp Phe Gly Thr His Tyr Ile Thr Glu Ala Val Leu Gly Gly Ile
        195                 200                 205

Tyr Glu Tyr Thr Leu Val Met Asn Lys Glu Ala Met Glu Arg Gly Asp
    210                 215                 220

Tyr Thr Leu Asn Asn Val His Ala Cys Ala Lys Asn Asp Phe Lys Ile
225                 230                 235                 240

Gly Gly Ala Ile Glu Glu Val Tyr Val Ser Leu Gly Val Ser Val Gly
                245                 250                 255

Lys Cys Arg Gly Ile Leu Asn Glu Ile Lys Asp Arg Asn Lys Arg Asp
            260                 265                 270

Thr Met Val Glu Asp Leu Val Val Leu Val Arg Gly Gly Ala Ser Glu
        275                 280                 285

His Ile Thr Thr Leu Ala Tyr Gln Glu Leu Pro Thr Ala Asp Leu Met
    290                 295                 300

Gln Glu Trp Gly Asp Ala Val Gln Tyr Asn Pro Ala Ile Ile Lys Val
305                 310                 315                 320

Lys Val Glu Pro Leu Tyr Glu Leu Val Thr Ala Thr Asp Phe Ala Tyr
                325                 330                 335

Ser Ser Thr Val Arg Gln Asn Met Lys Gln Ala Leu Glu Glu Phe Gln
            340                 345                 350

Lys Glu Val Ser Ser Cys His Cys Ala Pro Cys Gln Gly Asn Gly Val
        355                 360                 365

Pro Val Leu Lys Gly Ser Arg Cys Asp Cys Ile Cys Pro Val Gly Ser
    370                 375                 380

Gln Gly Leu Ala Cys Glu Val Ser Tyr Arg Lys Asn Thr Pro Ile Asp
385                 390                 395                 400

Gly Lys Trp Asn Cys Trp Ser Asn Trp Ser Ser Cys Ser Gly Arg Arg
                405                 410                 415
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Lys Thr Arg Gln Arg Gln Cys Asn Asn Pro Pro Pro Gln Asn Gly Gly
420 425 430

Ser Pro Cys Ser Gly Pro Ala Ser Glu Thr Leu Asp Cys Ser
435 440 445

<210> 1200
<211> 437
<212> PRT
<213> Homo sapiens

<400> 1200
Leu Gly Ser Ser Asp Ser Tyr Ala Ser Pro Gly Arg Ala Ala Ala Pro
1 5 10 15

Pro Ala Ala Ala Gly Pro Gly Asp Thr Ser Ala Cys Tyr Lys Ser Ser
20 25 30

Gly Pro Arg Cys Leu Leu Pro Asp Leu Ala Pro Ser Ser Glu Pro Gly
35 40 45

Ala Cys Leu Gly Gly Leu Ser Val Phe Thr Met Glu Gln Leu Ser Ser
50 55 60

Ala Asn Thr Arg Phe Ala Leu Asp Leu Phe Leu Ala Leu Ser Glu Asn
65 70 75 80

Asn Pro Ala Gly Asn Ile Phe Ile Ser Pro Phe Ser Ile Ser Ser Ala
85 90 95

Met Ala Met Val Phe Leu Gly Thr Arg Gly Asn Thr Ala Ala Gln Leu
100 105 110

Ser Lys Thr Phe His Phe Asn Thr Val Glu Glu Val His Ser Arg Phe
115 120 125

Gln Ser Leu Asn Ala Asp Ile Asn Lys Arg Gly Ala Ser Tyr Ile Leu
130 135 140

Lys Leu Ala Asn Arg Leu Tyr Gly Glu Lys Thr Tyr Asn Phe Leu Pro
145 150 155 160

Glu Phe Leu Val Ser Thr Gln Lys Thr Tyr Gly Ala Asp Leu Ala Ser
165 170 175

Val Asp Phe Gln His Ala Ser Glu Asp Ala Arg Lys Thr Ile Asn Gln
180 185 190

```
Trp Val Lys Gly Gln Thr Glu Gly Lys Ile Pro Glu Leu Leu Ala Ser
        195                 200                 205

Gly Met Val Asp Asn Met Thr Lys Leu Val Leu Val Asn Ala Ile Tyr
    210                 215                 220

Phe Lys Gly Asn Trp Lys Asp Lys Phe Met Lys Glu Ala Thr Thr Asn
225                 230                 235                 240

Ala Pro Phe Arg Leu Asn Lys Lys Asp Arg Lys Thr Val Lys Met Met
                245                 250                 255

Tyr Gln Lys Lys Lys Phe Ala Tyr Gly Tyr Ile Glu Asp Leu Lys Cys
            260                 265                 270

Arg Val Leu Glu Leu Pro Tyr Gln Gly Glu Glu Leu Ser Met Val Ile
        275                 280                 285

Leu Leu Pro Asp Asp Ile Glu Asp Glu Ser Thr Gly Leu Lys Lys Ile
    290                 295                 300

Glu Glu Gln Leu Thr Leu Glu Lys Leu His Glu Trp Thr Lys Pro Glu
305                 310                 315                 320

Asn Leu Asp Phe Ile Glu Val Asn Val Ser Leu Pro Arg Phe Lys Leu
                325                 330                 335

Glu Glu Ser Tyr Thr Leu Asn Ser Asp Leu Ala Arg Leu Gly Val Gln
            340                 345                 350

Asp Leu Phe Asn Ser Ser Lys Ala Asp Leu Ser Gly Met Ser Gly Ala
        355                 360                 365

Arg Asp Ile Phe Ile Ser Lys Ile Val His Lys Ser Phe Val Glu Val
    370                 375                 380

Asn Glu Glu Gly Thr Glu Ala Ala Ala Ala Thr Ala Gly Ile Ala Thr
385                 390                 395                 400

Phe Cys Met Leu Met Pro Glu Glu Asn Phe Thr Ala Asp His Pro Phe
                405                 410                 415

Leu Phe Phe Ile Arg His Asn Ser Ser Gly Ser Ile Leu Phe Leu Gly
            420                 425                 430

Arg Phe Ser Ser Pro
        435
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<210> 1201

<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (82)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1201
Gln Leu Gly Pro Val Val Gly Gly Trp Tyr Lys Val Leu Asp Arg Phe
1 5 10 15

Ile Pro Gly Thr Thr Lys Val Asp Ala Leu Lys Lys Met Leu Leu Asp
20 25 30

Gln Gly Gly Phe Ala Pro Cys Phe Leu Gly Cys Phe Leu Pro Leu Val
35 40 45

Gly Ala Leu Asn Gly Leu Ser Ala Gln Asp Asn Trp Pro Asn Tyr Ser
50 55 60

Gly Ile Ile Leu Met Pro Leu Ser Pro Thr Thr Ile Tyr Gly Leu Leu
65 70 75 80

Cys Xaa

<210> 1202
<211> 126
<212> PRT
<213> Homo sapiens

<400> 1202
Ile Ser Arg Ser Ser Ala Arg Arg Gln Pro Phe Arg His Gly Arg Leu
1 5 10 15

Trp Arg Ala Ala Ala Met Ala Leu Arg Tyr Pro Met Ala Val Gly Leu
20 25 30

Asn Lys Gly His Lys Val Thr Lys Asn Val Ser Lys Pro Arg His Ser
35 40 45

Arg Arg Arg Gly Arg Leu Thr Lys His Thr Lys Phe Val Arg Asp Met
50 55 60

Ile Arg Glu Val Cys Gly Phe Ala Pro Tyr Glu Arg Arg Ala Met Glu
65 70 75 80

Leu Leu Lys Val Ser Lys Asp Lys Arg Ala Leu Lys Phe Ile Lys Lys
85 90 95

Arg Val Gly Thr His Ile Arg Ala Lys Arg Lys Arg Glu Glu Leu Ser
100 105 110

Asn Val Leu Ala Ala Met Arg Lys Ala Ala Ala Lys Lys Asp
115 120 125

<210> 1203
<211> 130
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1203
Asp Trp Asn Pro Asp Leu Gln Ala Ser Ala Val Cys Ile Lys Arg Val
1 5 10 15

Gly Glu Ser Gly Pro Leu Ala Gln Glu Pro Xaa Leu Leu Lys Glu Gly
20 25 30

Phe Lys Ala Lys Trp Val Cys Gln Arg Cys Cys Leu Pro Phe Leu Glu
35 40 45

Met Leu Ile Ser Leu Ser Lys Thr Glu Lys Ser Arg Cys Tyr Arg Asn
50 55 60

Asn Leu Val Cys Cys Ile Asn Cys Ser Trp Ala Trp Ser Ser Ile Pro
65 70 75 80

Thr Leu Arg Phe Pro Ala Ser Leu Cys Cys Pro Gly Ser His Ser Cys
85 90 95

Arg Arg Pro Asn Pro Leu Ala Val Phe Cys Leu Lys Ile Trp Gly Ala
100 105 110

Pro Ser Leu Ser Ser Pro Gly Asn Ser Leu Ala Glu Gly Gly Asp Pro
115 120 125

Pro Gln
130

<210> 1204
<211> 228
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (189)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (196)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (199)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (225)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (228)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1204
Trp Ala Ala Phe Glu Pro Ala Thr Leu Ala Trp Lys Phe Pro Phe Gln
1 5 10 15

Ser Gly Phe Cys Leu Leu Leu Pro Ser Pro Ser Pro Arg Tyr Leu Phe
20 25 30

Thr Ser His Leu Ile Ser Leu Cys Ser Ser Val Ser Pro Thr His Ile
35 40 45

Ile Gly Asp Ser Gly Gly Ser Leu Thr Ser Leu Leu Ser Asn Ala Arg
50 55 60

Pro Ser Gly Leu Ala Ser Val Ala Ser His Ile Asp Val Thr Leu Glu
65 70 75 80

Leu Leu Pro Gln Arg Gly Arg Arg Asp Arg Leu Ser Pro His Leu Pro
85 90 95

Pro Tyr Ser Pro Leu Tyr Ser Arg Phe Asp His Leu Ser Pro Ser Ala
100 105 110

Ala Pro Ser His Phe Gly Gln Ser Gln Ala Pro Ile Arg Leu Pro Pro
115 120 125

Pro Pro Gly Ala Pro Ser Ile Ser Leu Ser Pro Leu Pro Gln Asn Leu
130 135 140

Cys Lys Gly Tyr Glu Arg Asp Pro Leu Pro Ser Arg Pro Pro Leu Arg
145 150 155 160

Ala Val Arg Ser Lys Lys Gln Lys Leu Val Gly Gly Trp Leu Gly Leu
165 170 175

Cys Pro Val Pro Arg Trp Asp Lys Leu Ala Phe Ser Xaa Ile Pro Ser
180 185 190

Trp Val Pro Xaa Ser Phe Xaa Ala Pro Gly Ala Arg Thr His Cys Ala
195 200 205

Val Phe Leu Phe Ser Phe Val Gly Lys Gly Thr Lys Val Phe Ala Lys
210 215 220

Xaa Pro Val Xaa
225

<210> 1205
<211> 270
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (128)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1205
Leu Pro Gly Ala Val Ala Ala Ser Ser Gly Ser Pro Pro Gly Ser Ala
1 5 10 15

Leu Ala Ala Val Ala Ser Gly Gly Asp Leu Phe Pro Gly Gln Pro Val
20 25 30

Ser Glu Leu Ile Ala Gln Leu Leu Arg Ala Glu Pro Tyr Pro Ala Ala
35 40 45

Ala Gly Arg Phe Gly Ala Gly Gly Gly Ala Ala Gly Ala Val Leu Gly
50 55 60

Ile Asp Asn Val Cys Glu Leu Ala Ala Arg Leu Leu Phe Ser Thr Val

65 70 75 80

Glu Trp Ala Arg His Ala Pro Phe Phe Pro Glu Leu Pro Val Ala Asp
85 90 95

Gln Val Ala Leu Leu Arg Leu Ser Trp Ser Glu Leu Phe Val Leu Asn
100 105 110

Ala Ala Gln Ala Ala Leu Pro Leu His Thr Ala Pro Leu Leu Ala Xaa
115 120 125

Ala Gly Leu His Ala Ala Pro Met Ala Ala Glu Arg Ala Val Ala Phe
130 135 140

Met Asp Gln Val Arg Ala Phe Gln Glu Gln Val Asp Lys Leu Gly Arg
145 150 155 160

Leu Gln Val Asp Ser Ala Glu Tyr Gly Cys Leu Lys Ala Ile Ala Leu
165 170 175

Phe Thr Pro Asp Ala Cys Gly Leu Ser Asp Pro Ala His Val Glu Ser
180 185 190

Leu Gln Glu Lys Ala Gln Val Ala Leu Thr Glu Tyr Val Arg Ala Gln
195 200 205

Tyr Pro Ser Gln Pro Gln Arg Phe Gly Arg Leu Leu Leu Arg Leu Pro
210 215 220

Ala Leu Arg Ala Val Pro Ala Ser Leu Ile Ser Gln Leu Phe Phe Met
225 230 235 240

Arg Leu Val Gly Lys Thr Pro Ile Glu Thr Leu Ile Arg Asp Met Leu
245 250 255

Leu Ser Gly Ser Thr Phe Asn Trp Pro Tyr Gly Ser Gly Gln
260 265 270

<210> 1206
<211> 89
<212> PRT
<213> Homo sapiens

<400> 1206
Met Phe His Cys Ser Asp Lys Tyr Phe Thr Phe Phe Ser Val His Gln
1 5 10 15

Arg Glu Arg Asp Pro Pro Thr Ala Val Thr Ser Lys Cys Ser Cys Ser
20 25 30

Ile Asn Gly Val Thr Asp Thr Glu Val His Ser Trp Phe Leu Ser Arg
35 40 45

Val Val Ile Leu Val Ser Trp Ser Leu Gly His Trp Gly Cys Thr Leu
50 55 60

Lys Ser Pro Asn Arg Leu Ala Ile Lys Ile Asn Lys Ala Ala Ala Pro
65 70 75 80

Phe Gln Phe Thr Phe His Leu Thr Gln
85

<210> 1207
<211> 145
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (137)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1207
Cys Val Gly Lys Ala Gly Val Glu Leu Gly Cys Ser Gly Glu Gly Val
1 5 10 15

Val Lys Lys Ala Ser Ser Arg Gly His Lys Ala Arg Phe Pro Leu Arg
20 25 30

Ser His Lys Val Leu Ser Pro Ala Pro Gly Ala Gly Gly Val His Gly
35 40 45

Pro Gly Phe Thr Ser Thr His Pro Ala His Pro Arg Gly Glu Gly Pro
50 55 60

Arg Ala Pro Gly Pro Ala Ala Asp Arg Ile Leu Cys Lys Leu Cys Ser
65 70 75 80

Val His Cys Lys Thr Pro Ala Gln Leu Ala Gly His Met Gln Thr His
85 90 95

Leu Gly Gly Ala Ala Pro Leu Ser Arg Glu Thr Pro Pro Ser His Ser
100 105 110

Pro Pro Ala Glu Gly Asp Pro Arg Thr His Gln Val Leu Val Arg Phe
115 120 125

Val Gln Trp Arg Arg Gln Arg Gln Xaa Arg Gln Arg Gln Gln Arg Gln

130 135 140

Gln
145

<210> 1208
<211> 378
<212> PRT
<213> Homo sapiens

<400> 1208
Ser Ala Ser Arg Ala Thr Ala Met Ser Ser Arg Gly Gly Lys Lys Lys
1 5 10 15

Ser Thr Lys Thr Ser Arg Ser Ala Lys Ala Gly Val Ile Phe Pro Val
20 25 30

Gly Arg Met Leu Arg Tyr Ile Lys Lys Gly His Pro Lys Tyr Arg Ile
35 40 45

Gly Val Gly Ala Pro Val Tyr Met Ala Ala Val Leu Glu Tyr Leu Thr
50 55 60

Ala Glu Ile Leu Glu Leu Ala Gly Asn Ala Ala Arg Asp Asn Lys Lys
65 70 75 80

Gly Arg Val Thr Pro Arg His Ile Leu Leu Ala Val Ala Asn Asp Glu
85 90 95

Glu Leu Asn Gln Leu Leu Lys Gly Val Thr Ile Ala Ser Gly Gly Val
100 105 110

Leu Pro Asn Ile His Pro Glu Leu Leu Ala Lys Lys Arg Gly Ser Lys
115 120 125

Gly Lys Leu Glu Ala Ile Ile Thr Pro Pro Pro Ala Lys Lys Ala Lys
130 135 140

Ser Pro Ser Gln Lys Lys Pro Val Ser Lys Lys Ala Gly Gly Lys Lys
145 150 155 160

Gly Ala Arg Lys Ser Lys Lys Gln Gly Glu Val Ser Lys Ala Ala Ser
165 170 175

Ala Asp Ser Thr Thr Glu Gly Thr Pro Ala Asp Gly Phe Thr Val Leu
180 185 190

Ser Thr Lys Ser Leu Phe Leu Gly Gln Lys Leu Asn Leu Ile His Ser
195 200 205

Glu Ile Ser Asn Leu Ala Gly Phe Glu Val Glu Ala Ile Ile Asn Pro
210 215 220

Thr Asn Ala Asp Ile Asp Leu Lys Asp Asp Leu Gly Asn Thr Leu Glu
225 230 235 240

Lys Lys Gly Gly Lys Glu Phe Val Glu Ala Val Leu Glu Leu Arg Lys
245 250 255

Lys Asn Gly Pro Leu Glu Val Ala Gly Ala Ala Val Ser Ala Gly His
260 265 270

Gly Leu Pro Ala Lys Phe Val Ile His Cys Asn Ser Pro Val Trp Gly
275 280 285

Ala Asp Lys Cys Glu Glu Leu Leu Glu Lys Thr Val Lys Asn Cys Leu
290 295 300

Ala Leu Ala Asp Asp Lys Lys Leu Lys Ser Ile Ala Phe Pro Ser Ile
305 310 315 320

Gly Ser Gly Arg Asn Gly Phe Pro Lys Gln Thr Ala Ala Gln Leu Ile
325 330 335

Leu Lys Ala Ile Ser Ser Tyr Phe Val Ser Thr Met Ser Ser Ser Ile
340 345 350

Lys Thr Val Tyr Phe Val Leu Phe Asp Ser Glu Ser Ile Gly Ile Tyr
355 360 365

Val Gln Glu Met Ala Lys Leu Asp Ala Asn
370 375

<210> 1209
<211> 220
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1209
Arg Gly Gly Lys Ile Xaa Asp Thr Phe Xaa Arg Tyr Ala Arg Arg Tyr
1   5   10   15

Arg Ser Gly Ile Pro Gly Ser Thr His Ala Xaa Ala Pro Gly Ala Met
            20   25   30

Arg Leu Ser Leu Pro Leu Leu Leu Leu Leu Leu Gly Ala Trp Ala Ile
        35   40   45

Pro Gly Gly Leu Gly Asp Arg Ala Pro Leu Thr Ala Thr Ala Pro Gln
    50   55   60

Leu Asp Asp Glu Glu Met Tyr Ser Ala His Met Pro Ala His Leu Arg
65   70   75   80

Cys Asp Ala Cys Arg Ala Val Ala Tyr Gln Met Trp Gln Asn Leu Ala
                85   90   95

Lys Ala Glu Thr Lys Leu His Thr Ser Asn Ser Gly Gly Arg Arg Glu
            100   105   110

Leu Ser Glu Leu Val Tyr Thr Asp Val Leu Asp Arg Ser Cys Ser Arg
        115   120   125

Asn Trp Gln Asp Tyr Gly Val Arg Glu Val Asp Gln Val Lys Arg Leu
    130   135   140

Thr Gly Pro Gly Leu Ser Glu Gly Pro Glu Pro Ser Ile Ser Val Met
145   150   155   160

Val Thr Gly Gly Pro Trp Pro Thr Arg Leu Ser Arg Thr Cys Leu His
                165   170   175

Tyr Leu Gly Glu Phe Gly Glu Asp Gln Ile Tyr Glu Ala His Gln Gln
            180   185   190

Gly Arg Gly Ala Leu Glu Ala Leu Leu Cys Gly Gly Pro Gln Gly Ala
        195   200   205

Cys Ser Glu Lys Val Ser Ala Thr Arg Glu Glu Leu
    210   215   220

<210> 1210

<211> 231
<212> PRT
<213> Homo sapiens

<400> 1210
Ala Leu Ser Pro Ala Met Val Val Pro Glu Asp Gln Leu Thr Arg Trp
1 5 10 15

His Pro Arg Phe Asn Val Asp Glu Val Pro Asp Ile Glu Pro Ala Ala
20 25 30

Leu Pro Gln Pro Pro Ala Thr Glu Lys Leu Thr Thr Ala Gln Glu Val
35 40 45

Leu Ala Arg Ala Arg Asn Leu Ile Ser Pro Arg Met Glu Lys Ala Leu
50 55 60

Ser Gln Leu Ala Leu Arg Ser Ala Ala Pro Ser Ser Pro Gly Ser Pro
65 70 75 80

Arg Pro Ala Leu Pro Ala Thr Pro Pro Ala Thr Pro Pro Ala Ala Ser
85 90 95

Pro Ser Ala Leu Lys Gly Val Ser Gln Asp Leu Leu Glu Arg Ile Arg
100 105 110

Ala Lys Glu Ala Gln Lys Gln Leu Ala Gln Met Thr Arg Cys Pro Glu
115 120 125

Gln Glu Gln Arg Leu Gln Arg Leu Glu Arg Leu Pro Glu Leu Ala Arg
130 135 140

Val Leu Arg Ser Val Phe Val Ser Glu Arg Lys Pro Ala Leu Ser Met
145 150 155 160

Glu Val Ala Cys Ala Arg Met Val Gly Ser Cys Cys Thr Ile Met Ser
165 170 175

Pro Gly Glu Met Glu Lys His Leu Leu Leu Leu Ser Glu Leu Leu Pro
180 185 190

Asp Trp Leu Ser Leu His Arg Ile Arg Thr Asp Thr Tyr Val Lys Leu
195 200 205

Asp Lys Ala Ala Asp Leu Ala His Ile Thr Ala Arg Leu Ala His Gln
210 215 220

Thr Arg Ala Glu Glu Gly Leu
225 230

<210> 1211
<211> 346
<212> PRT
<213> Homo sapiens

<400> 1211
Asn Cys Thr Thr Ile Ser Leu Val Tyr Leu His Phe Val Phe Tyr Asn
1 5 10 15

Ser Tyr Ser Leu Phe Pro Ser Lys Glu Asn Cys Val Tyr Glu Thr Val
20 25 30

Val Leu Pro Leu Asp Glu Arg Ala Phe Glu Lys Thr Leu Thr Pro Ile
35 40 45

Ile Gln Glu Tyr Phe Glu His Gly Asp Thr Asn Glu Val Ala Glu Met
50 55 60

Leu Arg Asp Leu Asn Leu Gly Glu Met Lys Ser Gly Val Pro Val Leu
65 70 75 80

Ala Val Ser Leu Ala Leu Glu Gly Lys Ala Ser His Arg Glu Met Thr
85 90 95

Ser Lys Leu Leu Ser Asp Leu Cys Gly Thr Val Met Ser Thr Thr Asp
100 105 110

Val Glu Lys Ser Phe Asp Lys Leu Leu Lys Asp Leu Pro Glu Leu Ala
115 120 125

Leu Asp Thr Pro Arg Ala Pro Gln Leu Val Gly Gln Phe Ile Ala Arg
130 135 140

Ala Val Gly Asp Gly Ile Leu Cys Asn Thr Tyr Ile Asp Ser Tyr Lys
145 150 155 160

Gly Thr Val Asp Cys Val Gln Ala Arg Ala Ala Leu Asp Lys Ala Thr
165 170 175

Val Leu Leu Ser Met Ser Lys Gly Gly Lys Arg Lys Asp Ser Val Trp
180 185 190

Gly Ser Gly Gly Gly Gln Gln Ser Val Asn His Leu Val Lys Glu Ile
195 200 205

Asp Met Leu Leu Lys Glu Tyr Leu Leu Ser Gly Asp Ile Ser Glu Ala
210 215 220

Glu His Cys Leu Lys Glu Leu Glu Val Pro His Phe His His Glu Leu
225 230 235 240

Val Tyr Glu Ala Ile Ile Met Val Leu Glu Ser Thr Gly Glu Ser Thr
245 250 255

Phe Lys Met Ile Leu Asp Leu Leu Lys Ser Leu Trp Lys Ser Ser Thr
260 265 270

Ile Thr Val Asp Gln Met Lys Arg Gly Tyr Glu Arg Ile Tyr Asn Glu
275 280 285

Ile Pro Asp Ile Asn Leu Asp Val Pro His Ser Tyr Ser Val Leu Glu
290 295 300

Arg Phe Val Glu Glu Cys Phe Gln Ala Gly Ile Ile Ser Lys Gln Leu
305 310 315 320

Arg Asp Leu Cys Pro Ser Arg Gly Arg Lys Arg Phe Val Ser Glu Gly
325 330 335

Asp Gly Gly Arg Leu Lys Pro Glu Ser Tyr
340 345

<210> 1212
<211> 175
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (63)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1212
Pro Arg Xaa Ile Val Ser Ala Ala Cys Gly Arg Asn His Thr Leu Ala
1 5 10 15

Leu Thr Glu Thr Gly Ser Val Phe Ala Phe Gly Glu Asn Lys Met Gly
20 25 30

Gln Leu Gly Leu Gly Asn Gln Thr Asp Ala Val Pro Ser Pro Ala Gln
35 40 45

Ile Met Tyr Asn Gly Gln Pro Ile Thr Lys Met Ala Cys Gly Xaa Glu
50 55 60

Phe Ser Met Ile Met Asp Cys Lys Gly Asn Leu Tyr Ser Phe Gly Cys
65 70 75 80

Pro Glu Tyr Gly Gln Leu Gly His Asn Ser Asp Gly Lys Phe Ile Ala
85 90 95

Arg Ala Gln Arg Ile Glu Tyr Asp Cys Glu Leu Val Pro Arg Arg Val
100 105 110

Ala Ile Phe Ile Glu Lys Thr Lys Asp Gly Gln Ile Leu Pro Val Pro
115 120 125

Asn Val Val Val Arg Asp Val Ala Cys Gly Ala Asn His Thr Leu Val
130 135 140

Leu Asp Ser Gln Lys Arg Val Phe Ser Trp Gly Phe Gly Gly Tyr Gly
145 150 155 160

Arg Leu Gly Thr Gln Ser Arg Arg Met Arg Trp Ser Pro Ala Trp
165 170 175

<210> 1213
<211> 127
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (41)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1213
Cys Phe Ile Cys Val Trp Cys Lys Arg Lys Leu Asp Gln Ile Asn Leu
1 5 10 15

Gln Leu Met Ser Pro Asn Ala Asn Thr Gly Thr His Met His Thr Pro
20 25 30

Ile Asn Thr His Thr Val His Leu Xaa Lys Gly Gln Val Ile Ser His
35 40 45

Pro Asn Phe Thr Ser Thr Asp Pro Leu Ala Pro Thr Pro Ala Ser Thr
50 55 60

Val Thr Ser Lys Ala Arg Ala Thr Cys Ala His Gln Thr Cys Ile Lys
65 70 75 80

Gln Leu Ala Gly Asp Gly Cys Gly Ala Gly Gly Leu Ser Asp Gly Ser

85 90 95

Leu Leu Leu Pro Leu Leu Arg Val Lys Leu Leu Ser Phe Leu Arg Val
100 105 110

Tyr Leu Cys Gln Val Cys Ala Phe Asn Cys Phe Tyr Phe Val Phe
115 120 125

<210> 1214
<211> 146
<212> PRT
<213> Homo sapiens

<400> 1214
Cys Thr Trp Asn Arg Cys Ser Ala Ser Pro Ala Gly Trp Gln Asn Ser
1 5 10 15

Phe Leu Gly His Leu Asn Pro Ser Ser Leu Leu Gln Asn Pro Pro Ala
20 25 30

Asn Arg Ile Gly Met Gly Ala Thr Leu Asp Ile Gln Arg Gln Gln Arg
35 40 45

Met Glu Leu Leu Asp Arg Gln Leu Met Phe Ser Gln Phe Ala Gln Gly
50 55 60

Arg Arg Gln Arg Gln Gln Gln Gly Gly Met Ile Asn Trp Asn Arg Leu
65 70 75 80

Phe Pro Pro Leu Arg Gln Arg Gln Asn Val Asn Tyr Gln Gly Gly Arg
85 90 95

Gln Ser Glu Pro Ala Ala Pro Pro Leu Glu Val Ser Glu Glu Gln Val
100 105 110

Ala Arg Leu Met Glu Met Gly Phe Ser Arg Gly Asp Ala Leu Glu Ala
115 120 125

Leu Arg Ala Ser Asn Asn Asp Leu Asn Val Ala Thr Asn Phe Leu Leu
130 135 140

Gln His
145

<210> 1215
<211> 116
<212> PRT

<213> Homo sapiens

<220>
<221> SITE
<222> (107)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1215
```
Leu Lys Asn His Gln Lys Thr His Thr Ser Glu Lys Ser Tyr Lys Cys
  1               5                  10                  15

Asn Glu Cys Arg Lys Ala Phe Ser Tyr Cys Ser Gly Leu Ile Gln Cys
             20                  25                  30

Gln Val Ile His Thr Ile Glu Lys Pro Tyr Glu Tyr Gly Lys Cys Gly
         35                  40                  45

Lys Ala Phe Arg Gln Arg Thr Asp Leu Lys Lys His Gln Lys Met His
     50                  55                  60

Thr Glu Glu Lys Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Ser
 65                  70                  75                  80

Gln Ser Thr Tyr Leu Thr Lys His Gln Lys Ile His Ser Glu Glu Lys
                 85                  90                  95

Ser Asn Ile His Thr Glu Cys Gly Glu Thr Xaa Xaa Gln Asn Ser Ser
            100                 105                 110

Phe Leu Gln Gln
        115
```

<210> 1216
<211> 201
<212> PRT
<213> Homo sapiens

<400> 1216
```
Ala Ala Gly Gly Glu Gly Phe Gly Ser Leu His Ala Ser Leu Val Gly
  1               5                  10                  15

Phe Arg Gly Val Val Ala Gly Cys Ala Arg His Phe Arg Ala Ser Arg
             20                  25                  30
```

Asn Gly Val Ala Asn Gly Leu Gln Ser Asn Met Pro Lys Phe Tyr Cys
35 40 45

Asp Tyr Cys Asp Thr Tyr Leu Thr His Asp Ser Pro Ser Val Arg Lys
50 55 60

Thr His Cys Ser Gly Arg Lys His Lys Glu Asn Val Lys Asp Tyr Tyr
65 70 75 80

Gln Lys Trp Met Glu Glu Gln Ala Gln Ser Leu Ile Asp Lys Thr Thr
85 90 95

Ala Ala Phe Gln Gln Gly Lys Ile Pro Pro Thr Pro Phe Ser Ala Pro
100 105 110

Pro Pro Ala Gly Ala Met Ile Pro Pro Pro Pro Ser Leu Pro Gly Pro
115 120 125

Pro Arg Pro Gly Met Met Pro Ala Pro His Met Gly Gly Pro Pro Met
130 135 140

Met Pro Met Met Gly Pro Pro Pro Pro Gly Met Met Pro Val Gly Pro
145 150 155 160

Ala Pro Gly Met Arg Pro Pro Met Gly Gly His Met Pro Met Met Pro
165 170 175

Gly Pro Pro Met Met Arg Pro Pro Ala Arg Pro Met Met Val Pro Thr
180 185 190

Arg Pro Gly Met Thr Arg Pro Asp Arg
195 200

<210> 1217
<211> 473
<212> PRT
<213> Homo sapiens

<400> 1217
Lys Phe Thr Met Lys Phe Leu Leu Ile Leu Leu Leu Gln Ala Thr Ala
1 5 10 15

Ser Gly Ala Leu Pro Leu Asn Ser Ser Thr Ser Leu Glu Lys Asn Asn
20 25 30

Val Leu Phe Gly Glu Arg Tyr Leu Glu Lys Phe Tyr Gly Leu Glu Ile
35 40 45

Asn Lys Leu Pro Val Thr Lys Met Lys Tyr Ser Gly Asn Leu Met Lys

50 55 60

Glu Lys Ile Gln Glu Met Gln His Phe Leu Gly Leu Lys Val Thr Gly
65 70 75 80

Gln Leu Asp Thr Ser Thr Leu Glu Met Met His Ala Pro Arg Cys Gly
85 90 95

Val Pro Asp Val His His Phe Arg Glu Met Pro Gly Gly Pro Val Trp
100 105 110

Arg Lys His Tyr Ile Thr Tyr Arg Ile Asn Asn Tyr Thr Pro Asp Met
115 120 125

Asn Arg Glu Asp Val Asp Tyr Ala Ile Arg Lys Ala Phe Gln Val Trp
130 135 140

Ser Asn Val Thr Pro Leu Lys Phe Ser Lys Ile Asn Thr Gly Met Ala
145 150 155 160

Asp Ile Leu Val Val Phe Ala Arg Gly Ala His Gly Asp Phe His Ala
165 170 175

Phe Asp Gly Lys Gly Gly Ile Leu Ala His Ala Phe Gly Pro Gly Ser
180 185 190

Gly Ile Gly Gly Asp Ala His Phe Asp Glu Asp Glu Phe Trp Thr Thr
195 200 205

His Ser Gly Gly Thr Asn Leu Phe Leu Thr Ala Val His Glu Ile Gly
210 215 220

His Ser Leu Gly Leu Gly His Ser Ser Asp Pro Lys Ala Val Met Phe
225 230 235 240

Pro Thr Tyr Lys Tyr Val Asp Ile Asn Thr Phe Arg Leu Ser Ala Asp
245 250 255

Asp Ile Arg Gly Ile Gln Ser Leu Tyr Gly Asp Pro Lys Glu Asn Gln
260 265 270

Arg Leu Pro Asn Pro Asp Asn Ser Glu Pro Ala Leu Cys Asp Pro Asn
275 280 285

Leu Ser Phe Asp Ala Val Thr Thr Val Gly Asn Lys Ile Phe Phe Phe
290 295 300

Lys Asp Arg Phe Phe Trp Leu Lys Val Ser Glu Arg Pro Lys Thr Ser
305 310 315 320

Val Asn Leu Ile Ser Ser Leu Trp Pro Thr Leu Pro Ser Gly Ile Glu

325 330 335

Ala Ala Tyr Glu Ile Glu Ala Arg Asn Gln Val Phe Leu Phe Lys Asp
340 345 350

Asp Lys Tyr Trp Leu Ile Ser Asn Leu Arg Pro Glu Pro Asn Tyr Pro
355 360 365

Lys Ser Ile His Ser Phe Gly Phe Pro Asn Phe Val Lys Lys Ile Asp
370 375 380

Ala Ala Val Phe Asn Pro Arg Phe Tyr Arg Thr Tyr Phe Phe Val Asp
385 390 395 400

Asn Gln Tyr Trp Arg Tyr Asp Glu Arg Arg Gln Met Met Asp Pro Gly
405 410 415

Tyr Pro Lys Leu Ile Thr Lys Asn Phe Gln Gly Ile Gly Pro Lys Ile
420 425 430

Asp Ala Val Phe Tyr Ser Lys Asn Lys Tyr Tyr Tyr Phe Phe Gln Gly
435 440 445

Ser Asn Gln Phe Glu Tyr Asp Phe Leu Leu Gln Arg Ile Thr Lys Thr
450 455 460

Leu Lys Ser Asn Ser Trp Phe Gly Cys
465 470

<210> 1218
<211> 598
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (144)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1218
Ala Thr Ser Arg Gln Pro Ser Tyr Xaa Arg Thr Trp Cys Arg Arg Cys
1 5 10 15

Cys Leu Pro Leu Ala Leu Asn Pro Val Pro Ala Ala Met Ala Pro Gly

```
            20                  25                  30

Gln Leu Ala Leu Phe Ser Val Ser Asp Lys Thr Gly Leu Val Glu Phe
        35                  40                  45

Ala Arg Asn Leu Thr Ala Leu Gly Leu Asn Leu Val Ala Ser Gly Gly
    50                  55                  60

Thr Ala Lys Ala Leu Arg Asp Ala Gly Leu Ala Val Arg Asp Val Ser
65                  70                  75                  80

Glu Leu Thr Gly Phe Pro Glu Met Leu Gly Gly Arg Val Lys Thr Leu
                85                  90                  95

His Pro Ala Val His Ala Gly Ile Leu Ala Arg Asn Ile Pro Glu Asp
            100                 105                 110

Asn Ala Asp Met Ala Arg Leu Asp Phe Asn Leu Ile Arg Val Val Ala
        115                 120                 125

Cys Asn Leu Tyr Pro Phe Val Lys Thr Val Ala Ser Pro Gly Val Xaa
    130                 135                 140

Val Glu Glu Ala Val Glu Gln Ile Asp Ile Gly Gly Val Thr Leu Leu
145                 150                 155                 160

Arg Ala Ala Ala Lys Asn His Ala Arg Val Thr Val Val Cys Glu Pro
                165                 170                 175

Glu Asp Tyr Val Val Val Ser Thr Glu Met Gln Ser Ser Glu Ser Lys
            180                 185                 190

Asp Thr Ser Leu Glu Thr Arg Arg Gln Leu Ala Leu Lys Ala Phe Thr
        195                 200                 205

His Thr Ala Gln Tyr Asp Glu Ala Ile Ser Asp Tyr Phe Arg Lys Gln
    210                 215                 220

Tyr Ser Lys Gly Val Ser Gln Met Pro Leu Arg Tyr Gly Met Asn Pro
225                 230                 235                 240

His Gln Thr Pro Ala Gln Leu Tyr Thr Leu Gln Pro Lys Leu Pro Ile
                245                 250                 255

Thr Val Leu Asn Gly Ala Pro Gly Phe Ile Asn Leu Cys Asp Ala Leu
            260                 265                 270

Asn Ala Trp Gln Leu Val Lys Glu Leu Lys Glu Ala Leu Gly Ile Pro
        275                 280                 285

Ala Ala Ala Ser Phe Lys His Val Ser Pro Ala Gly Ala Ala Val Gly
```

290 295 300

Ile Pro Leu Ser Glu Asp Glu Ala Lys Val Cys Met Val Tyr Asp Leu
305 310 315 320

Tyr Lys Thr Leu Thr Pro Ile Ser Ala Ala Tyr Ala Arg Ala Arg Gly
325 330 335

Ala Asp Arg Met Ser Ser Phe Gly Asp Phe Val Ala Leu Ser Asp Val
340 345 350

Cys Asp Val Pro Thr Ala Lys Ile Ile Ser Arg Glu Val Ser Asp Gly
355 360 365

Ile Ile Ala Pro Gly Tyr Glu Glu Glu Ala Leu Thr Ile Leu Ser Lys
370 375 380

Lys Lys Asn Gly Asn Tyr Cys Val Leu Gln Met Asp Gln Ser Tyr Lys
385 390 395 400

Pro Asp Glu Asn Glu Val Arg Thr Leu Phe Gly Leu His Leu Ser Gln
405 410 415

Lys Arg Asn Asn Gly Val Val Asp Lys Ser Leu Phe Ser Asn Val Val
420 425 430

Thr Lys Asn Lys Asp Leu Pro Glu Ser Ala Leu Arg Asp Leu Ile Val
435 440 445

Ala Thr Ile Ala Val Lys Tyr Thr Gln Ser Asn Ser Val Cys Tyr Ala
450 455 460

Lys Asn Gly Gln Val Ile Gly Ile Gly Ala Gly Gln Gln Ser Arg Ile
465 470 475 480

His Cys Thr Arg Leu Ala Gly Asp Lys Ala Asn Tyr Trp Trp Leu Arg
485 490 495

His His Pro Gln Val Leu Ser Met Lys Phe Lys Thr Gly Val Lys Arg
500 505 510

Ala Glu Ile Ser Asn Ala Ile Asp Gln Tyr Val Thr Gly Thr Ile Gly
515 520 525

Glu Asp Glu Asp Leu Ile Lys Trp Lys Ala Leu Phe Glu Glu Val Pro
530 535 540

Glu Leu Leu Thr Glu Ala Glu Lys Lys Glu Trp Val Glu Lys Leu Thr
545 550 555 560

Glu Val Ser Ile Ser Ser Asp Ala Phe Phe Pro Phe Arg Asp Asn Val

565 570 575

Asp Arg Ala Lys Arg Ser Gly Val Ala Tyr Ile Ala Ala Pro Pro Val
580 585 590

Leu Leu Leu Thr Lys Leu
595

<210> 1219
<211> 209
<212> PRT
<213> Homo sapiens

<400> 1219
Tyr Thr Ala Ile Met Ser Ile Met Ser Tyr Asn Gly Gly Ala Val Met
1 5 10 15

Ala Met Lys Gly Lys Asn Cys Val Ala Ile Ala Ala Asp Arg Arg Phe
20 25 30

Gly Ile Gln Ala Gln Met Val Thr Thr Asp Phe Gln Lys Ile Phe Pro
35 40 45

Met Gly Asp Arg Leu Tyr Ile Gly Leu Ala Gly Leu Ala Thr Asp Val
50 55 60

Gln Thr Val Ala Gln Arg Leu Lys Phe Arg Leu Asn Leu Tyr Glu Leu
65 70 75 80

Lys Glu Gly Arg Gln Ile Lys Pro Tyr Thr Leu Met Ser Met Val Ala
85 90 95

Asn Leu Leu Tyr Glu Lys Arg Phe Gly Pro Tyr Tyr Thr Glu Pro Val
100 105 110

Ile Ala Gly Leu Asp Pro Lys Thr Phe Lys Pro Phe Ile Cys Ser Leu
115 120 125

Asp Leu Ile Gly Cys Pro Met Val Thr Asp Asp Phe Val Val Ser Gly
130 135 140

Thr Cys Ala Glu Gln Met Tyr Gly Met Cys Glu Ser Leu Trp Glu Pro
145 150 155 160

Asn Met Asp Pro Asp His Leu Phe Glu Thr Ile Ser Gln Ala Met Leu
165 170 175

Asn Ala Val Asp Arg Asp Ala Val Ser Gly Met Gly Val Ile Val His
180 185 190

Ile Ile Glu Lys Asp Lys Ile Thr Thr Arg Thr Leu Lys Ala Arg Met
195 200 205

Asp

<210> 1220
<211> 140
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (51)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (64)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (77)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1220
Ile Ile Ser Ile Ile Ser Thr Ser Asn Lys Ile Lys Met Ser Glu Ala
1 5 10 15

Pro Arg Phe Phe Val Gly Pro Glu Asp Thr Glu Ile Asn Pro Gly Asn
20 25 30

Tyr Arg His Phe Phe His His Ala Asp Glu Asp Asp Glu Glu Glu Asp
35 40 45

Asp Ser Xaa Pro Glu Arg Gln Ile Val Val Gly Ile Cys Ser Met Xaa
50 55 60

Lys Lys Ser Lys Ser Lys Pro Met Lys Glu Ile Leu Xaa Arg Ile Ser
65 70 75 80

Leu Phe Lys Tyr Ile Thr Val Val Val Phe Glu Glu Glu Val Ile Leu
85 90 95

Asn Glu Pro Val Glu Asn Trp Pro Leu Cys Asp Cys Leu Ile Ser Phe
100 105 110

```
His Ser Lys Gly Phe Pro Leu Asp Lys Ala Val Ala Tyr Ala Lys Leu
        115                 120                 125

Arg Asn Pro Phe Val Ile Asn Asp Leu Asn Met Gln
    130                 135                 140



<210> 1221
<211> 45
<212> PRT
<213> Homo sapiens

<400> 1221
Gly Leu Met Glu Ile Glu Ile Thr Cys Lys Asp Ile Thr Val Phe Met
  1               5                  10                  15

Ser Tyr Ile Leu Val Leu Glu Ile Val Glu Cys Met Ile Asp Asn Ile
             20                  25                  30

Phe Leu Ile Phe Ile Phe Ser Ser Asn Thr Ser Thr Val
         35                  40                  45



<210> 1222
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1222
Val Ala Tyr Ile Cys Tyr Ser Lys Phe Cys Lys Tyr Ala Asn Gln Leu
  1               5                  10                  15

Tyr Arg Phe Ile Thr Ser Phe Leu Gly Phe Phe Trp Gly Arg Val Ile
             20                  25                  30

Ile Leu Leu Lys Ile Thr Met Asn Thr Leu Thr Val Arg Ile Cys Gly
         35                  40                  45

Lys Val Pro Leu Asn Ile Thr Lys Ile Ile Ser Leu Glu Gly Arg Asn
     50                  55                  60

Asn His Ser Asn Glu Leu
 65                  70



<210> 1223
<211> 88
<212> PRT
```

<213> Homo sapiens

<400> 1223
Phe Tyr Pro Ser Thr Tyr Leu Lys Ala Pro Ser Ser Leu Val Cys Gly
1 5 10 15

Val Leu Glu Pro Val Ser Ser Phe Trp Arg Phe Lys Leu Asn Ser Asn
20 25 30

Asn Tyr Val Thr Gln Ser Met Trp Arg Lys Ser Glu Thr Ser His Gly
35 40 45

Asp Ala Gly Pro Arg Ala Arg Pro Ala Val Trp Pro Ala Leu Leu Thr
50 55 60

Ser Val Ser Arg Ser Phe Pro Ser His Glu Val Pro Ser Gly His Gly
65 70 75 80

Asp Glu Gly Arg Glu Gly Thr Gly
85

<210> 1224
<211> 298
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (279)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1224
Ala Thr Arg Arg Arg Ala Ala Glu Ala Gly Met Ala Ala Val Leu Gln
1 5 10 15

Arg Val Glu Arg Leu Ser Asn Arg Val Val Arg Val Leu Gly Cys Asn
20 25 30

Pro Gly Pro Met Thr Leu Gln Gly Thr Asn Thr Tyr Leu Val Gly Thr
35 40 45

Gly Pro Arg Arg Ile Leu Ile Asp Thr Gly Glu Pro Ala Ile Pro Glu
50 55 60

Tyr Ile Ser Cys Leu Lys Gln Ala Leu Thr Glu Phe Asn Thr Ala Ile
65 70 75 80

Gln Glu Ile Val Val Thr His Trp His Arg Asp His Ser Gly Gly Ile
85 90 95

Gly Asp Ile Cys Lys Ser Ile Asn Asn Asp Thr Thr Tyr Cys Ile Lys
100 105 110

Lys Leu Pro Arg Asn Pro Gln Arg Glu Glu Ile Ile Gly Asn Gly Glu
115 120 125

Gln Gln Tyr Val Tyr Leu Lys Asp Gly Asp Val Ile Lys Thr Glu Gly
130 135 140

Ala Thr Leu Arg Val Leu Tyr Thr Pro Gly His Thr Asp Asp His Met
145 150 155 160

Ala Leu Leu Leu Glu Glu Glu Asn Ala Ile Phe Ser Gly Asp Cys Ile
165 170 175

Leu Gly Glu Gly Thr Thr Val Phe Glu Asp Leu Tyr Asp Tyr Met Asn
180 185 190

Ser Leu Lys Glu Leu Leu Lys Ile Lys Ala Asp Ile Ile Tyr Pro Gly
195 200 205

His Gly Pro Val Ile His Asn Ala Glu Ala Lys Ile Gln Gln Tyr Ile
210 215 220

Ser His Arg Asn Ile Arg Glu Gln Gln Ile Leu Thr Leu Phe Arg Glu
225 230 235 240

Asn Phe Glu Lys Ser Phe Thr Val Met Glu Leu Val Lys Ile Ile Tyr
245 250 255

Lys Asn Thr Pro Glu Asn Leu His Glu Met Ala Lys His Asn Leu Leu
260 265 270

Leu His Leu Lys Lys Leu Xaa Lys Glu Gly Lys Ile Phe Ser Asn Thr
275 280 285

Asp Pro Asp Lys Lys Trp Lys Ala His Leu
290 295

<210> 1225
<211> 27
<212> PRT
<213> Homo sapiens

<400> 1225
Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln Asp Gly Pro
1 5 10 15

Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Lys Val
20 25

<210> 1226
<211> 380
<212> PRT
<213> Homo sapiens

<400> 1226
Glu Gln Glu Leu Asp Thr Leu Lys Arg Lys Ser Pro Ser Asp Leu Trp
1 5 10 15

Lys Glu Asp Leu Ala Thr Phe Ile Glu Glu Leu Glu Ala Val Glu Ala
20 25 30

Lys Glu Lys Gln Asp Glu Gln Val Gly Leu Pro Gly Lys Val Gly Lys
35 40 45

Ala Lys Gly Lys Lys Thr Gln Met Ala Glu Val Leu Pro Ser Pro Arg
50 55 60

Gly Gln Arg Val Ile Pro Arg Ile Thr Ile Glu Met Lys Ala Glu Ala
65 70 75 80

Glu Lys Lys Asn Lys Lys Lys Ile Lys Asn Glu Asn Thr Glu Gly Ser
85 90 95

Pro Gln Glu Asp Gly Val Glu Leu Glu Gly Leu Lys Gln Arg Leu Glu
100 105 110

Lys Lys Gln Lys Arg Glu Pro Gly Thr Lys Thr Lys Lys Gln Thr Thr
115 120 125

Leu Ala Phe Lys Pro Ile Lys Lys Gly Lys Lys Arg Asn Pro Trp Ser
130 135 140

Asp Ser Glu Ser Asp Arg Ser Ser Asp Glu Ser Asn Phe Asp Val Pro
145 150 155 160

Pro Arg Glu Thr Glu Pro Arg Arg Ala Ala Thr Lys Thr Lys Phe Thr
165 170 175

Met Asp Leu Asp Ser Asp Glu Asp Phe Ser Asp Phe Asp Glu Lys Thr
180 185 190

Asp Asp Glu Asp Phe Val Pro Ser Asp Ala Ser Pro Pro Lys Thr Lys
195 200 205

Thr Ser Pro Lys Leu Ser Asn Lys Glu Leu Lys Pro Gln Lys Ser Val

210 215 220

Val Ser Asp Leu Glu Ala Asp Asp Val Lys Gly Ser Val Pro Leu Ser
225 230 235 240

Ser Ser Pro Pro Ala Thr His Phe Pro Asp Glu Thr Glu Ile Thr Asn
245 250 255

Pro Val Pro Lys Lys Asn Val Thr Val Lys Lys Thr Ala Ala Lys Ser
260 265 270

Gln Ser Ser Thr Ser Thr Thr Gly Ala Lys Lys Arg Ala Ala Pro Lys
275 280 285

Gly Thr Lys Arg Asp Pro Ala Leu Asn Ser Gly Val Ser Gln Lys Pro
290 295 300

Asp Pro Ala Lys Thr Lys Asn Arg Arg Lys Arg Lys Pro Ser Thr Ser
305 310 315 320

Asp Asp Ser Asp Ser Asn Phe Glu Lys Ile Val Ser Lys Ala Val Thr
325 330 335

Ser Lys Lys Ser Lys Gly Glu Ser Asp Asp Phe His Met Asp Phe Asp
340 345 350

Ser Ala Val Ala Pro Arg Ala Lys Ser Val Arg Ala Lys Lys Pro Ile
355 360 365

Lys Tyr Leu Glu Glu Ser Asp Glu Asp Asp Leu Phe
370 375 380

<210> 1227
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1227
Phe Asn Ser Leu Lys Cys Leu Phe Gly Ile Met Ile Gly Asn Leu Asp
1 5 10 15

Glu Phe Arg Gly Lys Lys Leu Ser Ala Xaa Met Leu Arg Ala His Leu
20 25 30

Ser Pro His Thr Pro Thr Glu Leu Thr Gly Leu Gln Cys Phe Ile Arg
35 40 45

Lys Phe Pro Ile Pro Leu Ser Cys Val Phe Met Leu Lys Ile Leu Leu
50 55 60

His Phe Ser Phe Glu Cys Gln Phe Leu Thr Ser Thr Ile Ser
65 70 75

<210> 1228
<211> 222
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (142)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1228
Ala Asn Glu Lys Val Ala Leu Gln Lys Ala Leu Leu Tyr Tyr Glu Ser
1 5 10 15

Ile His Gly Arg Pro Val Thr Lys Asn Glu Arg Gln Val Met Lys Pro
20 25 30

Leu Tyr Asp Arg Tyr Arg Leu Val Lys Gln Ile Leu Ser Arg Ala Asn
35 40 45

Thr Ile Pro Ile Ile Gly Ser Pro Ser Ser Lys Arg Arg Ser Pro Leu
50 55 60

Leu Gln Pro Ile Ile Glu Gly Glu Thr Ala Ser Phe Phe Lys Glu Ile
65 70 75 80

Lys Glu Glu Glu Glu Gly Ser Glu Asp Asp Ser Asn Val Lys Pro Asp
85 90 95

Phe Met Val Thr Leu Lys Thr Asp Phe Ser Ala Arg Cys Phe Leu Asp
100 105 110

Gln Phe Glu Asp Asp Ala Asp Gly Phe Ile Ser Pro Met Asp Asp Lys
115 120 125

Ile Pro Ser Lys Cys Ser Gln Asp Thr Gly Leu Ser Asn Xaa His Ala
130 135 140

Ala Ser Ile Pro Glu Leu Leu Glu His Leu Gln Glu Met Arg Glu Glu
145 150 155 160

Lys Lys Arg Ile Arg Lys Lys Leu Arg Asp Phe Glu Asp Asn Phe Phe
165 170 175

Arg Gln Asn Gly Arg Asn Val Gln Lys Glu Asp Arg Thr Pro Met Ala
180 185 190

Glu Glu Tyr Ser Glu Tyr Lys His Ile Lys Ala Lys Leu Arg Leu Leu
195 200 205

Glu Val Leu Ile Ser Lys Arg Asp Thr Asp Ser Lys Ser Met
210 215 220

<210> 1229
<211> 220
<212> PRT
<213> Homo sapiens

<400> 1229
Lys Gly Ser Thr Leu Gly His Leu Cys Thr Ala Met Ala Gly Met Met
1 5 10 15

Lys Gly Ile Arg Trp Ser Cys Pro Ala Ile Ala Ser Ile Ser Gln Thr
20 25 30

Arg Ser Ser Gln Glu Lys Asp Ser Ser Ser Pro Pro Trp Asp Leu Arg
35 40 45

Arg Ala Ala Thr Glu Gly Glu Ala Pro Asp Ala Leu Cys Gln Ser Gln
50 55 60

Val Arg Gly Gln Ser Ser Pro Cys His Pro Trp Cys Arg Pro Ala Pro
65 70 75 80

Ser Ser Phe Met Pro Gly Pro Ala Gly Thr Pro Ala Thr Thr Glu Ser
85 90 95

Thr Arg Ser Ala Leu Cys Ser Trp Arg Arg His Ser Arg Val Glu Ser
100 105 110

Cys Pro Ser Leu Ser Leu Gly His Leu Gly Gly Glu Ser Gly Leu Arg
115 120 125

Ser Glu Leu Asp Pro Gly Asp Leu Gly Ser Phe Phe Leu Ala His Gln
130 135 140

Pro Cys Arg Pro His Leu Ser Gln Asn Pro Leu Cys Leu Gly Gly Ser
145 150 155 160

Gly Ser Ala Leu Leu Cys Ser Arg Arg Leu Gly Ser Gly Gln His Gln
165 170 175

Val Gly Lys Trp Ser Pro Pro Ser Cys Phe Cys Arg Ile Leu Thr Val
180 185 190

Gly Leu Glu Glu Lys Ser Ile Asp Leu Ile Ser Pro Thr Thr His Pro
195 200 205

Ser Phe Ser Phe Phe His His Ser Pro Pro Gln Leu
210 215 220

<210> 1230
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (12)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (30)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1230
Glu Leu Lys Arg Leu Thr Ile Gly Lys Asn Xaa Xaa Arg Leu Thr Gly
1 5 10 15

Asn Arg Xaa Gly Ile Pro Gly Ser Thr His Ala Ser Glu Xaa Glu Val
20 25 30

Glu Glu Glu Gly Asp Val Asp Ser Asp Glu Glu Glu Glu Glu Asp Glu
35 40 45

Glu Ser Ser Ser Glu Gly Leu Glu Ala Glu Asp Trp Ala Gln Gly Val
50 55 60

Val Glu Ala Gly Gly Ser Phe Gly Ala Tyr Gly Ala Gln Glu Glu Ala
65 70 75 80

Gln Cys Pro Thr Leu His Phe Leu Glu Gly Gly Glu Asp Ser Asp Ser
85 90 95

Asp Ser Glu Glu Glu Asp Asp Glu Glu Glu Asp Asp Glu Asp Glu Asp
100 105 110

Asp Asp Asp Asp Glu Glu Asp Gly Asp Glu Val Pro Val Pro Ser Phe
115 120 125

Gly Glu Ala Met Ala Tyr Phe Ala Met Val Lys Arg Tyr Leu Thr Ser
130 135 140

Phe Pro Ile Asp Asp Arg Val Gln Ser His Ile Leu His Leu Glu His
145 150 155 160

Asp Leu Val His Val Thr Arg Lys Asn His Ala Arg Gln Ala Gly Val
165 170 175

Arg Gly Leu Gly His Gln Ser
180

<210> 1231
<211> 59
<212> PRT
<213> Homo sapiens

<400> 1231
Asn Leu Tyr Lys Leu Lys Leu Asn His Glu Leu Gln Lys Lys Ser Ile
1 5 10 15

Leu Pro Lys Leu Asp Val Thr Thr Leu Thr Ser Leu Lys Tyr Glu Val
20 25 30

Asp Cys Leu Lys Asp Ser Ala Tyr Ile Leu Val Cys Thr Phe Arg Asn
35 40 45

Ile Phe Leu Gly Lys Ser Thr Gln His Phe Leu
50 55

<210> 1232
<211> 135
<212> PRT
<213> Homo sapiens

<400> 1232
Gly Ser Thr His Ala Ser Gly Pro Pro Gln Ala Pro Gln Leu Ile Tyr
1 5 10 15

Gln Glu Tyr Val Asn Gln Pro Asp Val Arg Pro Gln Pro Pro Ser Pro
20 25 30

Arg Glu Gly Pro Leu Pro Ala Ala Arg Pro Ala Gly Ala Thr Leu Glu
35 40 45

Arg Ala Lys Thr Leu Ser Pro Gly Lys Asn Gly Val Val Lys Asp Val
50 55 60

Phe Ala Phe Gly Gly Ala Val Glu Asn Pro Glu Tyr Leu Thr Pro Gln
65 70 75 80

Gly Gly Ala Ala Pro Gln Pro His Pro Pro Pro Ala Phe Ser Pro Ala
85 90 95

Phe Asp Asn Leu Tyr Tyr Trp Asp Gln Asp Pro Pro Glu Arg Gly Ala
100 105 110

Pro Pro Ser Thr Phe Lys Gly Thr Pro Thr Ala Glu Asn Pro Glu Tyr
115 120 125

Leu Gly Leu Asp Val Pro Val
130 135

<210> 1233
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1233
Arg Gly Glu Thr Arg Glu Met Ala Gly Asn Leu Leu Ser Gly Ala Gly
1 5 10 15

Arg Arg Leu Trp Asp Trp Val Pro Leu Ala Cys Arg Ser Phe Ser Leu
20 25 30

Gly Val Pro Arg Leu Ile Gly Ile Arg Leu Thr Leu Pro Pro Pro Lys
35 40 45

Val Val Asp Arg Trp Asn Glu Lys Arg Ala Met Phe Gly Val Tyr Asp
50 55 60

Asn Ile Gly Ile Leu Gly Asn Phe Glu Lys His Pro Lys Glu Leu Ile
65 70 75 80

Arg Gly Pro Ile Trp Leu Arg Gly Trp Lys Gly Asn Glu Leu Gln Arg
85 90 95

Cys Ile Arg Lys Arg Lys Met Val Gly Ser Arg Met Phe Ala Asp Asp
100 105 110

Leu His Asn Leu Asn Lys Arg Ile Arg Tyr Leu Tyr Lys His Phe Asn
115 120 125

Arg His Gly Lys Phe Arg
130

<210> 1234
<211> 282
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (18)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1234
Thr Gly Pro Glu Phe Pro Gly Xaa Pro Thr Arg Pro Arg Thr Ala Ala
1 5 10 15

Ala Xaa Ser Ala Arg Thr Arg Thr Arg Gly Ser Pro Arg Met Gly Glu
20 25 30

Phe Asn Glu Lys Lys Thr Thr Cys Gly Thr Val Cys Leu Lys Tyr Leu
35 40 45

Leu Phe Thr Tyr Asn Cys Cys Phe Trp Leu Ala Gly Leu Ala Val Met
50 55 60

Ala Val Gly Ile Trp Thr Leu Ala Leu Lys Ser Asp Tyr Ile Ser Leu
65 70 75 80

Leu Ala Ser Gly Thr Tyr Leu Ala Thr Ala Tyr Ile Leu Val Val Ala
85 90 95

Gly Thr Val Val Met Val Thr Gly Val Leu Gly Cys Cys Ala Thr Phe
100 105 110

Lys Glu Arg Arg Asn Leu Leu Arg Leu Tyr Phe Ile Leu Leu Leu Ile
115 120 125

Ile Phe Leu Leu Glu Ile Ile Ala Gly Ile Leu Ala Tyr Ala Tyr Tyr
130 135 140

Gln Gln Leu Asn Thr Glu Leu Lys Glu Asn Leu Lys Asp Thr Met Thr
145 150 155 160

Lys Arg Tyr His Gln Pro Gly His Glu Ala Val Thr Ser Ala Val Asp
165 170 175

Gln Leu Gln Gln Glu Phe His Cys Cys Gly Ser Asn Asn Ser Gln Asp
180 185 190

Trp Arg Asp Ser Glu Trp Ile Arg Ser Gln Glu Ala Gly Gly Arg Val
195 200 205

Val Pro Asp Ser Cys Cys Lys Thr Val Val Ala Leu Cys Gly Gln Arg
210 215 220

Asp His Ala Ser Asn Ile Tyr Lys Val Glu Gly Gly Cys Ile Thr Lys
225 230 235 240

Leu Glu Thr Phe Ile Gln Glu His Leu Arg Val Ile Gly Ala Val Gly
245 250 255

Ile Gly Ile Ala Cys Val Gln Val Phe Gly Met Ile Phe Thr Cys Cys
260 265 270

Leu Tyr Arg Ser Leu Lys Leu Glu His Tyr
275 280

<210> 1235
<211> 66
<212> PRT
<213> Homo sapiens

<400> 1235
Ala Glu Ile Gln Val Phe Gln Val Gly Leu Val Ser Trp Gly Leu Tyr
1 5 10 15

Asn Pro Cys Leu Gly Ser Ala Asp Lys Asn Ser Arg Lys Arg Ala Pro
20 25 30

Arg Ser Lys Val Pro Pro Pro Arg Asp Phe His Ile Asn Leu Phe Arg
35 40 45

```
Met Gln Pro Trp Leu Arg Gln His Leu Gly Asp Val Leu Asn Phe Leu
     50                  55                  60

Pro Leu
 65



<210> 1236
<211> 108
<212> PRT
<213> Homo sapiens

<400> 1236
Ala Arg Arg Arg Arg Gly Gly Trp Ala Gly Gly Gly Gly Gly Thr Arg
  1               5                  10                  15

Arg Ala Leu Gly Val Pro Val Ala Arg Arg Arg Arg Met Trp Arg Ala
             20                  25                  30

Glu Gly Lys Trp Leu Pro Lys Thr Ser Arg Lys Ser Val Ser Gln Ser
         35                  40                  45

Val Phe Cys Gly Thr Ser Thr Tyr Cys Val Leu Asn Thr Val Pro Pro
     50                  55                  60

Ile Glu Asp Asp His Gly Asn Ser Asn Ser Ser His Val Lys Ile Phe
 65                  70                  75                  80

Leu Pro Lys Lys Leu Leu Glu Cys Leu Pro Lys Cys Ser Ser Leu Pro
                 85                  90                  95

Lys Glu Arg His Arg Trp Asn Thr Asn Glu Arg Ser
            100                 105



<210> 1237
<211> 116
<212> PRT
<213> Homo sapiens

<400> 1237
Arg Gly Gly Gly Ser Lys Gly Asn Glu Val Arg Pro Val Ala Gly Ser
  1               5                  10                  15

Ala Glu Ser Ala Ala Leu Arg Leu Arg Ala Pro Leu Gln Gln Val Gln
             20                  25                  30

Ala Gln Leu Ser Pro Leu Gln Asn Ile Ser Pro Trp Ile Leu Ala Val
         35                  40                  45
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Leu Thr Leu Gln Ile Gln Ser Leu Ile Ser Cys Trp Ala Phe Trp Thr
     50                  55                  60

Thr Trp Thr Gln Ser Cys Ser Ser Asn Ala Leu Pro Gln Ser Leu Pro
 65                  70                  75                  80

Ala Trp Arg Ser Ser Gln Arg Ser Thr Gln Lys Asp Pro Val Pro Tyr
                 85                  90                  95

Gln Pro Pro Phe Leu Cys Gln Trp Gly Arg His Gln Pro Ser Trp Lys
            100                 105                 110

Pro Leu Met Asn
        115



<210> 1238
<211> 311
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1238
Val Thr Ser Glu Gly Val Arg Val Arg Ser Ser Arg Gly Arg Ala Xaa
  1               5                  10                  15

Gly Val Trp Arg Phe Glu Arg Asp Glu Asp Gly Thr Gly Ala Gly Cys
             20                  25                  30

Gly Gln Trp Thr Arg Phe Cys Arg Glu Pro Lys Met Ala Val Asn Val
         35                  40                  45

Tyr Ser Thr Ser Val Thr Ser Asp Asn Leu Ser Arg His Asp Met Leu
     50                  55                  60

Ala Trp Ile Asn Glu Ser Leu Gln Leu Asn Leu Thr Lys Ile Glu Gln
 65                  70                  75                  80

Leu Cys Ser Gly Ala Ala Tyr Cys Gln Phe Met Asp Met Leu Phe Pro
                 85                  90                  95

Gly Ser Ile Ala Leu Lys Lys Val Lys Phe Gln Ala Lys Leu Glu His
            100                 105                 110

Glu Tyr Ile Gln Asn Phe Lys Ile Leu Gln Ala Gly Phe Lys Arg Met
```

```
        115                 120                 125

Gly Val Asp Lys Ile Ile Pro Val Asp Lys Leu Val Lys Gly Lys Phe
    130                 135                 140

Gln Asp Asn Phe Glu Phe Val Gln Trp Phe Lys Lys Phe Phe Asp Ala
145                 150                 155                 160

Asn Tyr Asp Gly Lys Asp Tyr Asp Pro Val Ala Ala Arg Gln Gly Gln
                165                 170                 175

Glu Thr Ala Val Ala Pro Ser Leu Val Ala Pro Ala Leu Asn Lys Pro
            180                 185                 190

Lys Lys Pro Leu Thr Ser Ser Ser Ala Ala Pro Gln Arg Pro Ile Ser
        195                 200                 205

Thr Gln Arg Thr Ala Ala Ala Pro Lys Ala Gly Pro Gly Val Val Arg
    210                 215                 220

Lys Asn Pro Gly Val Gly Asn Gly Asp Asp Glu Ala Ala Glu Leu Met
225                 230                 235                 240

Gln Gln Val Asn Val Leu Lys Leu Thr Val Glu Asp Leu Glu Lys Glu
                245                 250                 255

Arg Asp Phe Tyr Phe Gly Lys Leu Arg Asn Ile Glu Leu Ile Cys Gln
            260                 265                 270

Glu Asn Glu Gly Glu Asn Asp Pro Val Leu Gln Arg Ile Val Asp Ile
        275                 280                 285

Leu Tyr Ala Thr Asp Glu Gly Phe Val Ile Pro Asp Glu Gly Gly Pro
    290                 295                 300

Gln Glu Glu Gln Glu Glu Tyr
305                 310
```

<210> 1239
<211> 345
<212> PRT
<213> Homo sapiens

<400> 1239

```
Ala Ala Arg Leu Ala Val Glu Met Lys Thr Asp Leu Leu Ile Val Leu
  1               5                  10                  15

Ser Asp Val Glu Gly Leu Phe Asp Ser Pro Pro Gly Ser Asp Asp Ala
             20                  25                  30
```

Lys Leu Ile Asp Ile Phe Tyr Pro Gly Asp Gln Gln Ser Val Thr Phe
35 40 45

Gly Thr Lys Ser Arg Val Gly Met Gly Gly Met Glu Ala Lys Val Lys
50 55 60

Ala Ala Leu Trp Ala Leu Gln Gly Gly Thr Ser Val Val Ile Ala Asn
65 70 75 80

Gly Thr His Pro Lys Val Ser Gly His Val Ile Thr Asp Ile Val Glu
85 90 95

Gly Lys Lys Val Gly Thr Phe Phe Ser Glu Val Lys Pro Ala Gly Pro
100 105 110

Thr Val Glu Gln Gln Gly Glu Met Ala Arg Ser Gly Gly Arg Met Leu
115 120 125

Ala Thr Leu Glu Pro Glu Gln Arg Ala Glu Ile Ile His His Leu Ala
130 135 140

Asp Leu Leu Thr Asp Gln Arg Asp Glu Ile Leu Leu Ala Asn Lys Lys
145 150 155 160

Asp Leu Glu Glu Ala Glu Gly Arg Leu Ala Ala Pro Leu Leu Lys Arg
165 170 175

Leu Ser Leu Ser Thr Ser Lys Leu Asn Ser Leu Ala Ile Gly Leu Arg
180 185 190

Gln Ile Ala Ala Ser Ser Gln Asp Ser Val Gly Arg Val Leu Arg Arg
195 200 205

Thr Arg Ile Ala Lys Asn Leu Glu Leu Glu Gln Val Thr Val Pro Ile
210 215 220

Gly Val Leu Leu Val Ile Phe Glu Ser Arg Pro Asp Cys Leu Pro Gln
225 230 235 240

Val Ala Ala Leu Ala Ile Ala Ser Gly Asn Gly Leu Leu Leu Lys Gly
245 250 255

Gly Lys Glu Ala Ala His Ser Asn Arg Ile Leu His Leu Leu Thr Gln
260 265 270

Glu Ala Leu Ser Ile His Gly Val Lys Glu Ala Val Gln Leu Val Asn
275 280 285

Thr Arg Glu Glu Val Glu Asp Leu Cys Arg Leu Asp Lys Met Ile Asp
290 295 300

Leu Ile Ile Pro Arg Gly Ser Ser Gln Leu Val Arg Asp Ile Gln Lys
305 310 315 320

Ala Ala Lys Gly Ile Pro Val Met Gly His Ser Glu Gly Ile Cys Ala
325 330 335

His Val Cys Gly Phe Arg Gly Gln Cys
340 345

<210> 1240
<211> 87
<212> PRT
<213> Homo sapiens

<400> 1240
Gly Tyr Cys Phe Ile Ser Thr Ser Arg Thr Pro Lys Glu Thr Ile Trp
1 5 10 15

Val Lys Ala Thr Ser Thr Ala Leu Ala Leu His Arg Phe Leu Glu Phe
20 25 30

Leu Ser Phe Thr Phe Ser Leu Thr Gln His Cys Leu Leu Phe Val Phe
35 40 45

Val Ala Trp Phe Val Phe Phe Leu Pro Cys Ser Pro Asn Leu Cys Pro
50 55 60

Asn Ser Phe Gly Leu Met Gln Lys Tyr Leu Cys Gly Arg Glu Glu Leu
65 70 75 80

Phe Ser Trp Arg Ala Phe Arg
85

<210> 1241
<211> 196
<212> PRT
<213> Homo sapiens

<400> 1241
Arg Ala Gly Ser Pro Ala Ser Pro Ala His Val Ala Trp Pro Pro Ala
1 5 10 15

Pro Thr Trp Ser Arg Ala Leu Pro Arg Val Ala Pro Arg Ser Ser Ser
20 25 30

Arg Arg Gly Arg Arg Tyr Pro Glu Arg Ser Gln Arg Arg Arg Glu Val

35 40 45

Ala Ala Thr Ala Met Pro Lys Asn Lys Gly Lys Gly Gly Lys Asn Arg
50 55 60

Arg Arg Gly Lys Asn Glu Asn Glu Ser Glu Lys Arg Glu Leu Val Phe
65 70 75 80

Lys Glu Asp Gly Gln Glu Tyr Ala Gln Val Ile Lys Met Leu Gly Asn
85 90 95

Gly Arg Leu Glu Ala Met Cys Phe Asp Gly Val Lys Arg Leu Cys His
100 105 110

Ile Arg Gly Lys Leu Arg Lys Lys Val Trp Ile Asn Thr Ser Asp Ile
115 120 125

Ile Leu Val Gly Leu Arg Asp Tyr Gln Asp Asn Lys Ala Asp Val Ile
130 135 140

Leu Lys Tyr Asn Ala Asp Glu Ala Arg Ser Leu Lys Ala Tyr Gly Glu
145 150 155 160

Leu Pro Glu His Ala Lys Ile Asn Glu Thr Asp Thr Phe Gly Pro Gly
165 170 175

Asp Asp Asp Glu Ile Gln Phe Asp Asp Ile Gly Asp Asp Asp Glu Asp
180 185 190

Ile Asp Asp Ile
195

<210> 1242
<211> 218
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1242
Ala Val Xaa Phe Lys Asp Xaa Ile Tyr Glu Ile Phe Gln Lys Leu Asn

1 5 10 15

Thr Ser Ile Gln Val Val Leu Leu Ser Ala Thr Met Pro Thr Asp Val
20 25 30

Leu Glu Val Thr Lys Lys Phe Met Arg Asp Pro Ile Arg Ile Leu Val
35 40 45

Lys Lys Glu Glu Leu Thr Leu Glu Gly Ile Lys Gln Phe Tyr Ile Asn
50 55 60

Val Glu Arg Glu Glu Trp Lys Leu Asp Thr Leu Cys Asp Leu Tyr Glu
65 70 75 80

Thr Leu Thr Ile Thr Gln Ala Val Ile Phe Leu Asn Thr Arg Arg Lys
85 90 95

Val Asp Trp Leu Thr Glu Lys Met His Ala Arg Asp Phe Thr Val Ser
100 105 110

Ala Leu His Gly Asp Met Asp Gln Lys Glu Arg Asp Val Ile Met Arg
115 120 125

Glu Phe Arg Ser Gly Ser Ser Arg Val Leu Ile Thr Thr Asp Leu Leu
130 135 140

Ala Arg Gly Ile Asp Val Gln Gln Val Ser Leu Val Ile Asn Tyr Asp
145 150 155 160

Leu Pro Thr Asn Arg Glu Asn Tyr Ile His Arg Ile Gly Arg Gly Gly
165 170 175

Arg Phe Gly Arg Lys Gly Val Ala Ile Asn Phe Val Thr Glu Glu Asp
180 185 190

Lys Arg Ile Leu Arg Asp Ile Glu Thr Phe Tyr Asn Thr Thr Val Glu
195 200 205

Glu Met Pro Met Asn Val Ala Asp Leu Ile
210 215

<210> 1243
<211> 173
<212> PRT
<213> Homo sapiens

<400> 1243
Leu Asp Gly Ser Ala Arg Ala Glu Leu Ala Leu Ser Val Ala Val Asn
1 5 10 15

Val Ala Pro Gly Arg Leu Cys Ala Gly Arg Tyr Ser Ser Asp Val Gln
20 25 30

Glu Met Ile Leu Ser Ser Ala Thr Ala Asp Arg Ile Pro Ile Ala Val
35 40 45

Ser Gly Val Arg Gly Met Gly Phe Leu Met Arg His His Ile Glu Thr
50 55 60

Gly Gly Gly Gln Leu Pro Ala Lys Leu Ser Ser Leu Phe Val Lys Cys
65 70 75 80

Leu Gln Asn Pro Ser Ser Asp Ile Arg Leu Val Ala Glu Lys Met Ile
85 90 95

Trp Trp Ala Asn Lys Asp Pro Leu Pro Pro Leu Asp Pro Gln Ala Ile
100 105 110

Lys Pro Ile Leu Lys Ala Leu Leu Asp Asn Thr Lys Asp Lys Asn Thr
115 120 125

Val Val Arg Ala Tyr Ser Asp Gln Ala Ile Val Asn Leu Leu Lys Met
130 135 140

Arg Gln Gly Glu Glu Val Phe Gln Ser Leu Ser Lys Ile Leu Asp Val
145 150 155 160

Ala Ser Leu Glu Val Leu Asn Glu Val Asn Arg Ser Pro
165 170

<210> 1244
<211> 222
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1244
Tyr Ile Lys Ile Tyr Gln Gly Glu Glu Leu Pro His Pro Lys Ser Met
1 5 10 15

Xaa Gln Ala Thr Ala Glu Ala Asn Asn Leu Ala Ala Val Ala Thr Ala
20 25 30

Lys Asp Thr Tyr Asn Lys Lys Met Glu Glu Ile Cys Gly Gly Asp Lys
35 40 45

Pro Phe Leu Ala Pro Asn Asp Leu Gln Thr Lys His Leu Gln Leu Lys
50 55 60

Glu Glu Ser Val Lys Leu Phe Xaa Gly Val Lys Lys Met Gly Gly Glu
65 70 75 80

Glu Phe Ser Arg Arg Tyr Leu Gln Gln Leu Glu Ser Glu Ile Asp Glu
85 90 95

Leu Tyr Ile Gln Tyr Ile Lys His Asn Asp Ser Lys Asn Ile Phe His
100 105 110

Ala Ala Arg Thr Pro Ala Thr Leu Phe Val Val Ile Phe Ile Thr Tyr
115 120 125

Val Ile Ala Gly Val Thr Gly Phe Ile Gly Leu Asp Ile Ile Ala Ser
130 135 140

Leu Cys Asn Met Ile Met Gly Leu Thr Leu Ile Thr Leu Cys Thr Trp
145 150 155 160

Ala Tyr Ile Arg Tyr Ser Gly Glu Tyr Arg Glu Leu Gly Ala Val Ile
165 170 175

Asp Gln Val Ala Ala Ala Leu Trp Asp Gln Ala Leu Tyr Lys Leu Tyr
180 185 190

Ser Ala Ala Ala Thr His Arg His Leu Tyr His Gln Ala Phe Pro Thr
195 200 205

Pro Lys Ser Glu Ser Thr Glu Gln Ser Glu Lys Lys Lys Met
210 215 220

<210> 1245
<211> 278
<212> PRT
<213> Homo sapiens

<400> 1245
Ser Ala Glu Asp Val Glu Phe Gln Lys Glu Val Ala Gln Val Arg Lys
1 5 10 15

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Arg Ile Thr Gln Arg Lys Lys Gln Glu Gln Leu Thr Pro Gly Val Val
            20                  25                  30

Tyr Val Arg His Leu Pro Asn Leu Leu Asp Glu Thr Gln Ile Phe Ser
        35                  40                  45

Tyr Phe Ser Gln Phe Gly Thr Val Thr Arg Phe Arg Leu Ser Arg Ser
    50                  55                  60

Lys Arg Thr Gly Asn Ser Lys Gly Tyr Ala Phe Val Glu Phe Glu Ser
65                  70                  75                  80

Glu Asp Val Ala Lys Ile Val Ala Glu Thr Met Asn Asn Tyr Leu Phe
                85                  90                  95

Gly Glu Arg Leu Leu Glu Cys His Phe Met Pro Pro Glu Lys Val His
            100                 105                 110

Lys Glu Leu Phe Lys Asp Trp Asn Ile Pro Phe Lys Gln Pro Ser Tyr
        115                 120                 125

Pro Ser Val Lys Arg Tyr Asn Arg Asn Arg Thr Leu Thr Gln Lys Leu
    130                 135                 140

Arg Met Glu Glu Arg Phe Lys Lys Lys Glu Arg Leu Leu Arg Lys Lys
145                 150                 155                 160

Leu Ala Lys Lys Gly Ile Asp Tyr Asp Phe Pro Ser Leu Ile Leu Gln
                165                 170                 175

Lys Thr Glu Ser Ile Ser Lys Thr Asn Arg Gln Thr Ser Thr Lys Gly
            180                 185                 190

Gln Val Leu Arg Lys Lys Lys Lys Lys Val Ser Gly Thr Leu Asp Thr
        195                 200                 205

Pro Glu Lys Thr Val Asp Ser Gln Gly Pro Thr Pro Val Cys Thr Pro
    210                 215                 220

Thr Phe Leu Glu Arg Arg Lys Ser Gln Val Ala Glu Leu Asn Asp Asp
225                 230                 235                 240

Asp Lys Asp Asp Glu Ile Val Phe Lys Gln Pro Ile Ser Cys Val Lys
                245                 250                 255

Glu Glu Ile Gln Glu Thr Gln Thr Pro Thr His Ser Arg Lys Lys Arg
            260                 265                 270

Arg Arg Ser Ser Asn Gln
        275
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<210> 1246
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (100)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1246
Ser Pro Pro Pro Leu Ser Leu Ile Leu Leu Ser Pro Ile Lys Ala Lys
1 5 10 15

Tyr Gly Leu Thr Thr Ser Pro Lys Ser Val Leu Arg Pro Ser Leu Cys
20 25 30

Leu Cys Ala Leu Leu Gly Val Ser Gln Arg Ser Gly Gln Asp Cys Ala
35 40 45

Gly Pro Ala Ser Pro Cys Ala Ser Gln Glu His Arg Gln Gly Val Leu
50 55 60

Val Ala Val Ala Gly His Leu Ser Pro Ser Ser Leu Leu Asn Val Leu
65 70 75 80

Thr Ala Arg Gly Asn Gly Val Ser Phe Pro Thr Lys Lys Pro Leu Leu
85 90 95

Tyr Ile Phe Xaa Leu Gln Ser His Arg Leu Gln Thr Thr Leu Leu Phe
100 105 110

Phe Met Asp Phe Ser Ala His Phe Arg
115 120

<210> 1247
<211> 36
<212> PRT
<213> Homo sapiens

<400> 1247
Ile Phe His Arg Val Leu Leu Cys Asp Leu Asn Phe Ser Leu Gly Pro
1 5 10 15

Ala Ser Asp Ile Val Gly Gly Leu Ser Trp Phe Gln Glu Ile Arg Leu
20 25 30

Ala Phe Ser Ser
35

<210> 1248
<211> 184
<212> PRT
<213> Homo sapiens

<400> 1248
Trp Ile Pro Arg Ala Cys Arg Glu Phe Gly Thr Arg Phe Gly Gly Val
1 5 10 15

Thr Arg Gly Phe Asn Met Arg Ile Glu Lys Cys Tyr Phe Cys Ser Gly
20 25 30

Pro Ile Tyr Pro Gly His Gly Met Met Phe Val Arg Asn Asp Cys Lys
35 40 45

Val Phe Arg Phe Cys Lys Ser Lys Cys His Lys Asn Phe Lys Lys Lys
50 55 60

Arg Asn Pro Arg Lys Val Arg Trp Thr Lys Ala Phe Arg Lys Ala Ala
65 70 75 80

Gly Lys Glu Leu Thr Val Asp Asn Ser Phe Glu Phe Glu Lys Arg Arg
85 90 95

Asn Glu Pro Ile Lys Tyr Gln Arg Glu Leu Trp Asn Lys Thr Ile Asp
100 105 110

Ala Met Lys Arg Val Glu Glu Ile Lys Gln Lys Arg Gln Ala Lys Phe
115 120 125

Ile Met Asn Arg Leu Lys Lys Asn Lys Glu Leu Gln Lys Val Gln Asp
130 135 140

Ile Lys Glu Val Lys Gln Asn Ile His Leu Ile Arg Ala Pro Leu Ala
145 150 155 160

Gly Lys Gly Lys Gln Leu Glu Glu Lys Met Val Gln Gln Leu Gln Glu
165 170 175

Asp Val Asp Met Glu Asp Ala Pro
180

<210> 1249
<211> 188

<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (104)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1249
Gly Cys Pro Ala His Ser Pro Gly Ser Ala Lys Arg Trp Thr Gln Ala
1 5 10 15

Ala Met Ser Arg Pro Arg Met Arg Leu Val Val Thr Ala Asp Asp Phe
20 25 30

Gly Tyr Cys Pro Arg Arg Asp Glu Gly Ile Val Glu Ala Phe Leu Ala
35 40 45

Gly Ala Val Thr Ser Val Ser Leu Leu Val Asn Gly Ala Ala Thr Glu
50 55 60

Ser Ala Ala Glu Leu Ala Arg Arg His Ser Ile Pro Thr Gly Leu His
65 70 75 80

Ala Asn Leu Ser Glu Gly Arg Pro Val Gly Pro Ala Arg Arg Gly Ala
85 90 95

Ser Ser Leu Leu Gly Pro Glu Xaa Phe Phe Leu Gly Lys Met Gly Phe
100 105 110

Arg Glu Ala Val Ala Ala Gly Asp Val Asp Leu Pro Gln Val Arg Ser
115 120 125

Arg Ser Tyr Arg Arg Met Leu Ala Arg Thr Pro Arg Ala Pro Pro Gly
130 135 140

Gly Thr Val Arg Pro Leu Glu Leu Ala Val Asp Asp Phe Arg Ile Gln
145 150 155 160

Thr Leu Glu Pro Ser His Gly Ser Thr Arg Arg Val Ser Ser Ala Ala
165 170 175

Thr Pro Gly Arg Ser Arg Cys Leu Ser Leu Ala Leu
180 185

<210> 1250
<211> 201
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (96)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (97)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (101)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1250
Arg Lys Asn Leu Glu Ile Tyr Glu Ala Val Thr Ser Pro Gln Gly Pro
1 5 10 15

Ala Met Thr Trp Ser Met Phe Ala Val Gly Trp Met Glu Leu Lys Asp
20 25 30

Ala Cys Gly Xaa Arg Gly Leu Leu Asp Arg Ser Phe Ala Asn Met Ala
35 40 45

Glu Pro Phe Lys Val Trp Thr Glu Asn Ala Asp Gly Ser Gly Ala Val
50 55 60

Asn Phe Leu Thr Gly Met Gly Gly Phe Leu Gln Ala Val Val Phe Gly
65 70 75 80

Cys Thr Gly Phe Arg Val Ser Val Ser Gly Ile Phe Tyr Gln Gly Xaa
85 90 95

Xaa Leu Asn Phe Xaa Phe Ser Glu Asp Ser Val Thr Val Glu Val Thr
100 105 110

Ala Arg Ala Gly Pro Trp Ala Pro His Leu Glu Ala Glu Leu Trp Pro
115 120 125

Ser Gln Ser Arg Leu Ser Leu Leu Pro Gly His Lys Val Ser Phe Pro
130 135 140

Arg Ser Ala Gly Arg Ile Gln Met Ser Pro Pro Lys Leu Pro Gly Ser
145 150 155 160

Ser Ser Ser Glu Phe Pro Gly Arg Thr Phe Ser Asp Val Arg Asp Pro
165 170 175

Leu Gln Ser Pro Leu Trp Val Thr Leu Gly Ser Ser Ser Pro Thr Glu
180 185 190

Ser Leu Thr Val Asp Pro Ala Ser Glu
195 200

<210> 1251
<211> 266
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1251
Ser Val Gly Ser Val Ala Ala Ala Thr Arg Thr Gly Pro Val Ser Xaa
1 5 10 15

Lys Lys Phe Arg Glu Ala Ser Trp Arg Phe Thr Phe Tyr Leu Ile Ala
20 25 30

Phe Ile Ala Gly Met Ala Val Ile Val Asp Lys Pro Trp Phe Tyr Asp
35 40 45

Met Lys Lys Val Trp Glu Gly Tyr Pro Ile Gln Ser Thr Ile Pro Ser
50 55 60

Gln Tyr Trp Tyr Tyr Met Ile Glu Leu Ser Phe Tyr Trp Ser Leu Leu
65 70 75 80

Phe Ser Ile Ala Ser Asp Val Lys Arg Lys Asp Phe Lys Glu Gln Ile
85 90 95

Ile His His Val Ala Thr Ile Ile Leu Ile Ser Phe Ser Trp Phe Ala
100 105 110

Asn Tyr Ile Arg Ala Gly Thr Leu Ile Met Ala Leu His Asp Ser Ser
115 120 125

Asp Tyr Leu Leu Glu Ser Ala Lys Met Phe Asn Tyr Ala Gly Trp Lys
130 135 140

Asn Thr Cys Asn Asn Ile Phe Ile Val Phe Ala Ile Val Phe Ile Ile

145 150 155 160

Thr Arg Leu Val Ile Leu Pro Phe Trp Ile Leu His Cys Thr Leu Val
165 170 175

Tyr Pro Leu Glu Leu Tyr Pro Ala Phe Phe Gly Tyr Tyr Phe Phe Asn
180 185 190

Ser Met Met Gly Val Leu Gln Leu Leu His Ile Phe Trp Ala Tyr Leu
195 200 205

Ile Leu Arg Met Ala His Lys Phe Ile Thr Gly Lys Leu Val Glu Asp
210 215 220

Glu Arg Ser Asp Arg Glu Glu Thr Glu Ser Ser Glu Gly Glu Glu Ala
225 230 235 240

Ala Ala Gly Gly Gly Ala Lys Ser Arg Pro Leu Ala Asn Gly His Pro
245 250 255

Ile Leu Asn Asn Asn His Arg Lys Asn Asp
260 265

<210> 1252
<211> 163
<212> PRT
<213> Homo sapiens

<400> 1252
Lys Met Gly Thr Asn Lys Cys Ala Ser Gln Ala Gly Met Thr Ala Tyr
1 5 10 15

Gly Thr Arg Arg His Leu Tyr Asp Pro Lys Met Gln Thr Asp Lys Pro
20 25 30

Phe Asp Gln Thr Thr Ile Ser Leu Gln Met Gly Thr Asn Lys Gly Ala
35 40 45

Ser Gln Ala Gly Met Leu Ala Pro Gly Thr Arg Arg Asp Ile Tyr Asp
50 55 60

Gln Lys Leu Thr Leu Gln Pro Val Asp Asn Ser Thr Ile Ser Leu Gln
65 70 75 80

Met Gly Thr Asn Lys Val Ala Ser Gln Lys Gly Met Ser Val Tyr Gly
85 90 95

Leu Gly Arg Gln Val Tyr Asp Pro Lys Tyr Cys Ala Ala Pro Thr Glu
100 105 110

Pro Val Ile His Asn Gly Ser Gln Gly Thr Gly Thr Asn Gly Ser Glu
115 120 125

Ile Ser Asp Ser Asp Tyr Gln Ala Glu Tyr Pro Asp Glu Tyr His Gly
130 135 140

Glu Tyr Gln Asp Asp Tyr Pro Arg Asp Tyr Gln Tyr Ser Asp Gln Gly
145 150 155 160

Ile Asp Tyr

<210> 1253
<211> 298
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (109)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1253
Leu Glu Glu Thr Pro Cys Leu Arg Thr Ala Val Ala Cys Glu Gln Arg
1 5 10 15

Asp Pro Gly Thr Glu Ser Gln Pro Arg Arg Cys Cys Arg Arg Arg Arg
20 25 30

Pro Glu Thr Ala Glu Pro Val Arg Pro Pro Pro Pro Pro Thr Pro Asp
35 40 45

Thr Glu His Pro Val Met Asp Lys Asn Glu Leu Val Gln Lys Ala Lys
50 55 60

Leu Ala Glu Gln Ala Glu Arg Tyr Asp Asp Met Ala Ala Cys Met Lys
65 70 75 80

Ser Val Thr Glu Gln Gly Ala Glu Leu Ser Asn Glu Glu Arg Asn Leu
85 90 95

Leu Ser Val Ala Tyr Lys Asn Val Val Gly Ala Arg Xaa Ser Ser Trp
100 105 110

Arg Val Val Ser Ser Ile Glu Gln Lys Thr Glu Gly Ala Glu Lys Lys
115 120 125

Gln Gln Met Ala Arg Glu Tyr Arg Glu Lys Ile Glu Thr Glu Leu Arg

130 135 140

Asp Ile Cys Asn Asp Val Leu Ser Leu Leu Glu Lys Phe Leu Ile Pro
145 150 155 160

Asn Ala Ser Gln Ala Glu Ser Lys Val Phe Tyr Leu Lys Met Lys Gly
165 170 175

Asp Tyr Tyr Arg Tyr Leu Ala Glu Val Ala Ala Gly Asp Asp Lys Lys
180 185 190

Gly Ile Val Asp Gln Ser Gln Gln Ala Tyr Gln Glu Ala Phe Glu Ile
195 200 205

Ser Lys Lys Glu Met Gln Pro Thr His Pro Ile Arg Leu Gly Leu Ala
210 215 220

Leu Asn Phe Ser Val Phe Tyr Tyr Glu Ile Leu Asn Ser Pro Glu Lys
225 230 235 240

Ala Cys Ser Leu Ala Lys Thr Ala Phe Asp Glu Ala Ile Ala Glu Leu
245 250 255

Asp Thr Leu Ser Glu Glu Ser Tyr Lys Asp Ser Thr Leu Ile Met Gln
260 265 270

Leu Leu Arg Asp Asn Leu Thr Leu Trp Thr Ser Asp Thr Gln Gly Asp
275 280 285

Glu Ala Glu Ala Gly Glu Gly Gly Glu Asn
290 295

<210> 1254
<211> 173
<212> PRT
<213> Homo sapiens

<400> 1254
Ser Pro Ala Arg Pro Leu Ile Arg Ser Asp Lys Met Lys Glu Thr Ile
1 5 10 15

Met Asn Gln Glu Lys Leu Ala Lys Leu Gln Ala Gln Val Arg Ile Gly
20 25 30

Gly Lys Gly Thr Ala Arg Arg Lys Lys Lys Val Val His Arg Thr Ala
35 40 45

Thr Ala Asp Asp Lys Lys Leu Gln Phe Ser Leu Lys Lys Leu Gly Val
50 55 60

Asn Asn Ile Ser Gly Ile Glu Glu Val Asn Met Phe Thr Asn Gln Gly
65 70 75 80

Thr Val Ile His Phe Asn Asn Pro Lys Val Gln Ala Ser Leu Ala Ala
85 90 95

Asn Thr Phe Thr Ile Thr Gly His Ala Glu Thr Lys Gln Leu Thr Glu
100 105 110

Met Leu Pro Ser Ile Leu Asn Gln Leu Gly Ala Asp Ser Leu Thr Ser
115 120 125

Leu Arg Arg Leu Ala Glu Ala Leu Pro Lys Gln Ser Val Asp Gly Lys
130 135 140

Ala Pro Leu Ala Thr Gly Glu Asp Asp Asp Asp Glu Val Pro Asp Leu
145 150 155 160

Val Glu Asn Phe Asp Glu Ala Ser Lys Asn Glu Ala Asn
165 170

<210> 1255
<211> 66
<212> PRT
<213> Homo sapiens

<400> 1255
Leu Cys Cys Pro Phe His Ile Lys Glu Leu Leu Thr Thr Lys Ala Ala
1 5 10 15

Pro Ala Phe Pro Ile Cys Leu Ser Ile Trp Leu Ala Gly Lys Glu Arg
20 25 30

Thr Cys Met Leu Val Lys Glu Glu Val Gly Trp Lys Lys Trp Gly Gly
35 40 45

Thr Thr Val Lys Ser Arg Val Lys Pro Ser Trp Pro Lys Val Ser Cys
50 55 60

Arg Leu
65

<210> 1256
<211> 389
<212> PRT
<213> Homo sapiens

<400> 1256
Ala Glu Ala Gly Pro Gly Ala Arg Ala Ala Ala Ala Met Ala Ile Lys
1   5   10   15

Phe Leu Glu Val Ile Lys Pro Phe Cys Val Ile Leu Pro Glu Ile Gln
            20   25   30

Lys Pro Glu Arg Lys Ile Gln Phe Lys Glu Lys Val Leu Trp Thr Ala
        35   40   45

Ile Thr Leu Phe Ile Phe Leu Val Cys Cys Gln Ile Pro Leu Phe Gly
    50   55   60

Ile Met Ser Ser Asp Ser Ala Asp Pro Phe Tyr Trp Met Arg Val Ile
65   70   75   80

Leu Ala Ser Asn Arg Gly Thr Leu Met Glu Leu Gly Ile Ser Pro Ile
                85   90   95

Val Thr Ser Gly Leu Ile Met Gln Leu Leu Ala Gly Ala Lys Ile Ile
            100   105   110

Glu Val Gly Asp Thr Pro Lys Asp Arg Ala Leu Phe Asn Gly Ala Gln
        115   120   125

Lys Leu Phe Gly Met Ile Ile Thr Ile Gly Gln Ser Ile Val Tyr Val
    130   135   140

Met Thr Gly Met Tyr Gly Asp Pro Ser Glu Met Gly Ala Gly Ile Cys
145   150   155   160

Leu Leu Ile Thr Ile Gln Leu Phe Val Ala Gly Leu Ile Val Leu Leu
                165   170   175

Leu Asp Glu Leu Leu Gln Lys Gly Tyr Gly Leu Gly Ser Gly Ile Ser
            180   185   190

Leu Phe Ile Ala Thr Asn Ile Cys Glu Thr Ile Val Trp Lys Ala Phe
        195   200   205

Ser Pro Thr Thr Val Asn Thr Gly Arg Gly Met Glu Phe Glu Gly Ala
    210   215   220

Ile Ile Ala Leu Phe His Leu Leu Ala Thr Arg Thr Asp Lys Val Arg
225   230   235   240

Ala Leu Arg Glu Ala Phe Tyr Arg Gln Asn Leu Pro Asn Leu Met Asn
                245   250   255

Leu Ile Ala Thr Ile Phe Val Phe Ala Val Val Ile Tyr Phe Gln Gly

260 265 270

Phe Arg Val Asp Leu Pro Ile Lys Ser Ala Arg Tyr Arg Gly Gln Tyr
275 280 285

Asn Thr Tyr Pro Ile Lys Leu Phe Tyr Thr Ser Asn Ile Pro Ile Ile
290 295 300

Leu Gln Ser Ala Leu Val Ser Asn Leu Tyr Val Ile Ser Gln Met Leu
305 310 315 320

Ser Ala Arg Phe Ser Gly Asn Leu Leu Val Ser Leu Leu Gly Thr Trp
325 330 335

Ser Asp Thr Ser Ser Gly Gly Pro Ala Arg Ala Tyr Pro Val Gly Gly
340 345 350

Leu Cys Tyr Tyr Leu Ser Pro Pro Trp Ser Met Asn Ser Thr Gly Thr
355 360 365

Ser Pro Gln Pro Arg Pro Leu Val Gly Cys Ala Ser Gly Pro Ser Arg
370 375 380

Ser Trp Leu Thr Ser
385

<210> 1257
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1257
Gly Xaa Pro Ser Ser Ser Arg Ala His Ser Pro Met Ile Ala Val Gly
1 5 10 15

Ser Asp Asp Ser Ser Pro Asn Ala Met Ala Lys Val Gln Ile Phe Glu
20 25 30

Tyr Asn Glu Asn Thr Arg Lys Tyr Ala Lys Ala Glu Thr Leu Met Thr
35 40 45

Val Thr Asp Pro Val His Asp Ile Ala Phe Ala Pro Asn Leu Gly Arg
50 55 60

Ser Phe His Ile Leu Ala Ile Ala Thr Lys Asp Val Arg Ile Phe Thr
65 70 75 80

Leu Lys Pro Val Arg Lys Glu Leu Thr Ser Ser Gly Gly Pro Thr Lys
85 90 95

Phe Glu Ile His Ile Val Ala Gln Phe Asp Asn His Asn Ser Gln Val
100 105 110

Trp Arg Val Ser Trp Asn Ile Thr Gly Thr Val Leu Ala Ser Ser Gly
115 120 125

Asp Asp Gly Cys Val Arg Leu Trp Lys Ala Asn Tyr Met Asp Asn Trp
130 135 140

Lys Cys Thr Gly Ile Leu Lys Gly Asn Gly Ser Pro Val Asn Gly Ser
145 150 155 160

Ser Gln Gln Gly Thr Ser Asn Pro Ser Leu Gly Ser Asn Ile Pro Ser
165 170 175

Leu Gln Asn Ser Leu Asn Gly Ser Ser Ala Gly Arg Lys His Ser
180 185 190

<210> 1258
<211> 458
<212> PRT
<213> Homo sapiens

<400> 1258
Pro Gly Ala Arg His Gly Ser Ala Ser Ala Pro Thr Leu Phe Pro Leu
1 5 10 15

Val Ser Cys Glu Asn Ser Pro Ser Asp Thr Ser Ser Val Ala Val Gly
20 25 30

Cys Leu Ala Gln Asp Phe Leu Pro Asp Ser Ile Thr Phe Ser Trp Lys
35 40 45

Tyr Lys Asn Asn Ser Asp Ile Ser Ser Thr Arg Gly Phe Pro Ser Val
50 55 60

Leu Arg Gly Gly Lys Tyr Ala Ala Thr Ser Gln Val Leu Leu Pro Ser
65 70 75 80

Lys Asp Val Met Gln Gly Thr Asp Glu His Val Val Cys Lys Val Gln
85 90 95

His Pro Asn Gly Asn Lys Glu Lys Asn Val Pro Leu Pro Val Ile Ala

100 105 110

Glu Leu Pro Pro Lys Val Ser Val Phe Val Pro Pro Arg Asp Gly Phe
115 120 125

Phe Gly Asn Pro Arg Lys Ser Lys Leu Ile Cys Gln Ala Thr Gly Phe
130 135 140

Ser Pro Arg Gln Ile Gln Val Ser Trp Leu Arg Glu Gly Lys Gln Val
145 150 155 160

Gly Ser Gly Val Thr Thr Asp Gln Val Gln Ala Glu Ala Lys Glu Ser
165 170 175

Gly Pro Thr Thr Tyr Lys Val Thr Ser Thr Leu Thr Ile Lys Glu Ser
180 185 190

Asp Trp Leu Ser Gln Ser Met Phe Thr Cys Arg Val Asp His Arg Gly
195 200 205

Leu Thr Phe Gln Gln Asn Ala Ser Ser Met Cys Val Pro Asp Gln Asp
210 215 220

Thr Ala Ile Arg Val Phe Ala Ile Pro Pro Ser Phe Ala Ser Ile Phe
225 230 235 240

Leu Thr Lys Ser Thr Lys Leu Thr Cys Leu Val Thr Asp Leu Thr Thr
245 250 255

Tyr Asp Ser Val Thr Ile Ser Trp Thr Arg Gln Asn Gly Glu Ala Val
260 265 270

Lys Thr His Thr Asn Ile Ser Glu Ser His Pro Asn Ala Thr Phe Ser
275 280 285

Ala Val Gly Glu Ala Ser Ile Cys Glu Asp Asp Trp Asn Ser Gly Glu
290 295 300

Arg Phe Thr Cys Thr Val Thr His Thr Asp Leu Pro Ser Pro Leu Lys
305 310 315 320

Gln Thr Ile Ser Arg Pro Lys Gly Val Ala Leu His Arg Pro Asp Val
325 330 335

Tyr Leu Leu Pro Pro Ala Arg Glu Gln Leu Asn Leu Arg Glu Ser Ala
340 345 350

Thr Ile Thr Cys Leu Val Thr Gly Phe Ser Pro Ala Asp Val Phe Val
355 360 365

Gln Trp Met Gln Arg Gly Gln Pro Leu Ser Pro Glu Lys Tyr Val Thr

370 375 380

Ser Ala Pro Met Pro Glu Pro Gln Ala Pro Gly Arg Tyr Phe Ala His
385 390 395 400

Ser Ile Leu Thr Val Ser Glu Glu Glu Trp Asn Thr Gly Glu Thr Tyr
405 410 415

Thr Cys Val Val Ala His Glu Ala Leu Pro Asn Arg Val Thr Glu Arg
420 425 430

Thr Val Asp Lys Ser Thr Gly Lys Pro Thr Leu Tyr Asn Val Ser Leu
435 440 445

Val Met Ser Asp Thr Ala Gly Thr Cys Tyr
450 455

<210> 1259
<211> 247
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (25)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1259
Ala Gly Pro Ala Pro Glu Glu Pro Arg Gly Gly Ala Ala Ala Arg Trp
1 5 10 15

Asp Cys Gln Pro Cys Gln Ala Ala Xaa Val Val Glu Asn Ser Ala Gln
20 25 30

Arg Val Ile His Leu Ala Gly Gln Trp Glu Lys His Arg Val Pro Leu
35 40 45

Leu Ala Glu Tyr Arg His Leu Arg Lys Leu Gln Asp Cys Arg Glu Leu
50 55 60

Glu Ser Ser Arg Arg Leu Ala Glu Ile Gln Glu Leu His Gln Ser Val
65 70 75 80

Arg Ala Ala Ala Glu Glu Ala Arg Arg Lys Glu Glu Val Tyr Lys Gln
85 90 95

Leu Met Ser Glu Leu Glu Thr Leu Pro Arg Asp Val Ser Arg Leu Ala
100 105 110

Tyr Thr Gln Arg Ile Leu Glu Ile Val Gly Asn Ile Arg Lys Gln Lys
115 120 125

Glu Glu Ile Thr Lys Ile Leu Ser Asp Thr Lys Glu Leu Gln Lys Glu
130 135 140

Ile Asn Ser Leu Ser Gly Lys Leu Asp Arg Thr Phe Ala Val Thr Asp
145 150 155 160

Glu Leu Val Phe Lys Asp Ala Lys Lys Asp Asp Ala Val Arg Lys Ala
165 170 175

Tyr Lys Tyr Leu Ala Ala Leu His Glu Asn Cys Ser Gln Leu Ile Gln
180 185 190

Thr Ile Glu Asp Thr Gly Thr Ile Met Arg Glu Val Arg Asp Leu Glu
195 200 205

Glu Gln Ile Glu Thr Glu Leu Gly Lys Lys Thr Leu Ser Asn Leu Glu
210 215 220

Lys Ile Arg Glu Asp Tyr Arg Ala Leu Arg Gln Glu Asn Ala Gly Leu
225 230 235 240

Leu Gly Arg Val Arg Glu Ala
245

<210> 1260
<211> 62
<212> PRT
<213> Homo sapiens

<400> 1260
Val Gly Ile Lys Trp Ile Glu Glu Ala Val Leu Cys Ala Asn Val Ser
1 5 10 15

Phe Ala Ser Asp Arg Tyr Leu Phe Val Ile Arg Arg Val Ala Ser Phe
20 25 30

His Leu Gly Ala Glu Asn Ser Arg Gln Leu Leu Thr Asp Lys Phe Asn
35 40 45

Leu His Leu Gln Tyr Cys Met Leu Gly Ile Ser Ala Tyr Phe
50 55 60

<210> 1261
<211> 243

<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (76)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (210)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (226)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1261
Gln Glu Arg Pro Gly Asn Phe Tyr Val Ser Ser Glu Ser Ile Arg Lys
1 5 10 15

Gly Pro Pro Val Arg Pro Trp Arg Asp Arg Pro Gln Ser Ser Ile Tyr
20 25 30

Asp Pro Phe Ala Gly Met Lys Thr Pro Gly Gln Arg Gln Leu Ile Thr
35 40 45

Leu Gln Glu Gln Val Lys Leu Gly Ile Val Asn Val Asp Glu Ala Val
50 55 60

Leu His Phe Lys Glu Trp Gln Leu Asn Gln Lys Xaa Arg Ser Glu Ser
65 70 75 80

Phe Arg Phe Gln Gln Glu Asn Leu Lys Arg Leu Arg Asp Ser Ile Thr
85 90 95

Arg Arg Gln Arg Glu Lys Gln Lys Ser Gly Lys Gln Thr Asp Leu Glu
100 105 110

Ile Thr Val Pro Ile Arg His Ser Gln His Leu Pro Ala Lys Val Glu
115 120 125

Phe Gly Val Tyr Glu Ser Gly Pro Arg Lys Ser Val Ile Pro Pro Arg
130 135 140

Thr Glu Leu Arg Arg Gly Asp Trp Lys Thr Asp Ser Thr Ser Ser Thr
145 150 155 160

Ala Ser Ser Thr Ser Asn Arg Ser Ser Thr Arg Ser Leu Leu Ser Val
165 170 175

Ser Ser Gly Met Glu Gly Asp Asn Glu Asp Asn Glu Val Pro Glu Val
180 185 190

Thr Arg Ser Arg Ser Pro Gly Pro Pro Gln Val Asp Gly Thr Pro Thr
195 200 205

Met Xaa Leu Glu Arg Pro Pro Arg Val Pro Pro Arg Ala Ala Ser Gln
210 215 220

Arg Xaa Pro Thr Arg Glu Thr Phe His Pro Pro Pro Pro Val Pro Pro
225 230 235 240

Arg Gly Arg

<210> 1262
<211> 75
<212> PRT
<213> Homo sapiens

<400> 1262
Lys Tyr Val Arg Asn Asp Gln Asn Lys Arg Lys Phe Leu Phe Ser Cys
1 5 10 15

Lys Tyr Phe Ser Ser Val Ile Thr Leu Lys Tyr Lys Leu Lys Tyr Asn
20 25 30

Thr Pro Glu Cys Leu Arg His Asp Leu Asp Phe Lys Cys Val Val Phe
35 40 45

Ile Glu Lys Lys Leu Ser Thr His Leu Val Phe Gln Glu Asn Leu Lys
50 55 60

Arg Ser Gln Gly Lys Met Ile Cys Met Leu Lys
65 70 75

<210> 1263
<211> 475
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (249)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1263

Arg Thr Gly Leu Gly Arg Asp Val Gly Ala Gly Ala Arg Arg Ala Ala
1   5   10   15

Arg Cys Arg Ala Glu Ala Ala Ala Ala Val Gly Thr Ala Arg Ser Pro
            20   25   30

Ala Leu Gly Met Ala Leu Leu Val Leu Gly Leu Val Ser Cys Thr Phe
        35   40   45

Phe Leu Ala Val Asn Gly Leu Tyr Ser Ser Ser Asp Asp Val Ile Glu
    50   55   60

Leu Thr Pro Ser Asn Phe Asn Arg Glu Val Ile Gln Ser Asp Ser Leu
65   70   75   80

Trp Leu Val Glu Phe Tyr Ala Pro Trp Cys Gly His Cys Gln Arg Leu
                85   90   95

Thr Pro Glu Trp Lys Lys Ala Ala Thr Ala Leu Lys Asp Val Val Lys
            100   105   110

Val Gly Ala Val Asp Ala Asp Lys His His Ser Leu Gly Gly Gln Tyr
        115   120   125

Gly Val Gln Gly Phe Pro Thr Ile Lys Ile Phe Gly Ser Asn Lys Asn
    130   135   140

Arg Pro Glu Asp Tyr Gln Gly Gly Arg Thr Gly Glu Ala Ile Val Asp
145   150   155   160

Ala Ala Leu Ser Ala Leu Arg Gln Leu Val Lys Asp Arg Leu Gly Gly
                165   170   175

Arg Ser Gly Gly Tyr Ser Ser Gly Lys Gln Gly Arg Ser Asp Ser Ser
            180   185   190

Ser Lys Lys Asp Val Ile Glu Leu Thr Asp Asp Ser Phe Asp Lys Asn
        195   200   205

Val Leu Asp Ser Glu Asp Val Trp Met Val Glu Phe Tyr Ala Pro Trp
    210   215   220

Cys Gly His Cys Lys Asn Leu Glu Pro Glu Trp Ala Ala Ala Ala Ser
225   230   235   240

Glu Val Lys Glu Gln Thr Lys Gly Xaa Val Lys Leu Ala Ala Val Asp
                245   250   255

Ala Thr Val Asn Gln Val Leu Ala Ser Arg Tyr Gly Ile Arg Gly Phe
            260   265   270

Pro Thr Ile Lys Ile Phe Gln Lys Gly Glu Ser Pro Val Asp Tyr Asp
275 280 285

Gly Gly Arg Thr Arg Ser Asp Ile Val Ser Arg Ala Leu Asp Leu Phe
290 295 300

Ser Asp Asn Ala Pro Pro Pro Glu Leu Leu Glu Ile Ile Asn Glu Asp
305 310 315 320

Ile Ala Lys Arg Thr Cys Glu Glu His Gln Leu Cys Val Val Ala Val
325 330 335

Leu Pro His Ile Leu Asp Thr Gly Ala Ala Gly Arg Asn Ser Tyr Leu
340 345 350

Glu Val Leu Leu Lys Leu Ala Asp Lys Tyr Lys Lys Lys Met Trp Gly
355 360 365

Trp Leu Trp Thr Glu Ala Gly Ala Gln Ser Glu Leu Glu Thr Ala Leu
370 375 380

Gly Ile Gly Gly Phe Gly Tyr Pro Ala Met Ala Ala Ile Asn Ala Arg
385 390 395 400

Lys Met Lys Phe Ala Leu Leu Lys Gly Ser Phe Ser Glu Gln Gly Ile
405 410 415

Asn Glu Phe Leu Arg Glu Leu Ser Phe Gly Arg Gly Ser Thr Ala Pro
420 425 430

Val Gly Gly Gly Ala Phe Pro Thr Ile Val Glu Arg Glu Pro Trp Asp
435 440 445

Gly Arg Asp Gly Glu Leu Pro Val Glu Asp Asp Ile Asp Leu Ser Asp
450 455 460

Val Glu Leu Asp Asp Leu Gly Lys Asp Glu Leu
465 470 475

<210> 1264
<211> 398
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (28)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1264

His Phe Glu Arg Thr Ser Ser Lys Arg Val Ser Arg Ser Leu Asp Gly
1   5   10   15

Ala Pro Ile Gly Val Met Asp Gln Ser Leu Met Xaa Asp Phe Pro Gly
            20   25   30

Ala Ala Gly Glu Ile Ser Ala Tyr Gly Pro Gly Leu Val Ser Ile Ala
        35   40   45

Val Val Gln Asp Gly Asp Gly Arg Arg Glu Val Arg Ser Pro Thr Lys
    50   55   60

Ala Pro His Leu Gln Leu Ile Glu Gly Lys Ser Ser His Glu Thr Leu
65   70   75   80

Asn Ile Val Glu Glu Lys Lys Arg Ala Glu Val Gly Lys Asp Glu Arg
                85   90   95

Val Ile Thr Glu Glu Met Asn Gly Lys Glu Ile Ser Pro Gly Ser Gly
            100   105   110

Pro Gly Glu Ile Arg Lys Val Glu Pro Val Thr Gln Lys Asp Ser Thr
        115   120   125

Ser Leu Ser Ser Glu Ser Ser Ser Ser Ser Ser Glu Ser Glu Glu Glu
    130   135   140

Asp Val Gly Glu Tyr Arg Pro His His Arg Val Thr Glu Gly Thr Ile
145   150   155   160

Arg Glu Glu Gln Glu Tyr Glu Glu Glu Val Glu Glu Glu Pro Arg Pro
                165   170   175

Ala Ala Lys Val Val Glu Arg Glu Glu Ala Val Pro Glu Ala Ser Pro
            180   185   190

Val Thr Gln Ala Gly Ala Ser Val Ile Thr Val Glu Thr Val Ile Gln
        195   200   205

Glu Asn Val Gly Ala Gln Lys Ile Pro Gly Glu Lys Ser Val His Glu
    210   215   220

Gly Ala Leu Lys Gln Asp Met Gly Glu Glu Ala Glu Glu Glu Pro Gln
225   230   235   240

Lys Val Asn Gly Glu Val Ser His Val Asp Ile Asp Val Leu Pro Gln
                245   250   255

Ile Ile Cys Cys Ser Glu Pro Pro Val Val Lys Thr Glu Met Val Thr

260 265 270

Ile Ser Asp Ala Ser Gln Arg Thr Glu Ile Ser Thr Lys Glu Val Pro
275 280 285

Ile Val Gln Thr Glu Thr Lys Thr Ile Thr Tyr Glu Ser Pro Gln Ile
290 295 300

Asp Gly Gly Ala Gly Gly Asp Ser Gly Thr Leu Leu Thr Ala Gln Thr
305 310 315 320

Ile Thr Ser Glu Ser Val Ser Thr Thr Thr Thr Thr His Ile Thr Lys
325 330 335

Thr Val Lys Gly Gly Ile Ser Glu Thr Arg Ile Glu Lys Arg Ile Val
340 345 350

Ile Thr Gly Asp Gly Asp Ile Asp His Asp Gln Ala Leu Ala Gln Ala
355 360 365

Ile Arg Glu Ala Arg Glu Gln His Pro Asp Met Ser Val Thr Arg Val
370 375 380

Val Val His Lys Glu Thr Glu Leu Ala Glu Glu Gly Glu Asp
385 390 395

<210> 1265
<211> 207
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (99)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1265
Trp Thr Gly Thr Gly Arg Gly Ala Val Ala Ile Met Ala Asp Pro Asp
1 5 10 15

Pro Arg Tyr Pro Arg Ser Ser Ile Glu Asp Asp Phe Asn Tyr Gly Ser
20 25 30

Ser Val Ala Ser Ala Thr Val His Ile Arg Met Ala Phe Leu Arg Lys
35 40 45

Val Tyr Ser Ile Leu Ser Leu Gln Val Leu Leu Thr Thr Val Thr Ser
50 55 60

Thr Val Phe Leu Tyr Phe Glu Ser Val Arg Thr Phe Val His Glu Ser
65 70 75 80

Pro Ala Leu Ile Leu Leu Phe Ala Leu Gly Ser Leu Gly Leu Ile Phe
85 90 95

Ala Leu Xaa Leu Asn Arg His Lys Tyr Pro Leu Asn Leu Tyr Leu Leu
100 105 110

Phe Gly Phe Thr Leu Leu Glu Ala Leu Thr Val Ala Val Val Thr
115 120 125

Phe Tyr Asp Val Tyr Ile Ile Leu Gln Ala Phe Ile Leu Thr Thr Thr
130 135 140

Val Phe Phe Gly Leu Thr Val Tyr Thr Leu Gln Ser Lys Lys Asp Phe
145 150 155 160

Ser Lys Phe Gly Ala Gly Leu Phe Ala Leu Leu Trp Ile Leu Cys Leu
165 170 175

Ser Gly Phe Leu Lys Phe Phe Phe Tyr Ser Glu Ile Met Glu Leu Val
180 185 190

Leu Ala Ala Ala Gly Ala Leu Leu Phe Trp Gly Ile His His Leu
195 200 205

<210> 1266
<211> 289
<212> PRT
<213> Homo sapiens

<400> 1266
Ser Arg Asp Pro Asn Gly Trp Trp Arg Arg Leu Arg Val Ser Ala Glu
1 5 10 15

Leu Ala Met Ala Gln Leu Cys Gly Leu Arg Arg Ser Arg Ala Phe Leu
20 25 30

Ala Leu Leu Gly Ser Leu Leu Leu Ser Gly Val Leu Ala Ala Asp Arg
35 40 45

Glu Arg Ser Ile His Asp Phe Cys Leu Val Ser Lys Val Val Gly Arg
50 55 60

Cys Arg Ala Ser Met Pro Arg Trp Trp Tyr Asn Val Thr Asp Gly Ser
65 70 75 80

Cys Gln Leu Phe Val Tyr Gly Gly Cys Asp Gly Asn Ser Asn Asn Tyr

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                85                  90                  95

Leu Thr Lys Glu Glu Cys Leu Lys Lys Cys Ala Thr Val Thr Glu Asn
            100                 105                 110

Ala Thr Gly Asp Leu Ala Thr Ser Arg Asn Ala Ala Asp Ser Ser Val
        115                 120                 125

Pro Ser Ala Pro Arg Arg Gln Asp Ser Glu Asp His Ser Ser Asp Met
    130                 135                 140

Phe Asn Tyr Glu Glu Tyr Cys Thr Ala Asn Ala Val Thr Gly Pro Cys
145                 150                 155                 160

Arg Ala Ser Phe Pro Arg Trp Tyr Phe Asp Val Glu Arg Asn Ser Cys
                165                 170                 175

Asn Asn Phe Ile Tyr Gly Gly Cys Arg Gly Asn Lys Asn Ser Tyr Arg
            180                 185                 190

Ser Glu Glu Ala Cys Met Leu Arg Cys Phe Arg Gln Gln Glu Asn Pro
        195                 200                 205

Pro Leu Pro Leu Gly Ser Lys Val Val Val Leu Ala Gly Leu Phe Val
    210                 215                 220

Met Val Leu Ile Leu Phe Leu Gly Ala Ser Met Val Tyr Leu Ile Arg
225                 230                 235                 240

Val Ala Arg Arg Asn Gln Glu Arg Ala Leu Arg Thr Val Trp Ser Ser
                245                 250                 255

Gly Asp Asp Lys Glu Gln Leu Val Lys Asn Thr Tyr Val Leu Cys Arg
            260                 265                 270

Pro Val Ala Lys Arg Thr Gly Glu Gly Arg Gly Asp Met Cys Asp Phe
        275                 280                 285

Phe
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<210> 1267
<211> 284
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1267
Arg Gly Arg Arg Xaa Xaa Ala Ser Leu Arg Gly Trp Pro Val Arg Arg
1   5   10   15

Gly Met Gly Arg Val Gln Leu Phe Glu Ile Ser Leu Ser His Gly Arg
            20   25   30

Val Val Tyr Ser Pro Gly Glu Pro Leu Ala Gly Thr Val Arg Val Arg
        35   40   45

Leu Gly Ala Pro Leu Pro Phe Arg Ala Ile Arg Val Thr Cys Ile Gly
    50   55   60

Ser Cys Gly Val Ser Asn Lys Ala Asn Asp Thr Ala Trp Val Val Glu
65   70   75   80

Glu Gly Tyr Phe Asn Ser Ser Leu Ser Leu Ala Asp Lys Gly Ser Leu
                85   90   95

Pro Ala Gly Glu His Ser Phe Pro Phe Gln Phe Leu Leu Pro Ala Thr
            100   105   110

Ala Pro Thr Ser Phe Glu Gly Pro Phe Gly Lys Ile Val His Gln Val
        115   120   125

Arg Ala Ala Ile His Thr Pro Arg Phe Ser Lys Asp His Lys Cys Ser
    130   135   140

Leu Val Phe Tyr Ile Leu Ser Pro Leu Asn Leu Asn Ser Ile Pro Asp
145   150   155   160

Ile Glu Gln Pro Asn Val Ala Ser Ala Thr Lys Lys Phe Ser Tyr Lys
                165   170   175

Leu Val Lys Thr Gly Ser Val Val Leu Thr Ala Ser Thr Asp Leu Arg
            180   185   190

Gly Tyr Val Val Gly Gln Ala Leu Gln Leu His Ala Asp Val Glu Asn
        195   200   205

Gln Ser Gly Lys Asp Thr Ser Pro Val Val Ala Ser Leu Leu Gln Lys
    210   215   220

Val Ser Tyr Lys Ala Lys Arg Trp Ile His Asp Val Arg Thr Ile Ala

225 230 235 240

Glu Val Glu Gly Ala Gly Val Lys Ala Trp Arg Arg Ala Gln Trp His
245 250 255

Glu Gln Ile Leu Val Pro Ala Leu Pro Gln Ser Ala Leu Pro Ala Ala
260 265 270

Ala Ser Ser Thr Ser Thr Thr Thr Tyr Arg Ser Leu
275 280

<210> 1268
<211> 254
<212> PRT
<213> Homo sapiens

<400> 1268
Val Trp Leu Arg Val Glu Asn Val Cys Gln Gly Pro Gly Gln Glu Gly
1 5 10 15

Gly Pro Pro Val Thr Met Val Ser Met Ser Phe Lys Arg Asn Arg Ser
20 25 30

Asp Arg Phe Tyr Ser Thr Arg Cys Cys Gly Cys Cys His Val Arg Thr
35 40 45

Gly Thr Ile Ile Leu Gly Thr Trp Tyr Met Val Val Asn Leu Leu Met
50 55 60

Ala Ile Leu Leu Thr Val Glu Val Thr His Pro Asn Ser Met Pro Ala
65 70 75 80

Val Asn Ile Gln Tyr Glu Val Ile Gly Asn Tyr Tyr Ser Ser Glu Arg
85 90 95

Met Ala Asp Asn Ala Cys Val Leu Phe Ala Val Ser Val Leu Met Phe
100 105 110

Ile Ile Ser Ser Met Leu Val Tyr Gly Ala Ile Ser Tyr Gln Val Gly
115 120 125

Trp Leu Ile Pro Phe Phe Cys Tyr Arg Leu Phe Asp Phe Val Leu Ser
130 135 140

Cys Leu Val Ala Ile Ser Ser Leu Thr Tyr Leu Pro Arg Ile Lys Glu
145 150 155 160

Tyr Leu Asp Gln Leu Pro Asp Phe Pro Tyr Lys Asp Asp Leu Leu Ala
165 170 175

Leu Asp Ser Ser Cys Leu Leu Phe Ile Val Leu Val Phe Phe Ala Leu
            180   185   190

Phe Ile Ile Phe Lys Ala Tyr Leu Ile Asn Cys Val Trp Asn Cys Tyr
        195   200   205

Lys Tyr Ile Asn Asn Arg Asn Val Pro Glu Ile Ala Val Tyr Pro Ala
    210   215   220

Phe Glu Ala Pro Pro Gln Tyr Val Leu Pro Thr Tyr Glu Met Ala Val
225   230   235   240

Lys Met Pro Glu Lys Glu Pro Pro Pro Pro Tyr Leu Pro Ala
                245   250

<210> 1269
<211> 67
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (52)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (53)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1269
Lys Ser Ile Leu Val Ile Arg Val Tyr Phe Phe Tyr Arg Thr Arg Trp
1   5   10   15

Xaa Gly Gly Glu Pro Phe Thr Leu Leu Val Lys Leu Asn His Arg Lys
            20   25   30

Phe Thr Ile Cys Leu Ser Gln Thr Leu Ala Val Arg Gly Met Val Ala

35 40 45

Xaa Ala Cys Xaa Xaa Pro Ala Cys Trp Gly Gly Pro Ser Trp Gly Gly
50 55 60

Leu Pro Glu
65

<210> 1270
<211> 164
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (138)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (152)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (161)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (164)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1270

Gly Ser Pro Gly Thr Xaa Arg Ile Pro Xaa Thr Arg Xaa Glu Thr Cys
1   5   10   15

Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp Thr Tyr Glu
            20   25   30

Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile Gly Ala Gly
        35   40   45

Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His Glu Gly Gly
    50   55   60

Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His Glu Thr Gly
65   70   75   80

Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys Gly Glu Trp
                85   90   95

Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala Ala Gly Thr
            100   105   110

Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln Gly Trp Met
        115   120   125

Met Val Asp Cys Thr Cys Leu Gly Glu Xaa Ser Gly Arg Ile Thr Cys
    130   135   140

Thr Ser Arg Asn Arg Cys Asn Xaa Gln Asp Thr Arg Thr Ser Ile Glu
145   150   155   160

Xaa Glu Thr Xaa

<210> 1271
<211> 363
<212> PRT
<213> Homo sapiens

<400> 1271
Ala Arg Gly Ser Glu Cys Gly Gln Arg Ala Glu Ala Val Ser His Arg
1   5   10   15

Arg Arg Arg Arg Ala Gln Ala Ser Ser Phe Gly Trp Gly Ala Ala Glu
            20   25   30

Leu Thr Ser Asp Ile Ser Ala Pro Phe Thr Arg Arg Asn Pro Gly Ala
        35   40   45

Gly Ala Arg Ser Ala Gly Val Thr Met Thr Lys Ala Gly Ser Lys Gly

50 55 60

Gly Asn Leu Arg Asp Lys Leu Asp Gly Asn Glu Leu Asp Leu Ser Leu
65 70 75 80

Ser Asp Leu Asn Glu Val Pro Val Lys Glu Leu Ala Ala Leu Pro Lys
85 90 95

Ala Thr Ile Leu Asp Leu Ser Cys Asn Lys Leu Thr Thr Leu Pro Ser
100 105 110

Asp Phe Cys Gly Leu Thr His Leu Val Lys Leu Asp Leu Ser Lys Asn
115 120 125

Lys Leu Gln Gln Leu Pro Ala Asp Phe Gly Arg Leu Val Asn Leu Gln
130 135 140

His Leu Asp Leu Leu Asn Asn Lys Leu Val Thr Leu Pro Val Ser Phe
145 150 155 160

Ala Gln Leu Lys Asn Leu Lys Trp Leu Asp Leu Lys Asp Asn Pro Leu
165 170 175

Asp Pro Val Leu Ala Lys Val Ala Gly Asp Cys Leu Asp Glu Lys Gln
180 185 190

Cys Lys Gln Cys Ala Asn Lys Val Leu Gln His Met Lys Ala Val Gln
195 200 205

Ala Asp Gln Glu Arg Glu Arg Gln Arg Arg Leu Glu Val Glu Arg Glu
210 215 220

Ala Glu Lys Lys Arg Glu Ala Lys Gln Arg Ala Lys Glu Ala Gln Glu
225 230 235 240

Arg Glu Leu Arg Lys Arg Glu Lys Ala Glu Glu Lys Glu Arg Arg Arg
245 250 255

Lys Glu Tyr Asp Ala Leu Lys Ala Ala Lys Arg Glu Gln Glu Lys Lys
260 265 270

Pro Lys Lys Glu Ala Asn Gln Ala Pro Lys Ser Lys Ser Gly Ser Arg
275 280 285

Pro Arg Lys Pro Pro Pro Arg Lys His Thr Arg Ser Trp Ala Val Leu
290 295 300

Lys Leu Leu Leu Leu Leu Leu Leu Phe Gly Val Ala Gly Gly Leu Val
305 310 315 320

Ala Cys Arg Val Thr Glu Leu Gln Gln Gln Pro Leu Cys Thr Ser Val

325 330 335

Asn Thr Ile Tyr Asp Asn Ala Val Gln Gly Leu Arg Arg His Glu Ile
340 345 350

Leu Gln Trp Val Leu Gln Thr Asp Ser Gln Gln
355 360

<210> 1272
<211> 144
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (112)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (116)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (124)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1272
Gly Leu Val Met Ala Pro Ile Ala Cys Leu Leu Pro Ala Phe Ser Ser
1 5 10 15

Ala Pro Glu Ala Met His Pro Trp Glu Leu Phe Val Lys Tyr Tyr His
20 25 30

Ala Lys Asn Gly Arg Ala Tyr Val Glu Ser Pro Ala Arg Lys Leu Ser
35 40 45

Gln Ser Phe Ala Leu Pro Val Thr Gly Gly Thr Val Val Thr Pro Lys
50 55 60

Gln Ser Leu Leu Thr Ala Ile His Met Val Leu Thr Glu His Asp Pro
65 70 75 80

Phe Lys Arg Ser Ala Asp Ser Glu Leu Lys Ala Leu Val Cys Met Ala
85 90 95

Leu Asn Glu Pro Ala Ser Gly Val Leu Gly Glu Pro His Leu Gln Xaa
100 105 110

Arg Val Thr Xaa Arg Ala Ser Leu Pro Ala Leu Xaa Leu His Gly Thr
115 120 125

His Arg Leu Leu Lys Ile Ala Ser Thr Cys Ser Val Ala Ser Thr Thr
130 135 140

<210> 1273
<211> 252
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (32)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1273
Ala Arg Ala Pro Pro Arg Pro Arg Arg Ala Gly Arg Cys Gln Leu Pro
1 5 10 15

Gln Arg Pro Ala Glu Ala Arg Cys Met Leu Ser Arg Cys Arg Ser Xaa
20 25 30

Leu Leu His Val Leu Gly Leu Ser Phe Leu Leu Gln Thr Arg Arg Pro
35 40 45

Ile Leu Leu Cys Ser Pro Arg Leu Met Lys Pro Leu Val Val Phe Val
50 55 60

Leu Gly Gly Pro Gly Ala Gly Lys Gly Thr Gln Cys Ala Arg Ile Val
65 70 75 80

Glu Lys Tyr Gly Tyr Thr His Leu Ser Ala Gly Glu Leu Leu Arg Asp
85 90 95

Glu Arg Lys Asn Pro Asp Ser Gln Tyr Gly Glu Leu Ile Glu Lys Tyr
100 105 110

Ile Lys Glu Gly Lys Ile Val Pro Val Glu Ile Thr Ile Ser Leu Leu
115 120 125

Lys Arg Glu Met Asp Gln Thr Met Ala Ala Asn Ala Gln Lys Asn Lys
130 135 140

Phe Leu Ile Asp Gly Phe Pro Arg Asn Gln Asp Asn Leu Gln Gly Trp

145 150 155 160

Asn Lys Thr Met Asp Gly Lys Ala Asp Val Ser Phe Val Leu Phe Phe
165 170 175

Asp Cys Asn Asn Glu Ile Cys Ile Glu Arg Cys Leu Glu Arg Gly Lys
180 185 190

Ser Ser Gly Arg Ser Asp Asp Asn Arg Glu Ser Leu Glu Lys Arg Ile
195 200 205

Gln Thr Tyr Leu Gln Ser Thr Lys Pro Ile Ile Asp Leu Tyr Glu Glu
210 215 220

Met Gly Lys Val Lys Lys Ile Asp Ala Ser Lys Ser Val Asp Glu Val
225 230 235 240

Phe Asp Glu Val Val Gln Ile Phe Asp Lys Glu Gly
245 250

<210> 1274
<211> 425
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1274
Ala Ser Glu Arg Ser Glu Ala Arg Arg Lys Leu Arg Glu Cys Asp Gly
1 5 10 15

Leu Val Asp Ala Leu Ile Phe Ile Val Gln Ala Glu Ile Gly Gln Lys
20 25 30

Asp Ser Xaa Ser Lys Leu Val Glu Asn Cys Val Cys Leu Leu Arg Asn
35 40 45

Leu Ser Tyr Gln Val His Arg Glu Ile Pro Gln Ala Glu Arg Tyr Gln
50 55 60

Glu Ala Ala Pro Asn Val Ala Asn Asn Thr Gly Pro His Ala Ala Ser
65 70 75 80

Cys Phe Gly Ala Lys Lys Gly Lys Gly Lys Lys Pro Ile Glu Asp Pro
85 90 95

Ala Asn Asp Thr Val Asp Phe Pro Lys Arg Thr Ser Pro Ala Arg Gly
100 105 110

Tyr Glu Leu Leu Phe Gln Pro Glu Val Val Arg Ile Tyr Ile Ser Leu
115 120 125

Leu Lys Glu Ser Lys Thr Pro Ala Ile Leu Glu Ala Ser Ala Gly Ala
130 135 140

Ile Gln Asn Leu Cys Ala Gly Arg Trp Thr Tyr Gly Arg Tyr Ile Arg
145 150 155 160

Ser Ala Leu Arg Gln Glu Lys Ala Leu Ser Ala Ile Ala Asp Leu Leu
165 170 175

Thr Asn Glu His Glu Arg Val Val Lys Ala Ala Ser Gly Ala Leu Arg
180 185 190

Asn Leu Ala Val Asp Ala Arg Asn Lys Glu Leu Ile Gly Lys His Ala
195 200 205

Ile Pro Asn Leu Val Lys Asn Leu Pro Gly Gly Gln Gln Asn Ser Ser
210 215 220

Trp Asn Phe Ser Glu Asp Thr Val Ile Ser Ile Leu Asn Thr Ile Asn
225 230 235 240

Glu Val Ile Ala Glu Asn Leu Glu Ala Ala Lys Lys Leu Arg Glu Thr
245 250 255

Gln Gly Ile Glu Lys Leu Val Leu Ile Asn Lys Ser Gly Asn Arg Ser
260 265 270

Glu Lys Glu Val Arg Ala Ala Ala Leu Val Leu Gln Thr Ile Trp Gly
275 280 285

Tyr Lys Glu Leu Arg Lys Pro Leu Glu Lys Glu Gly Trp Lys Lys Ser
290 295 300

Asp Phe Gln Val Asn Leu Asn Asn Ala Ser Arg Ser Gln Ser Ser His
305 310 315 320

Ser Tyr Asp Asp Ser Thr Leu Pro Leu Ile Asp Arg Asn Gln Lys Ser
325 330 335

Asp Lys Lys Pro Asp Arg Glu Glu Ile Gln Met Ser Asn Met Gly Ser
340 345 350

Asn Thr Lys Ser Leu Asp Asn Asn Tyr Ser Thr Pro Asn Glu Arg Gly
355 360 365

Asp His Asn Arg Thr Leu Asp Arg Ser Gly Asp Leu Gly Asp Met Glu
    370   375   380

Pro Leu Lys Gly Thr Thr Pro Leu Met Gln Asp Glu Gly Gln Glu Ser
385   390   395   400

Leu Glu Glu Glu Leu Asp Val Leu Val Leu Asp Asp Glu Gly Gly Gln
                405   410   415

Val Ser Tyr Pro Ser Met Gln Lys Ile
            420   425

<210> 1275
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1275
Phe Phe Phe Ser Ser Leu Phe Ser Leu Xaa Phe Leu Lys Lys Gly Lys
  1   5   10   15

Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu
            20   25   30

Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val
        35   40   45

Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro
    50   55   60

Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met
65   70   75   80

Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp
                85   90   95

Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
            100   105   110

<210> 1276
<211> 766
<212> PRT

<213> Homo sapiens

<400> 1276

```
Gly Asp Phe Ile Met Leu Arg Ala Gly Arg Arg Ala Pro Leu Pro Ser
  1               5                  10                  15

Pro Pro Ser Leu Asp Ser Pro Gly Pro Gln Leu Met Pro Ser Pro Arg
             20                  25                  30

Pro Val Leu Leu Arg Gly Ala Arg Ala Ala Leu Leu Leu Leu Leu Pro
         35                  40                  45

Pro Arg Leu Leu Ala Arg Pro Ser Leu Leu Leu Arg Arg Ser Leu Ser
     50                  55                  60

Ala Ala Ser Cys Ala Pro Ile Ser Leu Pro Ala Ala Ala Ser Arg Ser
 65                  70                  75                  80

Ser Met Asp Gly Ala Gly Ala Glu Glu Val Leu Ala Pro Leu Arg Leu
                 85                  90                  95

Ala Val Arg Gln Gln Gly Asp Leu Val Arg Lys Leu Lys Glu Asp Lys
            100                 105                 110

Ala Pro Gln Val Asp Val Asp Lys Ala Val Ala Glu Leu Lys Ala Arg
        115                 120                 125

Lys Arg Val Leu Glu Ala Lys Glu Leu Ala Leu Gln Pro Lys Asp Asp
    130                 135                 140

Ile Val Asp Arg Ala Lys Met Glu Asp Thr Leu Lys Arg Arg Phe Phe
145                 150                 155                 160

Tyr Asp Gln Ala Phe Ala Ile Tyr Gly Gly Val Ser Gly Leu Tyr Asp
                165                 170                 175

Phe Gly Pro Val Gly Cys Ala Leu Lys Asn Asn Ile Ile Gln Thr Trp
            180                 185                 190

Arg Gln His Phe Ile Gln Glu Glu Gln Ile Leu Glu Ile Asp Cys Thr
        195                 200                 205

Met Leu Thr Pro Glu Pro Val Leu Lys Thr Ser Gly His Val Asp Lys
    210                 215                 220

Phe Ala Asp Phe Met Val Lys Asp Val Lys Asn Gly Glu Cys Phe Arg
225                 230                 235                 240

Ala Asp His Leu Leu Lys Ala His Leu Gln Lys Leu Met Ser Asp Lys
                245                 250                 255
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Lys Cys Ser Val Glu Lys Lys Ser Glu Met Glu Ser Val Leu Ala Gln
260 265 270

Leu Asp Asn Tyr Gly Gln Gln Glu Leu Ala Asp Leu Phe Val Asn Tyr
275 280 285

Asn Val Lys Ser Pro Ile Thr Gly Asn Asp Leu Ser Pro Pro Val Ser
290 295 300

Phe Asn Leu Met Phe Lys Thr Phe Ile Gly Pro Gly Gly Asn Met Pro
305 310 315 320

Gly Tyr Leu Arg Pro Glu Thr Ala Gln Gly Ile Phe Leu Asn Phe Lys
325 330 335

Arg Leu Leu Glu Phe Asn Gln Gly Lys Leu Pro Phe Ala Ala Ala Gln
340 345 350

Ile Gly Asn Ser Phe Arg Asn Glu Ile Ser Pro Arg Ser Gly Leu Ile
355 360 365

Arg Val Arg Glu Phe Thr Met Ala Glu Ile Glu His Phe Val Asp Pro
370 375 380

Ser Glu Lys Asp His Pro Lys Phe Gln Asn Val Ala Asp Leu His Leu
385 390 395 400

Tyr Leu Tyr Ser Ala Lys Ala Gln Val Ser Gly Gln Ser Ala Arg Lys
405 410 415

Met Arg Leu Gly Asp Ala Val Glu Gln Gly Val Ile Asn Asn Thr Val
420 425 430

Leu Gly Tyr Phe Ile Gly Arg Ile Tyr Leu Tyr Leu Thr Lys Val Gly
435 440 445

Ile Ser Pro Asp Lys Leu Arg Phe Arg Gln His Met Glu Asn Glu Met
450 455 460

Ala His Tyr Ala Cys Asp Cys Trp Asp Ala Glu Ser Lys Thr Ser Tyr
465 470 475 480

Gly Trp Ile Glu Ile Val Gly Cys Ala Asp Arg Ser Cys Tyr Asp Leu
485 490 495

Ser Cys His Ala Arg Ala Thr Lys Val Pro Leu Val Ala Glu Lys Pro
500 505 510

Leu Lys Glu Pro Lys Thr Val Asn Val Val Gln Phe Glu Pro Ser Lys
515 520 525

Gly Ala Ile Gly Lys Ala Tyr Lys Lys Asp Ala Lys Leu Val Met Glu
    530   535   540

Tyr Leu Ala Ile Cys Asp Glu Cys Tyr Ile Thr Glu Met Glu Met Leu
545   550   555   560

Leu Asn Glu Lys Gly Glu Phe Thr Ile Glu Thr Glu Gly Lys Thr Phe
                565   570   575

Gln Leu Thr Lys Asp Met Ile Asn Val Lys Arg Phe Gln Lys Thr Leu
            580   585   590

Tyr Val Glu Glu Val Val Pro Asn Val Ile Glu Pro Ser Phe Gly Leu
        595   600   605

Gly Arg Ile Met Tyr Thr Val Phe Glu His Thr Phe His Val Arg Glu
    610   615   620

Gly Asp Glu Gln Arg Thr Phe Phe Ser Phe Pro Ala Val Val Ala Pro
625   630   635   640

Phe Lys Cys Ser Val Leu Pro Leu Ser Gln Asn Gln Glu Phe Met Pro
                645   650   655

Phe Val Lys Glu Leu Ser Glu Ala Leu Thr Arg His Gly Val Ser His
            660   665   670

Lys Val Asp Asp Ser Ser Gly Ser Ile Gly Arg Arg Tyr Ala Arg Thr
        675   680   685

Asp Glu Ile Gly Val Ala Phe Gly Val Thr Ile Asp Phe Asp Thr Val
    690   695   700

Asn Lys Thr Pro His Thr Ala Thr Leu Arg Asp Arg Asp Ser Met Arg
705   710   715   720

Gln Ile Arg Ala Glu Ile Ser Glu Leu Pro Ser Ile Val Gln Asp Leu
                725   730   735

Ala Asn Gly Asn Ile Thr Trp Ala Asp Val Glu Ala Arg Tyr Pro Leu
            740   745   750

Phe Glu Gly Gln Glu Thr Gly Lys Lys Glu Thr Ile Glu Glu
        755   760   765

<210> 1277
<211> 386
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (75)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1277
Leu Gly Ser Arg Gln Ala Ala Gly Thr Met Arg Gly Gln Arg Ser Leu
1   5   10   15

Leu Leu Gly Pro Ala Arg Leu Cys Leu Arg Leu Leu Leu Leu Leu Gly
            20   25   30

Tyr Arg Arg Arg Cys Pro Pro Leu Leu Arg Gly Leu Val Gln Arg Trp
        35   40   45

Arg Tyr Gly Lys Val Cys Leu Arg Ser Leu Leu Tyr Asn Ser Phe Gly
    50   55   60

Gly Ser Asp Thr Ala Val Asp Ala Ala Phe Xaa Pro Val Tyr Trp Leu
65   70   75   80

Val Asp Asn Val Ile Arg Trp Phe Gly Val Val Phe Val Val Leu Val
                85   90   95

Ile Val Leu Thr Gly Ser Ile Val Ala Ile Ala Tyr Leu Cys Val Leu
            100   105   110

Pro Leu Ile Leu Arg Thr Tyr Ser Val Pro Arg Leu Cys Trp His Phe
        115   120   125

Phe Tyr Ser His Trp Asn Leu Ile Leu Ile Val Phe His Tyr Tyr Gln
    130   135   140

Ala Ile Thr Thr Pro Pro Gly Tyr Pro Pro Gln Gly Arg Asn Asp Ile
145   150   155   160

Ala Thr Val Ser Ile Cys Lys Lys Cys Ile Tyr Pro Lys Pro Ala Arg
                165   170   175

Thr His His Cys Ser Ile Cys Asn Arg Cys Val Leu Lys Met Asp His
            180   185   190

His Cys Pro Trp Leu Asn Asn Cys Val Gly His Tyr Asn His Arg Tyr
        195   200   205

Phe Phe Ser Phe Cys Phe Phe Met Thr Leu Gly Cys Val Tyr Cys Ser
    210   215   220

Tyr Gly Ser Trp Asp Leu Phe Arg Glu Ala Tyr Ala Ala Ile Glu Lys
225   230   235   240

Met Lys Gln Leu Asp Lys Asn Lys Leu Gln Ala Val Ala Asn Gln Thr
245 250 255

Tyr His Gln Thr Pro Pro Pro Thr Phe Ser Phe Arg Glu Arg Met Thr
260 265 270

His Lys Ser Leu Val Tyr Leu Trp Phe Leu Cys Ser Ser Val Ala Leu
275 280 285

Ala Leu Gly Ala Leu Thr Val Trp His Ala Val Leu Ile Ser Arg Gly
290 295 300

Glu Thr Ser Ile Glu Arg His Ile Asn Lys Lys Glu Arg Arg Arg Leu
305 310 315 320

Gln Ala Lys Gly Arg Val Phe Arg Asn Pro Tyr Asn Tyr Gly Cys Leu
325 330 335

Asp Asn Trp Lys Val Phe Leu Gly Val Asp Thr Gly Arg His Trp Leu
340 345 350

Thr Arg Val Leu Leu Pro Ser Ser His Leu Pro His Gly Asn Gly Met
355 360 365

Ser Trp Glu Pro Pro Pro Trp Val Thr Ala His Ser Ala Ser Val Met
370 375 380

Ala Val
385

<210> 1278
<211> 164
<212> PRT
<213> Homo sapiens

<400> 1278
Val Lys Ala Ser Ala Glu Thr Pro Arg Pro Gln Pro Val Asp Lys Leu
1 5 10 15

Glu Lys Ile Leu Glu Lys Leu Leu Thr Arg Phe Pro Gln Cys Asn Lys
20 25 30

Ala Gln Met Thr Asn Ile Leu Gln Gln Ile Lys Thr Ala Arg Thr Thr
35 40 45

Met Ala Gly Leu Thr Met Glu Glu Leu Ile Gln Leu Val Ala Ala Arg
50 55 60

```
Leu Ala Glu His Glu Arg Val Ala Ala Ser Thr Gln Pro Leu Gly Arg
 65                 70                  75                  80

Ile Arg Ala Leu Phe Pro Ala Pro Leu Ala Gln Ile Ser Thr Pro Met
                85                  90                  95

Phe Leu Pro Ser Ala Gln Val Ser Tyr Pro Gly Arg Ser Ser His Ala
            100                 105                 110

Pro Ala Thr Cys Lys Leu Cys Leu Met Cys Gln Lys Leu Val Gln Pro
        115                 120                 125

Ser Glu Leu His Pro Met Ala Cys Thr His Val Leu His Lys Glu Cys
    130                 135                 140

Ile Lys Phe Trp Ala Gln Thr Asn Thr Asn Asp Thr Cys Pro Phe Cys
145                 150                 155                 160

Pro Thr Leu Lys



<210> 1279
<211> 469
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (81)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1279
Pro Val Ala Val Gly Arg Val Arg Val Thr Ala Glu Gly Arg Xaa Met
  1               5                  10                  15

Val Leu Gln Thr Thr Lys Gly Leu Arg Leu Leu Phe Asp Gly Asp Ala
             20                  25                  30

His Leu Leu Met Ser Ile Pro Ser Pro Phe Arg Gly Arg Leu Cys Gly
        35                  40                  45

Leu Cys Gly Asn Phe Asn Gly Asn Trp Ser Asp Asp Phe Val Leu Pro
    50                  55                  60
```

Asn Gly Ser Ala Ala Ser Ser Val Glu Thr Phe Gly Ala Ala Trp Arg
65 70 75 80

Xaa Pro Gly Ser Ser Lys Gly Cys Gly Glu Gly Cys Gly Pro Gln Gly
85 90 95

Cys Pro Val Cys Leu Ala Glu Glu Thr Ala Pro Tyr Glu Ser Asn Glu
100 105 110

Ala Cys Gly Gln Leu Arg Asn Pro Gln Gly Pro Phe Ala Thr Cys Gln
115 120 125

Ala Val Leu Ser Pro Ser Glu Tyr Phe Arg Gln Cys Val Tyr Asp Leu
130 135 140

Cys Ala Gln Lys Gly Asp Lys Ala Phe Leu Cys Arg Ser Leu Ala Ala
145 150 155 160

Tyr Thr Ala Ala Cys Gln Ala Ala Gly Val Ala Val Lys Pro Trp Arg
165 170 175

Thr Asp Ser Phe Cys Pro Leu His Cys Pro Ala His Ser His Tyr Ser
180 185 190

Ile Cys Thr Arg Thr Cys Gln Gly Ser Cys Ala Ala Leu Ser Gly Leu
195 200 205

Thr Gly Cys Thr Thr Arg Cys Phe Glu Gly Cys Glu Cys Asp Asp Arg
210 215 220

Phe Leu Leu Ser Gln Gly Val Cys Ile Pro Val Gln Asp Cys Gly Cys
225 230 235 240

Thr His Asn Gly Arg Tyr Leu Pro Val Asn Ser Ser Leu Leu Thr Ser
245 250 255

Asp Cys Ser Glu Arg Cys Ser Cys Ser Ser Ser Ser Gly Leu Thr Cys
260 265 270

Gln Ala Ala Gly Cys Pro Pro Gly Arg Val Cys Glu Val Lys Ala Glu
275 280 285

Ala Arg Asn Cys Trp Ala Thr Arg Gly Leu Cys Val Leu Ser Val Gly
290 295 300

Ala Asn Leu Thr Thr Phe Asp Gly Ala Arg Gly Ala Thr Thr Ser Pro
305 310 315 320

Gly Val Tyr Glu Leu Ser Ser Arg Cys Pro Gly Leu Gln Asn Thr Ile
325 330 335

Pro Trp Tyr Arg Val Val Ala Glu Val Gln Ile Cys His Gly Lys Thr
340 345 350

Glu Ala Val Gly Gln Val His Ile Phe Phe Gln Asp Gly Met Val Thr
355 360 365

Leu Thr Pro Asn Lys Gly Val Trp Val Asn Gly Leu Arg Val Asp Leu
370 375 380

Pro Ala Glu Lys Leu Ala Ser Val Ser Val Ser Arg Thr Pro Asp Gly
385 390 395 400

Ser Leu Leu Val Arg Gln Lys Ala Gly Val Gln Val Trp Leu Gly Ala
405 410 415

Asn Gly Lys Val Ala Val Ile Val Ser Asn Asp His Ala Gly Lys Leu
420 425 430

Cys Gly Ala Cys Gly Asn Phe Asp Gly Asp Gln Thr Asn Asp Trp His
435 440 445

Asp Ser Gln Glu Lys Pro Ala Met Glu Lys Trp Arg Ala Gln Asp Phe
450 455 460

Ser Pro Cys Tyr Gly
465

<210> 1280
<211> 223
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (216)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (217)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1280
Gly Pro Arg Ala Leu Trp Pro Pro Pro Glu Val Gly Trp Gly Cys Ser
1 5 10 15

Pro Asn Pro Thr Leu Leu Pro Pro Leu Ser His Phe Pro Leu Leu Arg
20 25 30

```
Trp Gly Thr Asn Asn Lys Glu Leu Thr Leu Pro Ala Pro Asn Pro Pro
        35                  40                  45

Pro Ala Pro Pro Cys Pro Pro Arg Phe Trp Phe His Phe Ser Ser Val
    50                  55                  60

His Lys Leu Pro Leu Asp Ser Cys Val Val Phe Cys Ser Met Phe His
65                  70                  75                  80

Ser Ser Thr Ser Val Ile Ala Ala Ala Thr Ser Ala Lys Cys Ser Ser
                85                  90                  95

Ser Leu Pro Pro Val Leu Pro Thr Ile Pro Ser Pro Lys Ile Leu Phe
            100                 105                 110

Val Gly Lys Arg Gly Trp Gly Met Ala Gly Trp Val Thr Asp Tyr Pro
        115                 120                 125

Ser Pro Arg Glu Gly Gly Ala Leu Pro Leu Gly Cys Cys Ser Arg Val
    130                 135                 140

Ser Lys Gly Ala Arg Ile Asp His Lys Gly Cys Arg Gly His Leu Leu
145                 150                 155                 160

Pro Leu Phe Cys Trp Gly Gly Val Ala Met Ile Cys Pro Ser Leu Gly
                165                 170                 175

Leu Pro Leu Trp Phe Pro Ile Cys Ser Tyr Leu Asn Lys Lys Asn Ile
            180                 185                 190

Leu Phe Trp Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
        195                 200                 205

Lys Lys Lys Lys Lys Lys Lys Xaa Xaa Gly Gly Ala Pro Pro Pro
    210                 215                 220
```

<210> 1281
<211> 37
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (31)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1281

```
Thr Gln Ser Lys Trp Arg Leu Glu Val Gln Cys Gly Lys Glu Lys Gln
 1               5                  10                  15
```

Val Phe Ile Glu Ser Thr Asn Ser Thr Pro Phe Lys Asn Phe Xaa Gly
20 25 30

Thr Gln Pro Lys Gly
35

<210> 1282
<211> 458
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (249)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1282
Gly Pro Gln Arg Leu Ser Pro Gly Ala Met Leu Pro Ala Ala Thr Ala
1 5 10 15

Ser Leu Leu Gly Pro Leu Leu Thr Ala Cys Ala Leu Leu Pro Phe Ala
20 25 30

Gln Gly Gln Thr Pro Asn Tyr Thr Arg Pro Val Phe Leu Cys Gly Gly
35 40 45

Asp Val Lys Gly Glu Ser Gly Tyr Val Ala Ser Glu Gly Phe Pro Asn
50 55 60

Leu Tyr Pro Pro Asn Lys Glu Cys Ile Trp Thr Ile Thr Val Pro Glu
65 70 75 80

Gly Gln Thr Val Ser Leu Ser Phe Arg Val Phe Asp Leu Glu Leu His
85 90 95

Pro Ala Cys Arg Tyr Asp Ala Leu Glu Val Phe Ala Gly Ser Gly Thr
100 105 110

Ser Gly Gln Arg Leu Gly Arg Phe Cys Gly Thr Phe Arg Pro Ala Pro
115 120 125

Leu Val Ala Pro Gly Asn Gln Val Thr Leu Arg Met Thr Thr Asp Glu
130 135 140

Gly Thr Gly Gly Arg Gly Phe Leu Leu Trp Tyr Ser Gly Arg Ala Thr
145 150 155 160

Ser Gly Thr Glu His Gln Phe Cys Gly Gly Arg Leu Glu Lys Ala Gln

165 170 175

Gly Thr Leu Thr Thr Pro Asn Trp Pro Glu Ser Asp Tyr Pro Pro Gly
180 185 190

Ile Ser Cys Ser Trp His Ile Ile Ala Pro Pro Asp Gln Val Ile Ala
195 200 205

Leu Thr Phe Glu Lys Phe Asp Leu Glu Pro Asp Thr Tyr Cys Arg Tyr
210 215 220

Asp Ser Val Ser Val Phe Asn Gly Ala Val Ser Asp Asp Ser Arg Arg
225 230 235 240

Leu Gly Lys Phe Cys Gly Asp Ala Xaa Pro Gly Ser Ile Ser Ser Glu
245 250 255

Gly Asn Glu Leu Leu Val Gln Phe Val Ser Asp Leu Ser Val Thr Ala
260 265 270

Asp Gly Phe Ser Ala Ser Tyr Lys Thr Leu Pro Arg Gly Thr Ala Lys
275 280 285

Glu Gly Gln Gly Pro Gly Pro Lys Arg Gly Thr Glu Pro Lys Val Lys
290 295 300

Leu Pro Pro Lys Ser Gln Pro Pro Glu Lys Thr Glu Glu Ser Pro Ser
305 310 315 320

Ala Pro Asp Ala Pro Thr Cys Pro Lys Gln Cys Arg Arg Thr Gly Thr
325 330 335

Leu Gln Ser Asn Phe Cys Ala Ser Ser Leu Val Val Thr Ala Thr Val
340 345 350

Lys Ser Met Val Arg Glu Pro Gly Glu Gly Leu Ala Val Thr Val Ser
355 360 365

Leu Ile Gly Ala Tyr Lys Thr Gly Gly Leu Asp Leu Pro Ser Pro Pro
370 375 380

Thr Gly Ala Ser Leu Lys Phe Tyr Val Pro Cys Lys Gln Cys Pro Pro
385 390 395 400

Met Lys Lys Gly Val Ser Tyr Leu Leu Met Gly Gln Val Glu Glu Asn
405 410 415

Arg Gly Pro Val Leu Pro Pro Glu Ser Phe Val Val Leu His Arg Pro
420 425 430

Asn Gln Asp Gln Ile Leu Thr Asn Leu Ser Lys Arg Lys Cys Pro Ser

435 440 445

Gln Pro Val Arg Ala Ala Ala Ser Gln Asp
450 455

<210> 1283
<211> 229
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (45)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (154)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (155)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1283
Cys Arg Ala Pro Leu Gly Ala Gly Leu Ser Pro Ala Val Arg Arg Gln
1 5 10 15

Glu Pro Pro Phe Pro Leu Gly Val Thr Arg Gly Trp Gly Arg Trp Pro
20 25 30

Ile Gln Lys Arg Arg Glu Gly Ala Arg Pro Val Pro Xaa Ser Glu Arg
35 40 45

Ser Gln Glu Asp Gly Arg Gly Pro Ala Ala Arg Ser Ser Gly Thr Leu
50 55 60

Trp Arg Ile Arg Thr Arg Leu Ser Leu Cys Arg Asp Pro Glu Pro Pro
65 70 75 80

Pro Pro Leu Cys Leu Leu Arg Val Ser Leu Leu Cys Ala Leu Arg Ala
85 90 95

Gly Gly Arg Gly Ser Arg Trp Gly Glu Asp Gly Ala Arg Leu Leu Leu
100 105 110

Leu Pro Pro Ala Arg Ala Ala Gly Asn Gly Glu Ala Glu Pro Ser Gly
115 120 125

Gly Pro Ser Tyr Ala Gly Arg Met Leu Glu Ser Ser Gly Cys Lys Ala
    130   135   140

Leu Lys Glu Gly Val Leu Glu Lys Arg Xaa Xaa Gly Cys Cys Ser Ser
145   150   155   160

Gly Arg Lys Ser Val Ala Ser Ser Pro Arg Lys Gly Cys Cys Leu Ser
                165   170   175

Arg Pro Ser Ser Cys Asn Thr Ser Ser Ser Ser Asn Ser Ser Ser Ser
            180   185   190

Ser Ser Asn Asn Ser Pro Gly Arg Gly Arg Pro Ser Arg Pro Asn Pro
        195   200   205

Val Ala Pro Leu Ser Pro Ala Ser Ser Arg Arg Ser Ser Ser Arg Asn
    210   215   220

Cys Thr Ser Pro Thr
225

<210> 1284
<211> 390
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (52)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1284
Thr Ser Val Ala Ala Ala Ala Ala Arg Gly Arg Ala Gly Cys Pro Leu
  1   5   10   15

Thr Ala Ala Ser Ala Ala Arg Phe Lys Met Ala Ala Cys Ser His Ser
            20   25   30

Phe Ser Ala Glu Arg Leu Leu Thr Phe Ile Val Phe Ser Ala Arg Phe
        35   40   45

Asp Arg Leu Xaa Pro Ala Ala Leu Ser Gly Ile Phe Tyr Gln Ala Glu
     50   55   60

Met His Arg Thr Thr Arg Ile Lys Ile Thr Glu Leu Asn Pro His Leu
 65   70   75   80

Met Cys Val Leu Cys Gly Gly Tyr Phe Ile Asp Ala Thr Thr Ile Ile

85 90 95

Glu Cys Leu His Ser Phe Cys Lys Thr Cys Ile Val Arg Tyr Leu Glu
100 105 110

Thr Ser Lys Tyr Cys Pro Ile Cys Asp Val Gln Val His Lys Thr Arg
115 120 125

Pro Leu Leu Asn Ile Arg Ser Asp Lys Thr Leu Gln Asp Ile Val Tyr
130 135 140

Lys Leu Val Pro Gly Leu Phe Lys Asn Glu Met Lys Arg Arg Arg Asp
145 150 155 160

Phe Tyr Ala Ala His Pro Ser Ala Asp Ala Ala Asn Gly Ser Asn Glu
165 170 175

Asp Arg Gly Glu Val Ala Asp Glu Asp Lys Arg Ile Ile Thr Asp Asp
180 185 190

Glu Ile Ile Ser Leu Ser Ile Glu Phe Phe Asp Gln Asn Arg Leu Asp
195 200 205

Arg Lys Val Asn Lys Asp Lys Glu Lys Ser Lys Glu Glu Val Asn Asp
210 215 220

Lys Arg Tyr Leu Arg Cys Pro Ala Ala Met Thr Val Met His Leu Arg
225 230 235 240

Lys Phe Leu Arg Ser Lys Met Asp Ile Pro Asn Thr Phe Gln Ile Asp
245 250 255

Val Met Tyr Glu Glu Glu Pro Leu Lys Asp Tyr Tyr Thr Leu Met Asp
260 265 270

Ile Ala Tyr Ile Tyr Thr Trp Arg Arg Asn Gly Pro Leu Pro Leu Lys
275 280 285

Tyr Arg Val Arg Pro Thr Cys Lys Arg Met Lys Ile Ser His Gln Arg
290 295 300

Asp Gly Leu Thr Asn Ala Gly Glu Leu Glu Ser Asp Ser Gly Ser Asp
305 310 315 320

Lys Ala Asn Ser Pro Ala Gly Gly Ile Pro Ser Thr Ser Ser Cys Leu
325 330 335

Pro Ser Pro Ser Thr Pro Val Gln Ser Pro His Pro Gln Phe Pro His
340 345 350

Ile Ser Ser Thr Met Asn Gly Thr Ser Asn Ser Pro Ser Gly Asn His

355 360 365

Gln Ser Ser Phe Ala Asn Arg Pro Arg Lys Ser Ser Val Asn Gly Ser
370 375 380

Ser Ala Thr Ser Ser Gly
385 390

<210> 1285
<211> 39
<212> PRT
<213> Homo sapiens

<400> 1285
His Ala Ser Ala Gly Ser Gln Leu Phe Glu Met His Glu Lys Leu Ser
1 5 10 15

Cys Met Ala Asn Ser Val Ile Lys Asn Leu Gln Ser Arg Trp Arg Ser
20 25 30

Pro Ser His Glu Asn Ser Ile
35

<210> 1286
<211> 453
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (38)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (101)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (110)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (286)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1286

Arg Arg Ser Val Ile Cys Asp Ser Asn Ala Thr Ala Leu Glu Leu Pro
1 5 10 15

Gly Leu Pro Leu Ser Leu Pro Gln Pro Ser Ile Pro Ala Ala Val Pro
20 25 30

Gln Ser Ala Pro Pro Xaa Pro His Arg Glu Glu Thr Val Thr Ala Thr
35 40 45

Ala Thr Ser Gln Val Ala Gln Gln Pro Pro Ala Ala Ala Ala Pro Gly
50 55 60

Glu Gln Ala Val Ala Gly Pro Ala Pro Arg Leu Ser Pro Ala Val Pro
65 70 75 80

Ala Lys Thr Ala Gln Cys Pro Ser Leu Ala Leu Trp Gly Ala Lys Arg
85 90 95

Ser Arg Arg Arg Xaa Lys Val Ala Ala Ala Ala Gln Ala Xaa Lys Glu
100 105 110

Pro Gln Glu Glu Arg Ser Gln Gln Gln Asp Asp Ile Glu Glu Leu Glu
115 120 125

Thr Lys Ala Val Gly Met Ser Asn Asp Gly Arg Phe Leu Lys Phe Asp
130 135 140

Ile Glu Ile Gly Arg Gly Ser Phe Lys Thr Val Tyr Lys Gly Leu Asp
145 150 155 160

Thr Glu Thr Thr Val Glu Val Ala Trp Cys Glu Leu Gln Asp Arg Lys
165 170 175

Leu Thr Lys Ser Glu Arg Gln Arg Phe Lys Glu Glu Ala Glu Met Leu
180 185 190

Lys Gly Leu Gln His Pro Asn Ile Val Arg Phe Tyr Asp Ser Trp Glu
195 200 205

Ser Thr Val Lys Gly Lys Lys Cys Ile Val Leu Val Thr Glu Leu Met
210 215 220

Thr Ser Gly Thr Leu Lys Thr Tyr Leu Lys Arg Phe Lys Val Met Lys
225 230 235 240

Ile Lys Val Leu Arg Ser Trp Cys Arg Gln Ile Leu Lys Gly Leu Gln
245 250 255

Phe Leu His Thr Arg Thr Pro Pro Ile Ile His Arg Asp Leu Lys Cys

260 265 270

Asp Asn Ile Phe Ile Thr Gly Pro Thr Gly Ser Val Lys Xaa Gly Asp
275 280 285

Leu Gly Leu Ala Thr Leu Lys Arg Ala Ser Phe Ala Lys Ser Val Ile
290 295 300

Gly Thr Pro Glu Phe Met Ala Pro Glu Met Tyr Glu Glu Lys Tyr Asp
305 310 315 320

Glu Ser Val Asp Val Tyr Ala Phe Gly Met Cys Met Leu Glu Met Ala
325 330 335

Thr Ser Glu Tyr Pro Tyr Ser Glu Cys Gln Asn Ala Ala Gln Ile Tyr
340 345 350

Arg Arg Val Thr Ser Gly Val Lys Pro Ala Ser Phe Asp Lys Val Ala
355 360 365

Ile Pro Glu Val Lys Glu Ile Ile Glu Gly Cys Ile Arg Gln Asn Lys
370 375 380

Asp Glu Arg Tyr Ser Ile Lys Asp Leu Leu Asn His Ala Phe Phe Gln
385 390 395 400

Glu Glu Thr Gly Val Arg Val Glu Leu Ala Glu Glu Asp Asp Gly Glu
405 410 415

Lys Ile Ala Ile Lys Leu Trp Leu Arg Ile Glu Asp Ile Lys Lys Leu
420 425 430

Lys Gly Lys Tyr Lys Asp Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
435 440 445

Asn Thr His Arg Ala
450

<210> 1287
<211> 450
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (33)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (41)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (43)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (116)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (193)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (314)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (326)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (344)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1287
Ala Ala Glu Val Leu Cys Pro Ser Cys Phe Pro Ile Ser Pro Ala Pro
1 5 10 15

Trp Met Thr Val Gly Pro Ala Ser Ala Leu Phe Pro Cys Gln Thr Pro
20 25 30

Xaa Phe Pro Trp Thr Glu Trp Asn Xaa Trp Xaa Phe Thr Ala His Val
35 40 45

Leu Ser Gln Lys Phe Glu Lys Glu Leu Ser Lys Val Arg Glu Tyr Val
50 55 60

Gln Leu Ile Ser Val Tyr Glu Lys Lys Leu Leu Asn Leu Thr Val Arg
65 70 75 80

Ile Asp Ile Met Glu Lys Asp Thr Ile Ser Tyr Thr Glu Leu Asp Phe

85 90 95

Glu Leu Ile Lys Val Glu Val Lys Glu Met Glu Lys Leu Val Ile Gln
100 105 110

Leu Lys Glu Xaa Phe Gly Gly Ser Ser Glu Ile Val Asp Gln Leu Glu
115 120 125

Val Glu Ile Arg Asn Met Thr Leu Leu Val Glu Lys Leu Glu Thr Leu
130 135 140

Asp Lys Asn Asn Val Leu Ala Ile Arg Arg Glu Ile Val Ala Leu Lys
145 150 155 160

Thr Lys Leu Lys Glu Cys Glu Ala Ser Lys Asp Gln Asn Thr Pro Val
165 170 175

Val His Pro Pro Pro Thr Pro Gly Ser Cys Gly His Gly Gly Val Val
180 185 190

Xaa Ile Ser Lys Pro Ser Val Val Gln Leu Asn Trp Arg Gly Phe Ser
195 200 205

Tyr Leu Tyr Gly Ala Trp Gly Arg Asp Tyr Ser Pro Gln His Pro Asn
210 215 220

Lys Gly Leu Tyr Trp Val Ala Pro Leu Asn Thr Asp Gly Arg Leu Leu
225 230 235 240

Glu Tyr Tyr Arg Leu Tyr Asn Thr Leu Asp Asp Leu Leu Leu Tyr Ile
245 250 255

Asn Ala Arg Glu Leu Arg Ile Thr Tyr Gly Gln Gly Ser Gly Thr Ala
260 265 270

Val Tyr Asn Asn Asn Met Tyr Val Asn Met Tyr Asn Thr Gly Asn Ile
275 280 285

Ala Arg Val Asn Leu Thr Thr Asn Thr Ile Ala Val Thr Gln Thr Leu
290 295 300

Pro Asn Ala Ala Tyr Asn Asn Arg Phe Xaa Tyr Ala Asn Val Ala Trp
305 310 315 320

Gln Asp Ile Asp Phe Xaa Val Asp Glu Asn Gly Leu Trp Val Ile Tyr
325 330 335

Ser Thr Glu Ala Ser Thr Gly Xaa Met Val Ile Ser Lys Leu Asn Asp
340 345 350

Thr Thr Leu Gln Val Leu Asn Thr Trp Tyr Thr Lys Gln Tyr Lys Pro

355 360 365

Ser Ala Ser Asn Ala Phe Met Val Cys Gly Val Leu Tyr Ala Thr Arg
370 375 380

Thr Met Asn Thr Arg Thr Glu Glu Ile Phe Tyr Tyr Tyr Asp Thr Asn
385 390 395 400

Thr Gly Lys Glu Gly Lys Leu Asp Ile Val Met His Lys Met Gln Glu
405 410 415

Lys Val Gln Ser Ile Asn Tyr Asn Pro Phe Asp Gln Lys Leu Tyr Val
420 425 430

Tyr Asn Asp Gly Tyr Leu Leu Asn Tyr Asp Leu Ser Val Leu Gln Lys
435 440 445

Pro Gln
450

<210> 1288
<211> 164
<212> PRT
<213> Homo sapiens

<400> 1288
Leu Gln Gln Ala Leu Pro Asn Asn Gly Leu Leu Phe Thr Trp Thr Leu
1 5 10 15

Ser Lys Glu Gly Gly Arg Glu Gly Gln Ser Gly Val Ser Phe Gln His
20 25 30

Ser Ser Gln Lys Gly Glu Arg Phe Ser Gly Trp Cys His Ala Ile Gly
35 40 45

Ile Lys Gln Glu Ala His Gly Trp Leu Leu Asn Glu Glu Gln Asn Leu
50 55 60

Gly Ala Leu Trp Leu Thr Thr Ala Ile Cys Gly Ala Gly Thr His Thr
65 70 75 80

Ser Arg Gln Leu Gln Phe Cys Thr Phe Ser Leu Leu Asp Ser Lys Ser
85 90 95

Arg Cys Cys Leu Ala Ala Leu Arg Gly His Ser Leu Leu Arg Arg Ala
100 105 110

Leu Gln Ser Pro Ala Pro Gly Leu Gly Glu Trp Met Arg Leu Leu Pro
115 120 125

```
Tyr Asp Thr Cys Gln Asp Ala Leu Pro Pro Pro Leu Lys Val Gly Pro
    130                 135                 140

Gly Gln His Cys Ser Leu Leu Ser Ala Phe Ser Gly Leu Arg Ser Gln
145                 150                 155                 160

Tyr Glu Leu Pro



<210> 1289
<211> 40
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (30)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1289
Trp Met Ser Glu Tyr Xaa Gln Trp Val Phe Leu Ile Ser Leu Arg Ile
  1               5                  10                  15

Cys Leu Arg Val His Tyr Gln Gly Ile Ser Gly Thr Arg Xaa His Ser
             20                  25                  30

Leu His Gln Phe Leu Arg Val Leu
         35                  40



<210> 1290
<211> 266
<212> PRT
<213> Homo sapiens

<400> 1290
Asp Ile Met Glu Ser Gly Phe Thr Ser Lys Asp Thr Tyr Leu Ser His
  1               5                  10                  15

Phe Asn Pro Arg Asp Tyr Leu Glu Lys Tyr Tyr Lys Phe Gly Ser Arg
             20                  25                  30
```

His Ser Ala Glu Ser Gln Ile Leu Lys His Leu Leu Lys Asn Leu Phe
35 40 45

Lys Ile Phe Cys Leu Asp Gly Val Lys Gly Asp Leu Leu Ile Asp Ile
50 55 60

Gly Ser Gly Pro Thr Ile Tyr Gln Leu Leu Ser Ala Cys Glu Ser Phe
65 70 75 80

Lys Glu Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu
85 90 95

Glu Lys Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val
100 105 110

Val Thr Tyr Val Cys Asp Leu Glu Gly Asn Arg Val Lys Gly Pro Glu
115 120 125

Lys Glu Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp
130 135 140

Val Thr Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp
145 150 155 160

Cys Val Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro
165 170 175

Thr Tyr Cys Arg Ala Leu Arg Asn Leu Gly Ser Leu Leu Lys Pro Gly
180 185 190

Gly Phe Leu Val Ile Met Asp Ala Leu Lys Ser Ser Tyr Tyr Met Ile
195 200 205

Gly Glu Gln Lys Phe Ser Ser Leu Pro Leu Gly Arg Glu Ala Val Glu
210 215 220

Ala Ala Val Lys Glu Ala Gly Tyr Thr Ile Glu Trp Phe Glu Val Ile
225 230 235 240

Ser Gln Ser Tyr Ser Ser Thr Met Ala Asn Asn Glu Gly Leu Phe Ser
245 250 255

Leu Val Ala Arg Lys Leu Ser Arg Pro Leu
260 265

<210> 1291
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1291
Cys Gly Ser Thr Ile Leu Gln Gly Pro Gln Lys Ala Leu Arg Arg Gly
1   5   10   15

Leu Gly Glu Val Gly Asp Gln Gly Lys Ser Arg Gln Arg Ala Ser Lys
            20   25   30

Arg Leu Phe Ala Ser Lys Ala Leu Arg Gly His Leu Arg Pro Val Arg
        35   40   45

Gly Gln Gln Pro Gly Arg Xaa Gly Ser Asp Glu Asn Glu Glu Ser Ser
    50   55   60

Val Val Asp Tyr Val Glu Val Thr Val Gly Glu Glu Asp Ala Ile Ser
65   70   75   80

Asp Arg Ser Asp Ser Trp Ser Gln Ala Ala Ala Glu Gly Val Ser Glu
                85   90   95

Leu Ala Glu Ser Asp Ser Asp Cys Val Pro Ala Glu Ala Gly Gln Ala
            100   105   110

<210> 1292
<211> 217
<212> PRT
<213> Homo sapiens

<400> 1292
Gly Ser Thr His Ala Ser Gly Thr Met Arg Ala Ala Ala Ile Ser Thr
1   5   10   15

Pro Lys Leu Asp Lys Met Pro Gly Met Phe Phe Ser Ala Asn Pro Lys
            20   25   30

Glu Leu Lys Gly Thr Thr His Ser Leu Leu Asp Asp Lys Met Gln Lys
        35   40   45

Arg Arg Pro Lys Thr Phe Gly Met Asp Met Lys Ala Tyr Leu Arg Ser
    50   55   60

Met Ile Pro His Leu Glu Ser Gly Met Lys Ser Ser Lys Ser Lys Asp
65 70 75 80

Val Leu Ser Ala Ala Glu Val Met Gln Trp Ser Gln Ser Leu Glu Lys
85 90 95

Leu Leu Ala Asn Gln Thr Gly Gln Asn Val Phe Gly Ser Phe Leu Lys
100 105 110

Ser Glu Phe Ser Glu Glu Asn Ile Glu Phe Trp Leu Ala Cys Glu Asp
115 120 125

Tyr Lys Lys Thr Glu Ser Asp Leu Leu Pro Cys Lys Ala Glu Glu Ile
130 135 140

Tyr Lys Ala Phe Val His Ser Asp Ala Ala Lys Gln Ile Asn Ile Asp
145 150 155 160

Phe Arg Thr Arg Glu Ser Thr Ala Lys Lys Ile Lys Ala Pro Thr Pro
165 170 175

Thr Cys Phe Asp Glu Ala Gln Lys Val Ile Tyr Thr Leu Met Glu Lys
180 185 190

Asp Ser Tyr Pro Arg Phe Leu Lys Ser Asp Ile Tyr Leu Asn Leu Leu
195 200 205

Asn Asp Leu Gln Ala Asn Ser Leu Lys
210 215

<210> 1293
<211> 235
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (229)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1293
Leu His Leu Leu Ala Val Leu Glu Lys Met Ile Ser Gln Gly Asn Asn
1 5 10 15

Asn Lys Asn Gly Lys Asn Glu Thr Gly Asn Asn Asn Asn Lys Asp Gly
20 25 30

Ser Asn His Lys Ala Glu Ser Gly Ala Leu Ile Glu Ala Ala Lys Ser
35 40 45

```
Lys Ile His Gln Tyr Lys Val Arg Ala Tyr Ile Gln Met Lys Ser Leu
     50                  55                  60

Lys Ala Cys Lys Arg Glu Ile Lys Ser Val Met Asn Thr Ala Gly Asn
 65                  70                  75                  80

Ser Ala Pro Ser Leu Phe Leu Lys Ser Asn Phe Glu Tyr Leu Arg Gly
                 85                  90                  95

Asn Tyr Arg Lys Ala Val Lys Leu Leu Asn Ser Ser Asn Ile Ala Glu
            100                 105                 110

His Pro Gly Phe Met Lys Thr Gly Glu Cys Leu Arg Cys Met Phe Trp
        115                 120                 125

Asn Asn Leu Gly Cys Ile His Phe Ala Met Ser Lys His Asn Leu Gly
    130                 135                 140

Ile Phe Tyr Phe Lys Lys Ala Leu Gln Glu Asn Asp Asn Val Cys Ala
145                 150                 155                 160

Gln Leu Ser Ala Gly Ser Thr Asp Pro Gly Lys Lys Phe Ser Gly Arg
                165                 170                 175

Pro Met Cys Thr Leu Leu Thr Asn Lys Arg Tyr Glu Leu Leu Tyr Asn
            180                 185                 190

Cys Gly Ile Gln Leu Leu His Ile Gly Arg Pro Leu Ala Ala Phe Glu
        195                 200                 205

Cys Leu Ile Glu Ala Val Gln Val Tyr His Ala Asn Pro Arg Leu Trp
    210                 215                 220

Leu Arg Leu Ala Xaa Met Leu His Cys Cys Gln
225                 230                 235
```

<210> 1294
<211> 275
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (23)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (50)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1294

```
Ala Arg Gly Ala Arg Gly Arg Ala Leu Pro Ala Ser Gly Lys Ala Gly
1               5                   10                  15

Arg Ala Arg Gly Ser Ala Xaa Gly Ser Ala Ala Arg Gly His Trp Ser
            20                  25                  30

Leu Ala Arg Phe Pro Ala Pro Arg Gly Ser His Leu Pro Ala Arg Arg
        35                  40                  45

Xaa Xaa Gly Arg Val Ser Thr Pro Ile Leu Arg Pro Val Ser Ser Ile
    50                  55                  60

Pro Leu Ala Leu Ser Arg Glu Ser Arg Thr Ala Glu Glu Ser Ser Leu
65                  70                  75                  80

Thr Pro Gln Pro Gln Val Gly Leu Val His Ile Met Thr Ser Phe Glu
                85                  90                  95

Asp Ala Asp Thr Glu Glu Thr Val Thr Cys Leu Gln Met Thr Val Tyr
            100                 105                 110

His Pro Gly Gln Leu Gln Cys Gly Ile Phe Gln Ser Ile Ser Phe Asn
        115                 120                 125

Arg Glu Lys Leu Pro Ser Ser Glu Val Val Lys Phe Gly Arg Asn Ser
    130                 135                 140

Asn Ile Cys His Tyr Thr Phe Gln Asp Lys Gln Val Ser Arg Val Gln
145                 150                 155                 160

Phe Ser Leu Gln Leu Phe Lys Lys Phe Asn Ser Ser Val Leu Ser Phe
                165                 170                 175

Glu Ile Lys Asn Met Ser Lys Lys Thr Asn Leu Ile Val Asp Ser Arg
            180                 185                 190

Glu Leu Gly Tyr Leu Asn Lys Met Asp Leu Pro Tyr Arg Cys Met Val
        195                 200                 205

Arg Phe Gly Glu Tyr Gln Phe Leu Met Glu Lys Glu Asp Gly Glu Ser
    210                 215                 220
```

Leu Glu Phe Phe Glu Thr Gln Phe Ile Leu Ser Pro Arg Ser Leu Leu
225 230 235 240

Gln Glu Asn Asn Trp Pro Pro His Arg Pro Ile Pro Glu Tyr Gly Thr
245 250 255

Tyr Ser Leu Cys Ser Ser Gln Ser Ser Ser Pro Thr Glu Met Asp Glu
260 265 270

Asn Glu Ser
275

<210> 1295
<211> 677
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (144)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (161)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1295
Met Thr Arg Leu Pro Lys Leu Trp Ala Arg Pro Ala Gly Lys Ala Leu
1 5 10 15

Val Ser Pro Val Val Gln Asn Ile Thr Ser Pro Asp Glu Asp Gly Ile
20 25 30

Ser Pro Leu Gly Trp Leu Leu Asp Gln Tyr Leu Glu Cys Gln Glu Ala
35 40 45

Val Phe Asn Pro Gln Ser Arg Gly Pro Ala Phe Phe Ser Arg Val Arg
50 55 60

Arg Leu Thr His Leu Leu Val His Val Glu Pro Cys Glu Ala Pro Pro
65 70 75 80

Pro Val Val Ala Thr Pro Arg Pro Lys Gly Arg Asn Arg Ser His Asp
85 90 95

Trp Ser Ser Leu Ala Thr Arg Gly Leu Pro Ser Ser Ile Met Arg Asn
100 105 110

Leu Thr Arg Cys Trp Arg Ala Val Val Glu Lys Gln Val Asn Asn Phe
115 120 125

Leu Thr Ser Ser Trp Arg Asp Asp Asp Phe Val Pro Arg Tyr Cys Xaa
130 135 140

His Phe Asn Ile Leu Gln Asn Ser Ser Ser Glu Leu Phe Gly Pro Arg
145 150 155 160

Xaa Ala Phe Leu Leu Ala Leu Gln Asn Gly Cys Ala Gly Ala Leu Leu
165 170 175

Lys Leu Pro Phe Leu Lys Ala Ala His Val Ser Glu Gln Phe Ala Arg
180 185 190

His Ile Asp Gln Gln Ile Gln Gly Ser Arg Ile Gly Gly Ala Gln Glu
195 200 205

Met Glu Arg Leu Ala Gln Leu Gln Gln Cys Leu Gln Ala Val Leu Ile
210 215 220

Phe Ser Gly Leu Glu Ile Ala Thr Thr Phe Glu His Tyr Tyr Gln His
225 230 235 240

Tyr Met Ala Asp Arg Leu Leu Gly Val Val Ser Ser Trp Leu Glu Gly
245 250 255

Ala Val Leu Glu Gln Ile Gly Pro Cys Phe Pro Asn Arg Leu Pro Gln
260 265 270

Gln Met Leu Gln Ser Leu Ser Thr Ser Lys Glu Leu Gln Arg Gln Phe
275 280 285

His Val Tyr Gln Leu Gln Gln Leu Asp Gln Glu Leu Leu Lys Leu Glu
290 295 300

Asp Thr Glu Lys Lys Ile Gln Val Gly Leu Gly Ala Ser Gly Lys Glu
305 310 315 320

His Lys Ser Glu Lys Glu Glu Glu Ala Gly Ala Ala Ala Val Val Asp
325 330 335

Val Ala Glu Gly Glu Glu Glu Glu Glu Glu Asn Glu Asp Leu Tyr Tyr
340 345 350

Glu Gly Ala Met Pro Glu Val Ser Val Leu Val Leu Ser Arg His Ser
355 360 365

Trp Pro Val Ala Ser Ile Cys His Thr Leu Asn Pro Arg Thr Cys Leu
370 375 380

Pro Ser Tyr Leu Arg Gly Thr Leu Asn Arg Tyr Ser Asn Phe Tyr Asn
385 390 395 400

Lys Ser Gln Ser His Pro Ala Leu Glu Arg Gly Ser Gln Arg Arg Leu
405 410 415

Gln Trp Thr Trp Leu Gly Trp Ala Glu Leu Gln Phe Gly Asn Gln Thr
420 425 430

Leu His Val Ser Thr Val Gln Met Trp Leu Leu Leu Tyr Leu Asn Asp
435 440 445

Leu Lys Ala Val Ser Val Glu Ser Leu Leu Ala Phe Ser Gly Leu Ser
450 455 460

Ala Asp Met Leu Asn Gln Ala Ile Gly Pro Leu Thr Ser Ser Arg Gly
465 470 475 480

Pro Leu Asp Leu His Glu Gln Lys Asp Ile Pro Gly Gly Val Leu Lys
485 490 495

Ile Arg Asp Gly Ser Lys Glu Pro Arg Ser Arg Trp Asp Ile Val Arg
500 505 510

Leu Ile Pro Pro Gln Thr Tyr Leu Gln Ala Glu Gly Glu Asp Gly Gln
515 520 525

Asn Leu Glu Lys Arg Arg Asn Leu Leu Asn Cys Leu Ile Val Arg Ile
530 535 540

Leu Lys Ala His Gly Asp Glu Gly Leu His Ile Asp Gln Leu Val Cys
545 550 555 560

Leu Val Leu Glu Ala Trp Gln Lys Gly Pro Cys Pro Pro Arg Gly Leu
565 570 575

Val Ser Ser Leu Gly Lys Gly Ser Ala Cys Ser Ser Thr Asp Val Leu
580 585 590

Ser Cys Ile Leu His Leu Leu Gly Lys Gly Thr Leu Arg Arg His Asp
595 600 605

Asp Arg Pro Gln Val Leu Ser Tyr Ala Val Pro Val Thr Val Met Glu
610 615 620

Pro His Thr Glu Ser Leu Asn Pro Gly Ser Ser Gly Pro Asn Pro Pro
625 630 635 640

Leu Thr Phe His Thr Leu Gln Ile Arg Ser Arg Gly Val Pro Tyr Ala
645 650 655

Ser Cys Thr Ala Thr Gln Ser Phe Ser Thr Ser Gly Ser Pro Arg Leu
660 665 670

Gly Val Arg Gly Arg
675

<210> 1296
<211> 578
<212> PRT
<213> Homo sapiens

<400> 1296
Gly Thr Arg Glu Gly Ala Arg Val Gly Gly Ala Arg Gly Gly Arg Asp
1 5 10 15

Gly Arg Lys Met Ala Thr Ala Thr Ile Ala Leu Gln Val Asn Gly Gln
20 25 30

Gln Gly Gly Gly Ser Glu Pro Ala Ala Ala Ala Ala Val Val Ala Ala
35 40 45

Gly Asp Lys Trp Lys Pro Pro Gln Gly Thr Asp Ser Ile Lys Met Glu
50 55 60

Asn Gly Gln Ser Thr Ala Ala Lys Leu Gly Leu Pro Pro Leu Thr Pro
65 70 75 80

Glu Gln Gln Glu Ala Leu Gln Lys Ala Lys Lys Tyr Ala Met Glu Gln
85 90 95

Ser Ile Lys Ser Val Leu Val Lys Gln Thr Ile Ala His Gln Gln Gln
100 105 110

Gln Leu Thr Asn Leu Gln Met Ala Ala Val Thr Met Gly Phe Gly Asp
115 120 125

Pro Leu Ser Pro Leu Gln Ser Met Ala Ala Gln Arg Gln Arg Ala Leu
130 135 140

Ala Ile Met Cys Arg Val Tyr Val Gly Ser Ile Tyr Tyr Glu Leu Gly
145 150 155 160

Glu Asp Thr Ile Arg Gln Ala Phe Ala Pro Phe Gly Pro Ile Lys Ser
165 170 175

Ile Asp Met Ser Trp Asp Ser Val Thr Met Lys His Lys Gly Phe Ala
180 185 190

Phe Val Glu Tyr Glu Val Pro Glu Ala Ala Gln Leu Ala Leu Glu Gln

```
        195                 200                 205

Met Asn Ser Val Met Leu Gly Gly Arg Asn Ile Lys Val Gly Arg Pro
    210                 215                 220

Ser Asn Ile Gly Gln Ala Gln Pro Ile Ile Asp Gln Leu Ala Glu Glu
225                 230                 235                 240

Ala Arg Ala Phe Asn Arg Ile Tyr Val Ala Ser Val His Gln Asp Leu
                245                 250                 255

Ser Asp Asp Asp Ile Lys Ser Val Phe Glu Ala Phe Gly Lys Ile Lys
            260                 265                 270

Ser Cys Thr Leu Ala Arg Asp Pro Thr Thr Gly Lys His Lys Gly Tyr
        275                 280                 285

Gly Phe Ile Glu Tyr Glu Lys Ala Gln Ser Ser Gln Asp Ala Val Ser
    290                 295                 300

Ser Met Asn Leu Phe Asp Leu Gly Gly Gln Tyr Leu Arg Val Gly Lys
305                 310                 315                 320

Ala Val Thr Pro Pro Met Pro Leu Leu Thr Pro Ala Thr Pro Gly Gly
                325                 330                 335

Leu Pro Pro Ala Ala Ala Val Ala Ala Ala Ala Ala Thr Ala Lys Ile
            340                 345                 350

Thr Ala Gln Glu Ala Val Ala Gly Ala Ala Val Leu Gly Thr Leu Gly
        355                 360                 365

Thr Pro Gly Leu Val Ser Pro Ala Leu Thr Leu Ala Gln Pro Leu Gly
    370                 375                 380

Thr Leu Pro Gln Ala Val Met Ala Ala Gln Ala Pro Gly Val Ile Thr
385                 390                 395                 400

Gly Val Thr Pro Ala Arg Pro Pro Ile Pro Val Thr Ile Pro Ser Val
                405                 410                 415

Gly Val Val Asn Pro Ile Leu Ala Ser Pro Pro Thr Leu Gly Leu Leu
            420                 425                 430

Glu Pro Lys Lys Glu Lys Glu Glu Glu Glu Leu Phe Pro Glu Ser Glu
        435                 440                 445

Arg Pro Glu Met Leu Ser Glu Gln Glu His Met Ser Ile Ser Gly Ser
    450                 455                 460

Ser Ala Arg His Met Val Met Gln Lys Leu Leu Arg Lys Gln Glu Ser
```

465 470 475 480

Thr Val Met Val Leu Arg Asn Met Val Asp Pro Lys Asp Ile Asp Asp
485 490 495

Asp Leu Glu Gly Glu Val Thr Glu Glu Cys Gly Lys Phe Gly Ala Val
500 505 510

Asn Arg Val Ile Ile Tyr Gln Glu Lys Gln Gly Glu Glu Glu Asp Ala
515 520 525

Glu Ile Ile Val Lys Ile Phe Val Glu Phe Ser Ile Ala Ser Glu Thr
530 535 540

His Lys Ala Ile Gln Ala Leu Asn Gly Arg Trp Phe Ala Gly Arg Lys
545 550 555 560

Val Val Ala Glu Val Tyr Asp Gln Glu Arg Phe Asp Asn Ser Asp Leu
565 570 575

Ser Ala

<210> 1297
<211> 179
<212> PRT
<213> Homo sapiens

<400> 1297
Pro Arg Gly Thr Ser Arg Arg Ser Ala Trp Pro Lys Met Ala Ala Ser
1 5 10 15

Val Cys Ser Gly Leu Leu Gly Pro Arg Val Leu Ser Trp Ser Arg Glu
20 25 30

Leu Pro Cys Ala Trp Arg Ala Leu His Thr Ser Pro Val Cys Ala Lys
35 40 45

Asn Arg Ala Ala Arg Val Arg Val Ser Lys Gly Asp Lys Pro Val Thr
50 55 60

Tyr Glu Glu Ala His Ala Pro His Tyr Ile Ala His Arg Lys Gly Trp
65 70 75 80

Leu Ser Leu His Thr Gly Asn Leu Asp Gly Glu Asp His Ala Ala Glu
85 90 95

Arg Thr Val Glu Asp Val Phe Leu Arg Lys Phe Met Trp Gly Thr Phe
100 105 110

Pro Gly Cys Leu Ala Asp Gln Leu Val Leu Lys Arg Arg Gly Asn Gln
115 120 125

Leu Glu Ile Cys Ala Val Val Leu Arg Gln Leu Ser Pro His Lys Tyr
130 135 140

Tyr Phe Leu Val Gly Tyr Ser Glu Thr Leu Leu Ser Tyr Phe Tyr Lys
145 150 155 160

Cys Pro Val Arg Leu His Leu Gln Thr Val Pro Ser Lys Val Val Tyr
165 170 175

Lys Tyr Leu

<210> 1298
<211> 155
<212> PRT
<213> Homo sapiens

<400> 1298
Gly Leu Val Thr Ile Phe Gly Cys Pro Ser Arg Glu Lys Gly Arg Met
1 5 10 15

Pro Leu Glu Ser Ser Ser Ser Met Pro Leu Ser Phe Pro Ser Leu Leu
20 25 30

Pro Ser Val Pro His Asn Thr Asn Pro Ser Pro Pro Leu Met Ser Tyr
35 40 45

Ile Thr Ser Gln Glu Met Lys Cys Ile Leu His Trp Phe Ala Asn Trp
50 55 60

Ser Gly Pro Gln Arg Glu Arg Phe Leu Glu Asp Leu Val Ala Lys Ala
65 70 75 80

Val Pro Glu Lys Leu Gln Pro Leu Leu Asp Ser Leu Glu Gln Leu Ser
85 90 95

Val Ser Gly Ala Asp Arg Pro Pro Ser Ile Phe Glu Cys Gln Leu His
100 105 110

Leu Trp Asp Gln Trp Phe Arg Gly Trp Ala Glu Gln Glu Arg Asn Glu
115 120 125

Phe Val Arg Gln Leu Glu Phe Ser Glu Pro Asp Phe Val Ala Lys Phe
130 135 140

Tyr Gln Ala Val Ala Ala Thr Ala Gly Lys Asp
145 150 155

<210> 1299
<211> 449
<212> PRT
<213> Homo sapiens

<400> 1299
Ser Asn Arg Lys Phe Ile Pro His Gln Leu Leu Val Ala Ile Asp Leu
1 5 10 15

Leu Ala Arg Gln Ala Val Arg Tyr Ile Asn Glu Asn Leu Ile Val Asn
20 25 30

Thr Asp Glu Leu Gly Arg Asp Cys Leu Ile Asn Ala Ala Lys Thr Ser
35 40 45

Met Ser Ser Lys Ile Ile Gly Ile Asn Gly Asp Phe Phe Ala Asn Met
50 55 60

Val Val Asp Ala Val Leu Ala Ile Lys Tyr Thr Asp Ile Arg Gly Gln
65 70 75 80

Pro Arg Tyr Pro Val Asn Ser Val Asn Ile Leu Lys Ala His Gly Arg
85 90 95

Ser Gln Met Glu Ser Met Leu Ile Ser Gly Tyr Ala Leu Asn Cys Val
100 105 110

Val Gly Ser Gln Gly Met Pro Lys Arg Ile Val Asn Ala Lys Ile Ala
115 120 125

Cys Leu Asp Phe Ser Leu Gln Lys Thr Lys Met Lys Leu Gly Val Gln
130 135 140

Val Val Ile Thr Asp Pro Glu Lys Leu Asp Gln Ile Arg Gln Arg Glu
145 150 155 160

Ser Asp Ile Thr Lys Glu Arg Ile Gln Lys Ile Leu Ala Thr Gly Ala
165 170 175

Asn Val Ile Leu Thr Thr Gly Gly Ile Asp Asp Met Cys Leu Lys Tyr
180 185 190

Phe Val Glu Ala Gly Ala Met Ala Val Arg Arg Val Leu Lys Arg Asp
195 200 205

Leu Lys Arg Ile Ala Lys Ala Ser Gly Ala Thr Ile Leu Ser Thr Leu

210 215 220

Ala Asn Leu Glu Gly Glu Glu Thr Phe Glu Ala Ala Met Leu Gly Gln
225 230 235 240

Ala Glu Glu Val Val Gln Glu Arg Ile Cys Asp Asp Glu Leu Ile Leu
245 250 255

Ile Lys Asn Thr Lys Ala Arg Thr Ser Ala Ser Ile Ile Leu Arg Gly
260 265 270

Ala Asn Asp Phe Met Cys Asp Glu Met Glu Arg Ser Leu His Asp Ala
275 280 285

Leu Cys Val Val Lys Arg Val Leu Glu Ser Lys Ser Val Val Pro Gly
290 295 300

Gly Gly Ala Val Glu Ala Ala Leu Ser Ile Tyr Leu Glu Asn Tyr Ala
305 310 315 320

Thr Ser Met Gly Ser Arg Glu Gln Leu Ala Ile Ala Glu Phe Ala Arg
325 330 335

Ser Leu Leu Val Ile Pro Asn Thr Leu Ala Val Asn Ala Ala Gln Asp
340 345 350

Ser Thr Asp Leu Val Ala Lys Leu Arg Ala Phe His Asn Glu Ala Gln
355 360 365

Val Asn Pro Glu Arg Lys Asn Leu Lys Trp Ile Gly Leu Asp Leu Ser
370 375 380

Asn Gly Lys Pro Arg Asp Asn Lys Gln Ala Gly Val Phe Glu Pro Thr
385 390 395 400

Ile Val Lys Val Lys Ser Leu Lys Phe Ala Thr Glu Ala Ala Ile Thr
405 410 415

Ile Leu Arg Ile Asp Asp Leu Ile Lys Leu His Pro Glu Ser Lys Asp
420 425 430

Asp Lys His Gly Ser Tyr Glu Asp Ala Val His Ser Gly Ala Leu Asn
435 440 445

Asp

<210> 1300
<211> 96

<212> PRT
<213> Homo sapiens

<400> 1300
Leu Met Phe Tyr Val Leu Phe Trp Thr Leu Ser Ser Cys Lys Asn Phe
1 5 10 15

Tyr Lys Asn Cys Phe Leu His Pro Cys Gly Ala Tyr Ser Ser Glu Pro
20 25 30

Ser Pro Gln Ser Gln Cys Leu Cys Phe Leu Phe Tyr Phe Cys Ser Ile
35 40 45

Arg Phe Leu Leu Leu Leu Cys Leu Lys Ser Ser Leu Gly Ser Tyr Gln
50 55 60

Gly Phe Ser Phe Cys Val Ala Phe Ala Ala Trp Ile Lys His Trp Leu
65 70 75 80

Thr Val Leu Met Cys Glu Glu Lys Lys Phe Ser Lys Ala Gly Glu Leu
85 90 95

<210> 1301
<211> 332
<212> PRT
<213> Homo sapiens

<400> 1301
Gly Glu Pro Lys Met Thr Gly Ser Asn Glu Phe Lys Leu Asn Gln Pro
1 5 10 15

Pro Glu Asp Gly Ile Ser Ser Val Lys Phe Ser Pro Asn Thr Ser Gln
20 25 30

Phe Leu Leu Val Ser Ser Trp Asp Thr Ser Val Arg Leu Tyr Asp Val
35 40 45

Pro Ala Asn Ser Met Arg Leu Lys Tyr Gln His Thr Gly Ala Val Leu
50 55 60

Asp Cys Ala Phe Tyr Asp Pro Thr His Ala Trp Ser Gly Gly Leu Asp
65 70 75 80

His Gln Leu Lys Met His Asp Leu Asn Thr Asp Gln Glu Asn Leu Val
85 90 95

Gly Thr His Asp Ala Pro Ile Arg Cys Val Glu Tyr Cys Pro Glu Val
100 105 110

Asn Val Met Val Thr Gly Ser Trp Asp Gln Thr Val Lys Leu Trp Asp
115 120 125

Pro Arg Thr Pro Cys Asn Ala Gly Thr Phe Ser Gln Pro Glu Lys Val
130 135 140

Tyr Thr Leu Ser Val Ser Gly Asp Arg Leu Ile Val Gly Thr Ala Gly
145 150 155 160

Arg Arg Val Leu Val Trp Asp Leu Arg Asn Met Gly Tyr Val Gln Gln
165 170 175

Arg Arg Glu Ser Ser Leu Lys Tyr Gln Thr Arg Cys Ile Arg Ala Phe
180 185 190

Pro Asn Lys Gln Gly Tyr Val Leu Ser Ser Ile Glu Gly Arg Val Ala
195 200 205

Val Glu Tyr Leu Asp Pro Ser Pro Glu Val Gln Lys Lys Lys Tyr Ala
210 215 220

Phe Lys Cys His Arg Leu Lys Glu Asn Asn Ile Glu Gln Ile Tyr Pro
225 230 235 240

Val Asn Ala Ile Ser Phe His Asn Ile His Asn Thr Phe Ala Thr Gly
245 250 255

Gly Ser Asp Gly Phe Val Asn Ile Trp Asp Pro Phe Asn Lys Lys Arg
260 265 270

Leu Cys Gln Phe His Arg Tyr Pro Thr Ser Ile Ala Ser Leu Ala Phe
275 280 285

Ser Asn Asp Gly Thr Thr Leu Ala Ile Ala Ser Ser Tyr Met Tyr Glu
290 295 300

Met Asp Asp Thr Glu His Pro Glu Asp Gly Ile Phe Ile Arg Gln Val
305 310 315 320

Thr Asp Ala Glu Thr Lys Pro Lys Ser Pro Cys Thr
325 330

<210> 1302
<211> 565
<212> PRT
<213> Homo sapiens

<400> 1302
Leu His Cys Thr Met Cys Gly Ile Trp Ala Leu Phe Gly Ser Asp Asp
1 5 10 15

Cys Leu Ser Val Gln Cys Leu Ser Ala Met Lys Ile Ala His Arg Gly
20 25 30

Pro Asp Ala Phe Arg Phe Glu Asn Val Asn Gly Tyr Thr Asn Cys Cys
35 40 45

Phe Gly Phe His Arg Leu Ala Val Val Asp Pro Leu Phe Gly Met Gln
50 55 60

Pro Ile Arg Val Lys Lys Tyr Pro Tyr Leu Trp Leu Cys Tyr Asn Gly
65 70 75 80

Glu Ile Tyr Asn His Lys Lys Met Gln Gln His Phe Glu Phe Glu Tyr
85 90 95

Gln Thr Lys Val Asp Gly Glu Ile Ile Leu His Leu Tyr Asp Lys Gly
100 105 110

Gly Ile Glu Gln Thr Ile Cys Met Leu Asp Gly Val Phe Ala Phe Val
115 120 125

Leu Leu Asp Thr Ala Asn Lys Lys Val Phe Leu Gly Arg Asp Thr Tyr
130 135 140

Gly Val Arg Pro Leu Phe Lys Ala Met Thr Glu Asp Gly Phe Leu Ala
145 150 155 160

Val Cys Ser Glu Ala Lys Gly Leu Val Thr Leu Lys His Ser Ala Thr
165 170 175

Pro Phe Leu Lys Val Glu Pro Phe Leu Pro Gly His Tyr Glu Val Leu
180 185 190

Asp Leu Lys Pro Asn Gly Lys Val Ala Ser Val Glu Met Val Lys Tyr
195 200 205

His His Cys Arg Asp Glu Pro Leu His Ala Leu Tyr Asp Asn Val Glu
210 215 220

Lys Leu Phe Pro Gly Phe Glu Ile Glu Thr Val Lys Asn Asn Leu Arg
225 230 235 240

Ile Leu Phe Asn Asn Ala Val Lys Lys Arg Leu Met Thr Asp Arg Arg
245 250 255

Ile Gly Cys Leu Leu Ser Gly Gly Leu Asp Ser Ser Leu Val Ala Ala

260 265 270

Thr Leu Leu Lys Gln Leu Lys Glu Ala Gln Val Gln Tyr Pro Leu Gln
275 280 285

Thr Phe Ala Ile Gly Met Glu Asp Ser Pro Asp Leu Leu Ala Ala Arg
290 295 300

Lys Val Ala Asp His Ile Gly Ser Glu His Tyr Glu Val Leu Phe Asn
305 310 315 320

Ser Glu Glu Gly Ile Gln Ala Leu Asp Glu Val Ile Phe Ser Leu Glu
325 330 335

Thr Tyr Asp Ile Thr Thr Val Arg Ala Ser Val Gly Met Tyr Leu Ile
340 345 350

Ser Lys Tyr Ile Arg Lys Asn Thr Asp Ser Val Val Ile Phe Ser Gly
355 360 365

Glu Gly Ser Asp Glu Leu Thr Gln Gly Tyr Ile Tyr Phe His Lys Ala
370 375 380

Pro Ser Pro Glu Lys Ala Glu Glu Glu Ser Glu Arg Leu Leu Arg Glu
385 390 395 400

Leu Tyr Leu Phe Asp Val Leu Arg Ala Asp Arg Thr Thr Ala Ala His
405 410 415

Gly Leu Glu Leu Arg Val Pro Phe Leu Asp His Arg Phe Ser Ser Tyr
420 425 430

Tyr Leu Ser Leu Pro Pro Glu Met Arg Ile Pro Lys Asn Gly Ile Glu
435 440 445

Lys His Leu Leu Arg Glu Thr Phe Glu Asp Ser Asn Leu Ile Pro Lys
450 455 460

Glu Ile Leu Trp Arg Pro Lys Glu Ala Phe Ser Asp Gly Ile Thr Ser
465 470 475 480

Val Lys Asn Ser Trp Phe Lys Ile Leu Gln Glu Tyr Val Glu His Gln
485 490 495

Val Asp Asp Ala Met Met Ala Asn Ala Ala Gln Lys Phe Pro Phe Asn
500 505 510

Thr Pro Lys Thr Lys Glu Gly Tyr Tyr Tyr Arg Gln Val Phe Glu Arg
515 520 525

His Tyr Pro Gly Arg Ala Asp Trp Leu Ser His Tyr Trp Met Pro Lys

530 535 540

Trp Ile Asn Ala Thr Asp Pro Ser Ala Arg Thr Leu Thr His Tyr Lys
545 550 555 560

Ser Ala Val Lys Ala
565

<210> 1303
<211> 441
<212> PRT
<213> Homo sapiens

<400> 1303
Arg Arg Arg Arg Ala Cys Arg Ser Ala Glu Gly Thr Gly Leu Arg Ser
1 5 10 15

Leu Leu Leu Pro Pro Arg Leu Gln Leu Pro Ala Gly Pro Phe Ser Arg
20 25 30

Cys Arg Trp Asp Pro Val Ser Ser Pro Arg Pro Ser Thr Met Pro Pro
35 40 45

Lys Lys Gly Gly Asp Gly Ile Lys Pro Pro Pro Ile Ile Gly Arg Phe
50 55 60

Gly Thr Ser Leu Lys Ile Gly Ile Val Gly Leu Pro Asn Val Gly Lys
65 70 75 80

Ser Thr Phe Phe Asn Val Leu Thr Asn Ser Gln Ala Ser Ala Glu Asn
85 90 95

Phe Pro Phe Cys Thr Ile Asp Pro Asn Glu Ser Arg Val Pro Val Pro
100 105 110

Asp Glu Arg Phe Asp Phe Leu Cys Gln Tyr His Lys Pro Ala Ser Lys
115 120 125

Ile Pro Ala Phe Leu Asn Val Val Asp Ile Ala Gly Leu Val Lys Gly
130 135 140

Ala His Asn Gly Gln Gly Leu Gly Asn Ala Phe Leu Ser His Ile Ser
145 150 155 160

Ala Cys Asp Gly Ile Phe His Leu Thr Arg Ala Phe Glu Asp Asp Asp
165 170 175

Ile Thr His Val Glu Gly Ser Val Asp Pro Ile Arg Asp Ile Glu Ile
180 185 190

Ile His Glu Glu Leu Gln Leu Lys Asp Glu Glu Met Ile Gly Pro Ile
195 200 205

Ile Asp Lys Leu Glu Lys Val Ala Val Arg Gly Gly Asp Lys Lys Leu
210 215 220

Lys Pro Glu Tyr Asp Ile Met Cys Lys Val Lys Ser Trp Val Ile Asp
225 230 235 240

Gln Lys Lys Pro Val Arg Phe Tyr His Asp Trp Asn Asp Lys Glu Ile
245 250 255

Glu Val Leu Asn Lys His Leu Phe Leu Thr Ser Lys Pro Met Val Tyr
260 265 270

Leu Val Asn Leu Ser Glu Lys Asp Tyr Ile Arg Lys Lys Asn Lys Trp
275 280 285

Leu Ile Lys Ile Lys Glu Trp Val Asp Lys Tyr Asp Pro Gly Ala Leu
290 295 300

Val Ile Pro Phe Ser Gly Ala Leu Glu Leu Lys Leu Gln Glu Leu Ser
305 310 315 320

Ala Glu Glu Arg Gln Lys Tyr Leu Glu Ala Asn Met Thr Gln Ser Ala
325 330 335

Leu Pro Lys Ile Ile Lys Ala Gly Phe Ala Ala Leu Gln Leu Glu Tyr
340 345 350

Phe Phe Thr Ala Gly Pro Asp Glu Val Arg Ala Trp Thr Ile Arg Lys
355 360 365

Gly Thr Lys Ala Pro Gln Ala Ala Gly Lys Ile His Thr Asp Phe Glu
370 375 380

Lys Gly Phe Ile Met Ala Glu Val Met Lys Tyr Glu Asp Phe Lys Glu
385 390 395 400

Glu Gly Ser Glu Asn Ala Val Lys Ala Ala Gly Lys Tyr Arg Gln Gln
405 410 415

Gly Arg Asn Tyr Ile Val Glu Asp Gly Asp Ile Ile Phe Phe Lys Phe
420 425 430

Asn Thr Pro Gln Gln Pro Lys Lys Lys
435 440

<210> 1304
<211> 94
<212> PRT
<213> Homo sapiens

<400> 1304
Glu Lys Lys Arg Gly Arg Glu Asp Lys Pro Gly Thr Met Ala Thr Phe
1   5   10   15

Pro Pro Ala Thr Ser Ala Pro Gln Gln Pro Pro Gly Pro Glu Asp Glu
            20   25   30

Asp Ser Ser Leu Asp Glu Ser Asp Leu Tyr Ser Leu Ala His Ser Tyr
        35   40   45

Leu Gly Gly Gly Gly Arg Lys Gly Arg Thr Lys Arg Glu Ala Ala Ala
    50   55   60

Asn Thr Asn Arg Pro Ser Pro Gly Gly His Glu Arg Lys Leu Val Thr
65   70   75   80

Lys Leu Gln Asn Ser Glu Arg Lys Lys Arg Gly Ala Arg Arg
                85   90

<210> 1305
<211> 82
<212> PRT
<213> Homo sapiens

<400> 1305
Val Ile Leu Glu Met Val Ile Val Phe Cys Leu Val Thr Phe Ala Thr
1   5   10   15

Val Pro Phe Lys Thr Met Trp Lys Pro Gln Val Cys Gly Gln His Arg
            20   25   30

Trp Asn Asp Ile Leu Cys Phe Leu Arg Leu Pro Ser Thr Arg His Ile
        35   40   45

Ser Leu Val Leu Gln Met Ser Ala Gln Val Leu Val Thr Ser Phe Ser
    50   55   60

Cys Cys Pro Gly Lys Ser Val Cys Ala Gly Ala Gly Ala Leu Ala Leu
65   70   75   80

Phe Arg

<210> 1306
<211> 231
<212> PRT
<213> Homo sapiens

<400> 1306
Ala Arg Glu Met Ala Ala Gln Gln Arg Asp Cys Gly Gly Ala Ala Gln
1 5 10 15

Leu Ala Gly Pro Ala Ala Glu Ala Asp Pro Leu Gly Arg Phe Thr Cys
20 25 30

Pro Val Cys Leu Glu Val Tyr Glu Lys Pro Val Gln Val Pro Cys Gly
35 40 45

His Val Phe Cys Ser Ala Cys Leu Gln Glu Cys Leu Lys Pro Lys Lys
50 55 60

Pro Val Cys Gly Val Cys Arg Ser Ala Leu Ala Pro Gly Val Arg Ala
65 70 75 80

Val Glu Leu Glu Arg Gln Ile Glu Ser Thr Glu Thr Ser Cys His Gly
85 90 95

Cys Arg Lys Asn Phe Phe Leu Ser Lys Ile Arg Ser His Val Ala Thr
100 105 110

Cys Ser Lys Tyr Gln Asn Tyr Ile Met Glu Gly Val Lys Ala Thr Ile
115 120 125

Lys Asp Ala Ser Leu Gln Pro Arg Asn Val Pro Asn Arg Tyr Thr Phe
130 135 140

Pro Cys Pro Tyr Cys Pro Glu Lys Asn Phe Asp Gln Glu Gly Leu Val
145 150 155 160

Glu His Cys Lys Leu Phe His Ser Thr Asp Thr Lys Ser Val Val Cys
165 170 175

Pro Ile Cys Ala Ser Met Pro Trp Gly Asp Pro Asn Tyr Arg Ser Ala
180 185 190

Asn Phe Arg Glu His Ile Gln Arg Arg His Arg Phe Ser Tyr Asp Thr
195 200 205

Phe Val Asp Tyr Asp Val Asp Glu Glu Asp Met Met Asn Gln Val Leu
210 215 220

Gln Arg Ser Ile Ile Asp Gln
225 230

<210> 1307
<211> 170
<212> PRT
<213> Homo sapiens

<400> 1307
Gln Lys Gln Arg Thr Phe Trp Lys Tyr Tyr Tyr Asp Gly Lys Asp Tyr
1   5   10   15

Ile Glu Phe Asn Lys Glu Ile Pro Ala Trp Val Pro Phe Asp Pro Ala
            20   25   30

Ala Gln Ile Thr Lys Gln Lys Trp Glu Ala Glu Pro Val Tyr Val Gln
        35   40   45

Arg Ala Lys Ala Tyr Leu Glu Glu Glu Cys Pro Ala Thr Leu Arg Lys
    50   55   60

Tyr Leu Lys Tyr Ser Lys Asn Ile Leu Asp Arg Gln Asp Pro Pro Ser
65   70   75   80

Val Val Val Thr Ser His Gln Ala Pro Gly Glu Lys Lys Lys Leu Lys
                85   90   95

Cys Leu Ala Tyr Asp Phe Tyr Pro Gly Lys Ile Asp Val His Trp Thr
            100   105   110

Arg Ala Gly Glu Val Gln Glu Pro Glu Leu Arg Gly Asp Val Leu His
        115   120   125

Asn Gly Asn Gly Thr Tyr Gln Ser Trp Val Val Val Ala Val Pro Pro
    130   135   140

Gln Asp Thr Ala Pro Tyr Ser Cys His Val Gln His Ser Ser Leu Ala
145   150   155   160

Gln Pro Leu Val Val Pro Trp Glu Ala Ser
                165   170

<210> 1308
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (95)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (104)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1308
Cys Ser Cys Thr Val Arg Ala Arg Arg Arg Leu Asn Arg Gly Leu Arg
1 5 10 15

Arg Lys Gln His Ser Leu Leu Lys Arg Leu Arg Lys Ala Lys Lys Glu
20 25 30

Ala Pro Pro Met Glu Lys Pro Glu Val Val Lys Thr His Leu Arg Asp
35 40 45

Met Ile Ile Leu Pro Glu Met Val Gly Ser Met Val Gly Val Tyr Asn
50 55 60

Gly Lys Thr Phe Asn Gln Val Glu Ile Lys Pro Glu Met Ile Gly His
65 70 75 80

Tyr Leu Gly Glu Phe Ser Ile Thr Tyr Lys Pro Val Lys His Xaa Arg
85 90 95

Pro Gly Ile Gly Ala Thr His Xaa Ser Arg Phe Ile Pro Leu Lys
100 105 110

<210> 1309
<211> 121
<212> PRT
<213> Homo sapiens

<400> 1309
Pro Val Ser Pro Gln Glu Arg Pro Pro Pro Tyr Leu Ala Val Pro Gly
1 5 10 15

His Gly Glu Glu Tyr Pro Val Ala Gly Ala His Ser Ser Pro Pro Lys
20 25 30

Ala Arg Phe Leu Arg Val Pro Ser Glu His Pro Tyr Leu Thr Pro Ser
35 40 45

Pro Glu Ser Pro Glu His Trp Ala Ser Pro Ser Pro Pro Ser Leu Ser
50 55 60

Asp Trp Ser Glu Ser Thr Pro Ser Pro Ala Thr Ala Thr Gly Ala Met

```
 65                  70                  75                  80

Ala Thr Thr Thr Gly Ala Leu Pro Ala Gln Pro Leu Pro Leu Ser Val
                85                  90                  95

Pro Ser Ser Leu Ala Gln Ala Gln Thr Gln Leu Gly Pro Gln Pro Glu
            100                 105                 110

Val Thr Pro Lys Arg Gln Val Leu Ala
        115                 120



<210> 1310
<211> 206
<212> PRT
<213> Homo sapiens

<400> 1310
Gln Cys Pro Gly Arg Ala Gly Ala Pro Gln Thr Arg Ala Pro Arg Ala
  1               5                  10                  15

Arg Glu Arg Gly Gly Ala Met Ala Thr Ala Asn Gly Ala Val Glu Asn
            20                  25                  30

Gly Gln Pro Asp Arg Lys Pro Pro Ala Leu Pro Arg Pro Ile Arg Asn
        35                  40                  45

Leu Glu Val Lys Phe Thr Lys Ile Phe Ile Asn Asn Glu Trp His Glu
    50                  55                  60

Ser Lys Ser Gly Lys Lys Phe Ala Thr Cys Asn Pro Ser Thr Arg Glu
 65                  70                  75                  80

Gln Ile Cys Glu Val Glu Glu Gly Asp Lys Pro Asp Val Asp Lys Ala
                85                  90                  95

Val Glu Ala Ala Gln Val Ala Phe Gln Arg Gly Ser Pro Trp Arg Arg
            100                 105                 110

Leu Asp Ala Leu Ser Arg Gly Arg Leu Leu His Gln Leu Ala Asp Leu
        115                 120                 125

Val Glu Arg Asp Arg Ala Thr Leu Ala Ala Leu Glu Thr Met Asp Thr
    130                 135                 140

Gly Lys Pro Phe Leu His Ala Phe Phe Ile Asp Leu Glu Gly Cys Ile
145                 150                 155                 160

Arg Thr Leu Arg Tyr Phe Ala Gly Trp Ala Asp Lys Ile Gln Gly Lys
                165                 170                 175
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Thr Ile Pro Thr Asp Asp Asn Val Cys Ala Ser Pro Gly Met Ser Pro
180 185 190

Leu Val Ser Val Gly Pro Ser Leu His Gly Thr Ser Pro Cys
195 200 205

<210> 1311
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1311
Ser Trp Glu Thr Glu Lys Met Gln Thr Ala Gly Ala Leu Phe Ile Ser
1 5 10 15

Pro Ala Leu Ile Arg Cys Cys Thr Arg Gly Leu Ile Arg Pro Val Ser
20 25 30

Ala Ser Phe Leu Asn Ser Pro Val Asn Ser Ser Lys Gln Pro Ser Tyr
35 40 45

Ser Asn Phe Pro Leu Gln Val Ala Arg Arg Glu Phe Gln Thr Ser Val
50 55 60

Val Ser Arg Asp Ile Asp Thr Ala Ala Lys Phe Ile Gly Ala Gly Ala
65 70 75 80

Ala Thr Val Gly Val Ala Gly Ser Gly Ala Gly Ile Gly Thr Val Phe
85 90 95

Gly Ser Leu Ile Ile Gly Tyr Ala Arg Asn Pro Ser Leu Lys Gln Gln
100 105 110

Leu Phe Ser Tyr Ala Ile Leu Gly Phe Ala Leu Ser Glu Ala Met Gly
115 120 125

Leu Phe Cys Leu Met Val Ala Phe Leu Ile Leu Phe Ala Met
130 135 140

<210> 1312
<211> 495
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (121)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (392)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (460)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1312
Arg Arg Met Glu Gly Gln Asp Glu Val Ser Ala Arg Glu Gln His Phe
1 5 10 15

His Ser Gln Val Arg Glu Ser Thr Ile Cys Phe Leu Leu Phe Ala Ile
20 25 30

Leu Tyr Val Val Ser Tyr Phe Ile Ile Thr Arg Tyr Lys Arg Lys Ser
35 40 45

Asp Glu Gln Glu Asp Glu Asp Ala Ile Val Asn Arg Ile Ser Leu Phe
50 55 60

Leu Ser Thr Phe Thr Leu Ala Val Ser Ala Gly Ala Val Leu Leu Leu
65 70 75 80

Pro Phe Ser Ile Ile Ser Asn Glu Ile Leu Leu Ser Phe Pro Gln Asn
85 90 95

Tyr Tyr Ile Gln Trp Leu Asn Gly Ser Leu Ile His Gly Leu Trp Asn
100 105 110

Leu Ala Ser Leu Phe Ser Asn Leu Xaa Leu Phe Val Leu Met Pro Phe
115 120 125

Ala Phe Phe Phe Leu Glu Ser Glu Gly Phe Ala Gly Leu Lys Lys Gly
130 135 140

Ile Arg Ala Arg Ile Leu Glu Thr Leu Val Met Leu Leu Leu Leu Ala
145 150 155 160

Leu Leu Ile Leu Gly Ile Val Trp Val Ala Ser Ala Leu Ile Asp Asn
165 170 175

Asp Ala Ala Ser Met Glu Ser Leu Tyr Asp Leu Trp Glu Phe Tyr Leu
180 185 190

Pro Tyr Leu Tyr Ser Cys Ile Ser Leu Met Gly Cys Leu Leu Leu Leu

```
        195                 200                 205

Leu Cys Thr Pro Val Gly Leu Ser Arg Met Phe Thr Val Met Gly Gln
    210                 215                 220

Leu Leu Val Lys Pro Thr Ile Leu Glu Asp Leu Asp Glu Gln Ile Tyr
225                 230                 235                 240

Ile Ile Thr Leu Glu Glu Glu Ala Leu Gln Arg Arg Leu Asn Gly Leu
                245                 250                 255

Ser Ser Ser Val Glu Tyr Asn Ile Met Glu Leu Glu Gln Glu Leu Glu
            260                 265                 270

Asn Val Lys Thr Leu Lys Thr Lys Leu Asp Pro Trp Ser Ser Phe Ser
        275                 280                 285

Val Leu Gln Ser Pro Val Trp His Phe Ala Ala Gln Thr Pro Ala Asp
    290                 295                 300

Ile Val Ser Pro Asp Ser His Phe Met Leu Ser Thr Gln Gly Met Ser
305                 310                 315                 320

Trp Ala Gln Leu Val Phe Leu Leu Pro Ala Ser Arg Pro Gly Asn Ser
                325                 330                 335

Gln Asp Lys Arg Arg Lys Lys Ala Ser Ala Trp Glu Arg Asn Leu Val
            340                 345                 350

Tyr Pro Ala Val Met Val Leu Leu Leu Ile Glu Thr Ser Ile Ser Val
        355                 360                 365

Leu Leu Val Ala Cys Asn Ile Leu Cys Leu Leu Val Asp Glu Thr Ala
    370                 375                 380

Met Pro Lys Gly Thr Arg Gly Xaa Gly Ile Gly Asn Ala Ser Leu Ser
385                 390                 395                 400

Thr Phe Gly Phe Val Gly Ala Ala Leu Glu Ile Ile Leu Ile Phe Tyr
                405                 410                 415

Leu Met Val Ser Ser Val Val Gly Phe Tyr Ser Leu Arg Phe Phe Gly
            420                 425                 430

Asn Phe Thr Pro Lys Lys Asp Asp Thr Thr Met Thr Lys Ile Ile Gly
        435                 440                 445

Asn Cys Val Ser Ile Leu Val Leu Ser Ser Ala Xaa Pro Val Met Ser
    450                 455                 460

Arg Thr Leu Gly Leu His Lys Leu His Leu Pro Asn Thr Ser Arg Asp
```

465 470 475 480

Ser Glu Thr Ala Lys Pro Ser Val Asn Gly His Gln Lys Ala Leu
485 490 495

<210> 1313
<211> 790
<212> PRT
<213> Homo sapiens

<400> 1313
Gly Thr Arg Gly Thr Ala Thr Glu Arg Leu Lys Met Ile Pro Phe Leu
1 5 10 15

Pro Met Phe Ser Leu Leu Leu Leu Leu Ile Val Asn Pro Ile Asn Ala
20 25 30

Asn Asn His Tyr Asp Lys Ile Leu Ala His Ser Arg Ile Arg Gly Arg
35 40 45

Asp Gln Gly Pro Asn Val Cys Ala Leu Gln Gln Ile Leu Gly Thr Lys
50 55 60

Lys Lys Tyr Phe Ser Thr Cys Lys Asn Trp Tyr Lys Lys Ser Ile Cys
65 70 75 80

Gly Gln Lys Thr Thr Val Leu Tyr Glu Cys Cys Pro Gly Tyr Met Arg
85 90 95

Met Glu Gly Met Lys Gly Cys Pro Ala Val Leu Pro Ile Asp His Val
100 105 110

Tyr Gly Thr Leu Gly Ile Val Gly Ala Thr Thr Thr Gln Arg Tyr Ser
115 120 125

Asp Ala Ser Lys Leu Arg Glu Glu Ile Glu Gly Lys Gly Ser Phe Thr
130 135 140

Tyr Phe Ala Pro Ser Asn Glu Ala Trp Asp Asn Leu Asp Ser Asp Ile
145 150 155 160

Arg Arg Gly Leu Glu Ser Asn Val Asn Val Glu Leu Leu Asn Ala Leu
165 170 175

His Ser His Met Ile Asn Lys Arg Met Leu Thr Lys Asp Leu Lys Asn
180 185 190

Gly Met Ile Ile Pro Ser Met Tyr Asn Asn Leu Gly Leu Phe Ile Asn
195 200 205

His Tyr Pro Asn Gly Val Val Thr Val Asn Cys Ala Arg Ile Ile His
    210   215   220

Gly Asn Gln Ile Ala Thr Asn Gly Val Val His Val Ile Asp Arg Val
225   230   235   240

Leu Thr Gln Ile Gly Thr Ser Ile Gln Asp Phe Ile Glu Ala Glu Asp
                245   250   255

Asp Leu Ser Ser Phe Arg Ala Ala Ala Ile Thr Ser Asp Ile Leu Glu
            260   265   270

Ala Leu Gly Arg Asp Gly His Phe Thr Leu Phe Ala Pro Thr Asn Glu
        275   280   285

Ala Phe Glu Lys Leu Pro Arg Gly Val Leu Glu Arg Ile Met Gly Asp
    290   295   300

Lys Val Ala Ser Glu Ala Leu Met Lys Tyr His Ile Leu Asn Thr Leu
305   310   315   320

Gln Cys Ser Glu Ser Ile Met Gly Gly Ala Val Phe Glu Thr Leu Glu
                325   330   335

Gly Asn Thr Ile Glu Ile Gly Cys Asp Gly Asp Ser Ile Thr Val Asn
            340   345   350

Gly Ile Lys Met Val Asn Lys Lys Asp Ile Val Thr Asn Asn Gly Val
        355   360   365

Ile His Leu Ile Asp Gln Val Leu Ile Pro Asp Ser Ala Lys Gln Val
    370   375   380

Ile Glu Leu Ala Gly Lys Gln Gln Thr Thr Phe Thr Asp Leu Val Ala
385   390   395   400

Gln Leu Gly Leu Ala Ser Ala Leu Arg Pro Asp Gly Glu Tyr Thr Leu
                405   410   415

Leu Ala Pro Val Asn Asn Ala Phe Ser Asp Asp Thr Leu Ser Met Asp
            420   425   430

Gln Arg Leu Leu Lys Leu Ile Leu Gln Asn His Ile Leu Lys Val Lys
        435   440   445

Val Gly Leu Asn Glu Leu Tyr Asn Gly Gln Ile Leu Glu Thr Ile Gly
    450   455   460

Gly Lys Gln Leu Arg Val Phe Val Tyr Arg Thr Ala Val Cys Ile Glu
465   470   475   480

```
Asn Ser Cys Met Glu Lys Gly Ser Lys Gln Gly Arg Asn Gly Ala Ile
                485                 490                 495

His Ile Phe Arg Glu Ile Ile Lys Pro Ala Glu Lys Ser Leu His Glu
            500                 505                 510

Lys Leu Lys Gln Asp Lys Arg Phe Ser Thr Phe Leu Ser Leu Leu Glu
        515                 520                 525

Ala Ala Asp Leu Lys Glu Leu Leu Thr Gln Pro Gly Asp Trp Thr Leu
    530                 535                 540

Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met Thr Ser Glu Glu Lys
545                 550                 555                 560

Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln Asn Ile Ile Leu Tyr
                565                 570                 575

His Leu Thr Pro Gly Val Phe Ile Gly Lys Gly Phe Glu Pro Gly Val
            580                 585                 590

Thr Asn Ile Leu Lys Thr Thr Gln Gly Ser Lys Ile Phe Leu Lys Glu
        595                 600                 605

Val Asn Asp Thr Leu Leu Val Asn Glu Leu Lys Ser Lys Glu Ser Asp
    610                 615                 620

Ile Met Thr Thr Asn Gly Val Ile His Val Val Asp Lys Leu Leu Tyr
625                 630                 635                 640

Pro Ala Asp Thr Pro Val Gly Asn Asp Gln Leu Leu Glu Ile Leu Asn
                645                 650                 655

Lys Leu Ile Lys Tyr Ile Gln Ile Lys Phe Val Arg Gly Ser Thr Phe
            660                 665                 670

Lys Glu Ile Pro Val Thr Val Tyr Lys Pro Ile Ile Lys Lys Tyr Thr
        675                 680                 685

Lys Ile Ile Asp Gly Val Pro Val Glu Ile Thr Glu Lys Glu Thr Arg
    690                 695                 700

Glu Glu Arg Ile Ile Thr Gly Pro Glu Ile Lys Tyr Thr Arg Ile Ser
705                 710                 715                 720

Thr Gly Gly Gly Glu Thr Glu Glu Thr Leu Lys Lys Leu Leu Gln Glu
                725                 730                 735

Glu Val Thr Lys Val Thr Lys Phe Ile Glu Gly Gly Asp Gly His Leu
            740                 745                 750
```

Phe Glu Asp Glu Glu Ile Lys Arg Leu Leu Gln Gly Asp Thr Pro Val
755 760 765

Arg Lys Leu Gln Ala Asn Lys Lys Val Gln Gly Ser Arg Arg Arg Leu
770 775 780

Arg Glu Gly Arg Ser Gln
785 790

<210> 1314
<211> 73
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (20)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1314
Thr Ser Trp Ala Phe Asp Glu Thr Gly Xaa Asn Thr Ala Val Phe Leu
1 5 10 15

Leu Glu Ile Xaa Trp Gly Ile Phe Phe Glu Leu Met Gly Thr Ile Arg
20 25 30

His Asn Cys Leu His Lys Leu Gly Ile Xaa Asp Phe Gly Ile Thr Ile
35 40 45

Tyr Gln Asn Gly Asp Ile Ser Pro Leu Val Leu Arg Cys Lys Pro Lys
50 55 60

Asn Ile Met Thr Ser Phe Gln Ala Ser
65 70

<210> 1315

<211> 268
<212> PRT
<213> Homo sapiens

<400> 1315

```
Pro Gly Arg Pro Thr Arg Pro Arg Thr Arg Gly Ile Asn Lys Leu Ile
  1               5                  10                  15

Arg Ile Gly Arg Asn Glu Cys Val Val Val Ile Arg Val Asp Lys Glu
             20                  25                  30

Lys Gly Tyr Ile Asp Leu Ser Lys Arg Arg Val Ser Pro Glu Glu Ala
         35                  40                  45

Ile Lys Cys Glu Asp Lys Phe Thr Lys Ser Lys Thr Val Tyr Ser Ile
     50                  55                  60

Leu Arg His Val Ala Glu Val Leu Glu Tyr Thr Lys Asp Glu Gln Leu
 65                  70                  75                  80

Glu Ser Leu Phe Gln Arg Thr Ala Trp Val Phe Asp Asp Lys Tyr Lys
                 85                  90                  95

Arg Pro Gly Tyr Gly Ala Tyr Asp Ala Phe Lys His Ala Val Ser Asp
            100                 105                 110

Pro Ser Ile Leu Asp Ser Leu Asp Leu Asn Glu Asp Glu Arg Glu Val
        115                 120                 125

Leu Ile Asn Asn Ile Asn Arg Arg Leu Thr Pro Gln Ala Val Lys Ile
    130                 135                 140

Arg Ala Asp Ile Glu Val Ala Cys Tyr Gly Tyr Glu Gly Ile Asp Ala
145                 150                 155                 160

Val Lys Glu Ala Leu Arg Ala Gly Leu Asn Cys Ser Thr Glu Asn Met
                165                 170                 175

Pro Ile Lys Ile Asn Leu Ile Ala Pro Pro Arg Tyr Val Met Thr Thr
            180                 185                 190

Thr Thr Leu Glu Arg Thr Glu Gly Leu Ser Val Leu Ser Gln Ala Met
        195                 200                 205

Ala Val Ile Lys Glu Lys Ile Glu Glu Lys Arg Gly Val Phe Asn Val
    210                 215                 220

Gln Met Glu Pro Lys Val Val Thr Asp Thr Asp Glu Thr Glu Leu Ala
225                 230                 235                 240

Arg Gln Met Glu Arg Leu Glu Arg Glu Asn Ala Glu Val Asp Gly Asp
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245 250 255

Asp Asp Ala Glu Glu Met Glu Ala Lys Ala Glu Asp
260 265

<210> 1316
<211> 315
<212> PRT
<213> Homo sapiens

<400> 1316
Gly Gln Arg Ala Gly Met Pro His Ala Gln Gly Gly Trp Ser Gly Pro
1 5 10 15

Ala Ala Asp Ser Ala Glu Pro Ala Leu Pro Ala Gly Glu Pro Gly Gly
20 25 30

Pro Thr Leu Met Arg Leu Asn Ser Val Gln Ser Ser Glu Arg Pro Leu
35 40 45

Phe Leu Val His Pro Ile Glu Gly Ser Thr Thr Val Phe His Ser Leu
50 55 60

Ala Ser Arg Leu Ser Ile Pro Thr Tyr Gly Leu Gln Cys Thr Arg Ala
65 70 75 80

Ala Pro Leu Asp Ser Ile His Ser Leu Ala Ala Tyr Tyr Ile Asp Cys
85 90 95

Ile Arg Gln Val Gln Pro Glu Gly Pro Tyr Arg Val Ala Gly Tyr Ser
100 105 110

Tyr Gly Ala Cys Val Ala Phe Glu Met Cys Ser Gln Leu Gln Ala Gln
115 120 125

Gln Ser Pro Ala Pro Thr His Asn Ser Leu Phe Leu Phe Asp Gly Ser
130 135 140

Pro Thr Tyr Val Leu Ala Tyr Thr Gln Ser Tyr Arg Ala Lys Leu Thr
145 150 155 160

Pro Gly Cys Glu Ala Glu Ala Glu Thr Glu Ala Ile Cys Phe Phe Val
165 170 175

Gln Gln Phe Thr Asp Met Glu His Asn Arg Val Leu Glu Ala Leu Leu
180 185 190

Pro Leu Lys Gly Leu Glu Glu Arg Val Ala Ala Ala Val Asp Leu Ile
195 200 205

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Ile Lys Ser His Gln Gly Leu Asp Arg Gln Glu Leu Ser Phe Ala Ala
    210                 215                 220

Arg Ser Phe Tyr Tyr Lys Leu Arg Ala Ala Glu Gln Tyr Thr Pro Lys
225                 230                 235                 240

Ala Lys Tyr His Gly Asn Val Met Leu Leu Arg Ala Lys Thr Gly Gly
                245                 250                 255

Ala Tyr Gly Glu Asp Leu Gly Ala Asp Tyr Asn Leu Ser Gln Val Cys
            260                 265                 270

Asp Gly Lys Val Ser Val His Val Ile Glu Gly Asp His Arg Thr Leu
        275                 280                 285

Leu Glu Gly Ser Gly Leu Glu Ser Ile Ile Ser Ile Ile His Ser Ser
    290                 295                 300

Leu Ala Glu Pro Arg Val Ser Val Arg Glu Gly
305                 310                 315
```

<210> 1317
<211> 191
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (20)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (25)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (186)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1317
Thr Thr Xaa Val Xaa Asp Arg Leu Leu Xaa Thr Ser Gly Ser Pro Gly
1 5 10 15

Thr Asp Arg Xaa Phe Gly His Glu Xaa Glu Met Ala Pro Asn Ala Ser
20 25 30

Cys Leu Cys Val His Val Arg Ser Glu Glu Trp Asp Leu Met Thr Phe
35 40 45

Asp Ala Asn Pro Tyr Asp Ser Val Lys Lys Ile Lys Glu His Val Arg
50 55 60

Ser Lys Thr Lys Val Pro Val Gln Asp Gln Val Leu Leu Leu Gly Ser
65 70 75 80

Lys Ile Leu Lys Pro Arg Arg Ser Leu Ser Ser Tyr Gly Ile Asp Lys
85 90 95

Glu Lys Thr Ile His Leu Thr Leu Lys Val Val Lys Pro Ser Asp Glu
100 105 110

Glu Leu Pro Leu Phe Leu Val Glu Ser Gly Asp Glu Ala Lys Arg His
115 120 125

Leu Leu Gln Val Arg Arg Ser Ser Ser Val Ala Gln Val Lys Ala Met
130 135 140

Ile Glu Thr Lys Thr Gly Ile Ile Pro Glu Thr Gln Ile Val Thr Cys
145 150 155 160

Asn Gly Lys Arg Leu Glu Asp Gly Lys Met Met Ala Asp Tyr Gly Ile
165 170 175

Arg Lys Gly Asn Leu Leu Phe Leu Ala Xaa Tyr Cys Ile Gly Gly
180 185 190

<210> 1318
<211> 230
<212> PRT
<213> Homo sapiens

<400> 1318

Arg Asn Leu Gln Glu Thr Ala Ile Met Ala Glu Lys Pro Lys Leu His
1   5   10   15

Tyr Phe Asn Ala Arg Gly Arg Met Glu Ser Thr Arg Trp Leu Leu Ala
            20   25   30

Ala Ala Gly Val Glu Phe Glu Glu Lys Phe Ile Lys Ser Ala Glu Asp
        35   40   45

Leu Asp Lys Leu Arg Asn Asp Gly Tyr Leu Met Phe Gln Gln Val Pro
    50   55   60

Met Val Glu Ile Asp Gly Met Lys Leu Val Gln Thr Arg Ala Ile Leu
65   70   75   80

Asn Tyr Ile Ala Ser Lys Tyr Asn Leu Tyr Gly Lys Asp Ile Lys Glu
                85   90   95

Arg Ala Leu Ile Asp Met Tyr Ile Glu Gly Ile Ala Asp Leu Gly Glu
            100   105   110

Met Ile Leu Leu Leu Pro Val Cys Pro Pro Glu Glu Lys Asp Ala Lys
        115   120   125

Leu Ala Leu Ile Lys Glu Lys Ile Lys Asn Arg Tyr Phe Pro Ala Phe
    130   135   140

Glu Lys Val Leu Lys Ser His Gly Gln Asp Tyr Leu Val Gly Asn Lys
145   150   155   160

Leu Ser Arg Ala Asp Ile His Leu Val Glu Leu Leu Tyr Tyr Val Glu
                165   170   175

Glu Leu Asp Ser Ser Leu Ile Ser Ser Phe Pro Leu Leu Lys Ala Leu
            180   185   190

Lys Thr Arg Ile Ser Asn Leu Pro Thr Val Lys Lys Phe Leu Gln Pro
        195   200   205

Gly Ser Pro Arg Lys Pro Pro Met Asp Glu Lys Ser Leu Glu Glu Ala
    210   215   220

Arg Lys Ile Phe Arg Phe
225   230

<210> 1319
<211> 279

<212> PRT
<213> Homo sapiens

<400> 1319
Glu Gly Pro Ala Glu Gly Asn Met Ala Ala Lys Val Phe Glu Ser Ile
1   5   10   15

Gly Lys Phe Gly Leu Ala Leu Ala Val Ala Gly Gly Val Val Asn Ser
            20   25   30

Ala Leu Tyr Asn Val Asp Ala Gly His Arg Ala Val Ile Phe Asp Arg
        35   40   45

Phe Arg Gly Val Gln Asp Ile Val Val Gly Glu Gly Thr His Phe Leu
    50   55   60

Ile Pro Trp Val Gln Lys Pro Ile Ile Phe Asp Cys Arg Ser Arg Pro
65   70   75   80

Arg Asn Val Pro Val Ile Thr Gly Ser Lys Asp Leu Gln Asn Val Asn
                85   90   95

Ile Thr Leu Arg Ile Leu Phe Arg Pro Val Ala Ser Gln Leu Pro Arg
            100   105   110

Ile Phe Thr Ser Ile Gly Glu Asp Tyr Asp Glu Arg Val Leu Pro Ser
        115   120   125

Ile Thr Thr Glu Ile Leu Lys Ser Val Val Ala Arg Phe Asp Ala Gly
    130   135   140

Glu Leu Ile Thr Gln Arg Glu Leu Val Ser Arg Gln Val Ser Asp Asp
145   150   155   160

Leu Thr Glu Arg Ala Ala Thr Phe Gly Leu Ile Leu Asp Asp Val Ser
                165   170   175

Leu Thr His Leu Thr Phe Gly Lys Glu Phe Thr Glu Ala Val Glu Ala
            180   185   190

Lys Gln Val Ala Gln Gln Glu Ala Glu Arg Ala Arg Phe Val Val Glu
        195   200   205

Lys Ala Glu Gln Gln Lys Lys Ala Ala Ile Ile Ser Ala Glu Gly Asp
    210   215   220

Ser Lys Ala Ala Glu Leu Ile Ala Asn Ser Leu Ala Thr Ala Gly Asp
225   230   235   240

Gly Leu Ile Glu Leu Arg Lys Leu Glu Ala Ala Glu Asp Ile Ala Tyr
                245   250   255

Gln Leu Ser Arg Ser Arg Asn Ile Thr Tyr Leu Pro Ala Gly Gln Ser
260 265 270

Val Leu Leu Gln Leu Pro Gln
275

<210> 1320
<211> 406
<212> PRT
<213> Homo sapiens

<400> 1320
Val Thr Ala Cys Ala Ala Pro Ala Ala Trp Leu Pro Ile Leu Val Ala
1 5 10 15

Asp Ile Trp Ser Ser Tyr Asn Met Ala Asp Ile Asp Asn Lys Glu Gln
20 25 30

Ser Glu Leu Asp Gln Asp Leu Asp Asp Val Glu Glu Val Glu Glu Glu
35 40 45

Glu Thr Gly Glu Glu Thr Lys Leu Lys Ala Arg Gln Leu Thr Val Gln
50 55 60

Met Met Gln Asn Pro Gln Ile Leu Ala Ala Leu Gln Glu Arg Leu Asp
65 70 75 80

Gly Leu Val Glu Thr Pro Thr Gly Tyr Ile Glu Ser Leu Pro Arg Val
85 90 95

Val Lys Arg Arg Val Asn Ala Leu Lys Asn Leu Gln Val Lys Cys Ala
100 105 110

Gln Ile Glu Ala Lys Phe Tyr Glu Glu Val His Asp Leu Glu Arg Lys
115 120 125

Tyr Ala Val Leu Tyr Gln Pro Leu Phe Asp Lys Arg Phe Glu Ile Ile
130 135 140

Asn Ala Ile Tyr Glu Pro Thr Glu Glu Glu Cys Glu Trp Lys Pro Asp
145 150 155 160

Glu Glu Asp Glu Ile Ser Glu Glu Leu Lys Glu Lys Ala Lys Ile Glu
165 170 175

Asp Glu Lys Lys Asp Glu Glu Lys Glu Asp Pro Lys Gly Ile Pro Glu
180 185 190

Phe Trp Leu Thr Val Phe Lys Asn Val Asp Leu Leu Ser Asp Met Val
195 200 205

Gln Glu His Asp Glu Pro Ile Leu Lys His Leu Lys Asp Ile Lys Val
210 215 220

Lys Phe Ser Asp Ala Gly Gln Pro Met Ser Phe Val Leu Glu Phe His
225 230 235 240

Phe Glu Pro Asn Glu Tyr Phe Thr Asn Glu Val Leu Thr Lys Thr Tyr
245 250 255

Arg Met Arg Ser Glu Pro Asp Asp Ser Asp Pro Phe Ser Phe Asp Gly
260 265 270

Pro Glu Ile Met Gly Cys Thr Gly Cys Gln Ile Asp Trp Lys Lys Gly
275 280 285

Lys Asn Val Thr Leu Lys Thr Ile Lys Lys Lys Gln Lys His Lys Gly
290 295 300

Arg Gly Thr Val Arg Thr Val Thr Lys Thr Val Ser Asn Asp Ser Phe
305 310 315 320

Phe Asn Phe Phe Ala Pro Pro Glu Val Pro Glu Ser Gly Asp Leu Asp
325 330 335

Asp Asp Ala Glu Ala Ile Leu Ala Ala Asp Phe Glu Ile Gly His Phe
340 345 350

Leu Arg Glu Arg Ile Ile Pro Arg Ser Val Leu Tyr Phe Thr Gly Glu
355 360 365

Ala Ile Glu Asp Asp Asp Asp Asp Tyr Asp Glu Glu Gly Glu Glu Ala
370 375 380

Asp Glu Gly Tyr Gln Leu Phe Glu Glu Val Lys Ser Cys Ser Lys Leu
385 390 395 400

Phe Gln Arg Trp Leu Gln
405

<210> 1321
<211> 173
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1321
Gln Ser Ala Cys Ser Leu Leu Pro Glu Met Pro Arg Ile Leu Thr Arg
1 5 10 15

Thr Pro Ser Ser Arg Met Ile Val Leu Arg Leu Met Pro Val Gly Gly
20 25 30

Arg Arg Pro Ile Val Thr Ser Phe Gly Gly Cys Ser Thr Ala Pro Arg
35 40 45

Ala Asn Phe Pro Leu Pro Xaa Pro Ala Leu Arg Gln Ser Arg Ser Lys
50 55 60

Met Ala Val Val Gly Val Ser Ser Val Ser Arg Leu Leu Gly Arg Ser
65 70 75 80

Arg Pro Gln Leu Gly Arg Pro Met Ser Ser Gly Ala His Gly Glu Glu
85 90 95

Gly Ser Ala Arg Met Trp Lys Thr Leu Thr Phe Phe Val Ala Leu Pro
100 105 110

Gly Val Ala Val Ser Met Leu Asn Val Tyr Leu Lys Ser His His Gly
115 120 125

Glu His Glu Arg Pro Glu Phe Ile Ala Tyr Pro His Leu Arg Ile Arg
130 135 140

Thr Lys Pro Phe Pro Trp Gly Asp Gly Asn His Thr Leu Phe His Asn
145 150 155 160

Pro His Val Asn Pro Leu Pro Thr Gly Tyr Glu Asp Glu
165 170

<210> 1322
<211> 209
<212> PRT
<213> Homo sapiens

<400> 1322
Lys Thr Gln Ala Ala Ser Val Glu Ala Val Lys Met Leu Asp Glu Ile
1 5 10 15

Leu Leu Gln Leu Ser Ala Ser Val Pro Val Asp Val Met Pro Gly Glu
20 25 30

Phe Asp Pro Thr Asn Tyr Thr Leu Pro Gln Gln Pro Leu His Pro Cys
35 40 45

Met Phe Pro Leu Ala Thr Ala Tyr Ser Thr Leu Gln Leu Val Thr Asn
50 55 60

Pro Tyr Gln Ala Thr Ile Asp Gly Val Arg Phe Leu Gly Thr Ser Gly
65 70 75 80

Gln Asn Val Ser Asp Ile Phe Arg Tyr Ser Ser Met Glu Asp His Leu
85 90 95

Glu Ile Leu Glu Trp Thr Leu Arg Val Arg His Ile Ser Pro Thr Ala
100 105 110

Pro Asp Thr Leu Gly Cys Tyr Pro Phe Tyr Lys Thr Asp Pro Phe Ile
115 120 125

Phe Pro Glu Cys Pro His Val Tyr Phe Cys Gly Asn Thr Pro Ser Phe
130 135 140

Gly Ser Lys Ile Ile Arg Gly Pro Glu Asp Gln Thr Val Leu Leu Val
145 150 155 160

Thr Val Pro Asp Phe Ser Ala Thr Gln Thr Ala Cys Leu Val Asn Leu
165 170 175

Arg Ser Leu Ala Cys Gln Pro Ile Ser Phe Ser Gly Phe Gly Ala Glu
180 185 190

Asp Asp Asp Leu Gly Gly Leu Gly Trp Ala Pro Asp Ser Lys Lys Trp
195 200 205

Phe

<210> 1323
<211> 291
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (30)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (57)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1323

Asn Asn Val Ala Thr Thr His Glu Pro Ala Ser Val Pro Ala Pro Gln
1 5 10 15

Gly Asp Leu Leu Ser Gly Ala Glu Pro Glu Gly Gly Asn Xaa Ala Arg
20 25 30

Arg Pro Pro Gly Ala Arg Glu Gln Pro Gln Ser Pro Pro Pro Ala Arg
35 40 45

Gly Gly Ala Gly Ser Leu Ala Thr Xaa Ala Pro Pro Ser Ser Gly Leu
50 55 60

Ser Cys Pro Gly Cys Phe Arg Leu Arg Leu Trp Met Leu Arg Leu Ser
65 70 75 80

Glu Arg Asn Met Lys Val Leu Leu Ala Ala Ala Leu Ile Ala Gly Ser
85 90 95

Val Phe Phe Leu Leu Leu Pro Gly Pro Ser Ala Ala Asp Glu Lys Lys
100 105 110

Lys Gly Pro Lys Val Thr Val Lys Val Tyr Phe Asp Leu Arg Ile Gly
115 120 125

Asp Glu Asp Val Gly Arg Val Ile Phe Gly Leu Phe Gly Lys Thr Val
130 135 140

Pro Lys Thr Val Asp Asn Phe Val Ala Leu Ala Thr Gly Glu Lys Gly
145 150 155 160

Phe Gly Tyr Lys Asn Ser Lys Phe His Arg Val Ile Lys Asp Phe Met
165 170 175

Ile Gln Gly Gly Asp Phe Thr Arg Gly Asp Gly Thr Gly Gly Lys Ser
180 185 190

Ile Tyr Gly Glu Arg Phe Pro Asp Glu Asn Phe Lys Leu Lys His Tyr
195 200 205

Gly Pro Gly Trp Val Ser Met Ala Asn Ala Gly Lys Asp Thr Asn Gly
210 215 220

Ser Gln Phe Phe Ile Thr Thr Val Lys Thr Ala Trp Leu Asp Gly Lys
225 230 235 240

His Val Val Phe Gly Lys Val Leu Glu Gly Met Glu Val Val Arg Lys
245 250 255

Val Glu Ser Thr Lys Thr Asp Ser Arg Asp Lys Pro Leu Lys Asp Val
260 265 270

Ile Ile Ala Asp Cys Gly Lys Ile Glu Val Glu Lys Pro Phe Ala Ile
275 280 285

Ala Lys Glu
290

<210> 1324
<211> 150
<212> PRT
<213> Homo sapiens

<400> 1324
Glu Cys Leu Val Arg Ser Lys Asn Ile Thr Gln Ile Val Gly His Ser
1 5 10 15

Gly Cys Glu Ala Lys Ser Ile Gln Asn Arg Ala Cys Leu Gly Gln Cys
20 25 30

Phe Ser Tyr Ser Val Pro Asn Thr Phe Pro Gln Ser Thr Glu Ser Leu
35 40 45

Val His Cys Asp Ser Cys Met Pro Ala Gln Ser Met Trp Glu Ile Val
50 55 60

Thr Leu Glu Cys Pro Gly His Glu Glu Val Pro Arg Val Asp Lys Leu
65 70 75 80

Val Glu Lys Ile Leu His Cys Ser Cys Gln Ala Cys Gly Lys Glu Pro
85 90 95

Ser His Glu Gly Leu Ser Val Tyr Val Gln Gly Glu Asp Gly Pro Gly
100 105 110

Ser Gln Pro Gly Thr His Pro His Pro His Pro His Pro His Pro Gly
115 120 125

Gly Gln Thr Pro Glu Pro Glu Asp Pro Pro Gly Ala Pro His Thr Glu
130 135 140

Glu Glu Gly Ala Glu Asp
145 150

<210> 1325
<211> 56

<212> PRT
<213> Homo sapiens

<400> 1325
Glu Ile Asn Ile Ser Arg Lys Gly Glu Ser Arg Phe Tyr Lys Met Ser
1 5 10 15

Gln Leu Ser Asn Ile Trp Gly Ser Asp Ser Phe Phe Val Arg Thr Phe
20 25 30

Glu Thr Ser Lys Gln Pro Leu Phe Leu Lys Asn Ser Gly Phe Thr Leu
35 40 45

Thr His Val Ser Phe Thr Pro Phe
50 55

<210> 1326
<211> 486
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (34)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (438)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (447)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1326
Arg Leu Pro Leu Gly Ser Arg Ser Pro Ser Glu Ala Ala Gly Ala Glu
1 5 10 15

Thr Ala Pro Ser Ser Leu Ser Ala Ala Met Thr Pro Leu Val Ser Arg
20 25 30

Leu Xaa Arg Leu Trp Ala Ile Met Arg Lys Pro Arg Ala Ala Val Gly
35 40 45

Ser Gly His Arg Lys Gln Ala Ala Ser Gln Glu Gly Arg Gln Lys His
50 55 60

Ala Lys Asn Asn Ser Gln Ala Lys Pro Ser Ala Cys Asp Gly Leu Ala
65 70 75 80

Arg Gln Pro Glu Glu Val Val Leu Gln Ala Ser Val Ser Ser Tyr His
85 90 95

Leu Phe Arg Asp Val Ala Glu Val Thr Ala Phe Arg Gly Ser Leu Leu
100 105 110

Ser Trp Tyr Asp Gln Glu Lys Arg Asp Leu Pro Trp Arg Arg Arg Ala
115 120 125

Glu Asp Glu Met Asp Leu Asp Arg Arg Ala Tyr Ala Val Trp Val Ser
130 135 140

Glu Val Met Leu Gln Gln Thr Gln Val Ala Thr Val Ile Asn Tyr Tyr
145 150 155 160

Thr Gly Trp Met Gln Lys Trp Pro Thr Leu Gln Asp Leu Ala Ser Ala
165 170 175

Ser Leu Glu Glu Val Asn Gln Leu Trp Ala Gly Leu Gly Tyr Tyr Ser
180 185 190

Arg Gly Arg Arg Leu Gln Glu Gly Ala Arg Lys Val Val Glu Glu Leu
195 200 205

Gly Gly His Met Pro Arg Thr Ala Glu Thr Leu Gln Gln Leu Leu Pro
210 215 220

Gly Val Gly Arg Tyr Thr Ala Gly Ala Ile Ala Ser Ile Ala Phe Gly
225 230 235 240

Gln Ala Thr Gly Val Val Asp Gly Asn Val Ala Arg Val Leu Cys Arg
245 250 255

Val Arg Ala Ile Gly Ala Asp Pro Ser Ser Thr Leu Val Ser Gln Gln
260 265 270

Leu Trp Gly Leu Ala Gln Gln Leu Val Asp Pro Ala Arg Pro Gly Asp
275 280 285

Phe Asn Gln Ala Ala Met Glu Leu Gly Ala Thr Val Cys Thr Pro Gln
290 295 300

Arg Pro Leu Cys Ser Gln Cys Pro Val Glu Ser Leu Cys Arg Ala Arg
305 310 315 320

Gln Arg Val Glu Gln Glu Gln Leu Leu Ala Ser Gly Ser Leu Ser Gly
325 330 335

Ser Pro Asp Val Glu Glu Cys Ala Pro Asn Thr Gly Gln Cys His Leu
340 345 350

Cys Leu Pro Pro Ser Glu Pro Trp Asp Gln Thr Leu Gly Val Val Asn
355 360 365

Phe Pro Arg Lys Ala Ser Arg Lys Pro Pro Arg Glu Glu Ser Ser Ala
370 375 380

Thr Cys Val Leu Glu Gln Pro Gly Ala Leu Gly Ala Gln Ile Leu Leu
385 390 395 400

Val Gln Arg Pro Asn Ser Gly Leu Leu Ala Gly Leu Trp Glu Phe Pro
405 410 415

Ser Val Thr Trp Glu Pro Ser Glu Gln Leu Gln Arg Lys Ala Leu Leu
420 425 430

Gln Glu Leu Gln Arg Xaa Ala Gly Pro Leu Pro Ala Thr His Xaa Arg
435 440 445

His Leu Gly Glu Val Val His Thr Phe Ser His Ile Lys Leu Thr Tyr
450 455 460

Gln Val Tyr Gly Leu Ala Leu Glu Gly Gln Thr Pro Val Thr Thr Val
465 470 475 480

Pro Pro Gly Ala Arg Cys
485

<210> 1327
<211> 88
<212> PRT
<213> Homo sapiens

<400> 1327
Lys Thr Leu Phe Thr Tyr Ser Phe His Gly Tyr Asn Thr Leu Ala Asp
1 5 10 15

Phe Leu Leu Ala Leu Gly Ala Met Ile Leu Ile Thr Phe Cys Lys Val
20 25 30

Thr Asn Val Ile His Ser Thr Leu Cys Gly Ser His Leu Phe Arg Leu
35 40 45

Met Cys Phe Gly Glu Arg Lys Lys Phe Leu Ala Glu Tyr Tyr Phe Glu
50 55 60

Leu Ser Arg Thr Leu Ser His Gln Arg Gln Phe Phe Ser Val Gln Phe

65 70 75 80

Pro Ile Pro Asp Asn Leu Leu Lys
85

<210> 1328
<211> 424
<212> PRT
<213> Homo sapiens

<400> 1328
Ile Arg Val Ser Phe Met Asn Asn Gln Lys Gln Gln Lys Pro Thr Leu
1 5 10 15

Ser Gly Gln Arg Phe Lys Thr Arg Lys Arg Asp Glu Lys Glu Arg Phe
20 25 30

Asp Pro Thr Gln Phe Gln Asp Cys Ile Ile Gln Gly Leu Thr Glu Thr
35 40 45

Gly Thr Asp Leu Glu Ala Val Ala Lys Phe Leu Asp Ala Ser Gly Ala
50 55 60

Lys Leu Asp Tyr Arg Arg Tyr Ala Glu Thr Leu Phe Asp Ile Leu Val
65 70 75 80

Ala Gly Gly Met Leu Ala Pro Gly Gly Thr Leu Ala Asp Asp Met Met
85 90 95

Arg Thr Asp Val Cys Val Phe Ala Ala Gln Glu Asp Leu Glu Thr Met
100 105 110

Gln Ala Phe Ala Gln Val Phe Asn Lys Leu Ile Arg Arg Tyr Lys Tyr
115 120 125

Leu Glu Lys Gly Phe Glu Asp Glu Val Lys Lys Leu Leu Leu Phe Leu
130 135 140

Lys Gly Phe Ser Glu Ser Glu Arg Asn Lys Leu Ala Met Leu Thr Gly
145 150 155 160

Val Leu Leu Ala Asn Gly Thr Leu Asn Ala Ser Ile Leu Asn Ser Leu
165 170 175

Tyr Asn Glu Asn Leu Val Lys Glu Gly Val Ser Ala Ala Phe Ala Val
180 185 190

Lys Leu Phe Lys Ser Trp Ile Asn Glu Lys Asp Ile Asn Ala Val Ala
195 200 205

Ala Ser Leu Arg Lys Val Ser Met Asp Asn Arg Leu Met Glu Leu Phe
    210   215   220

Pro Ala Asn Lys Gln Ser Val Glu His Phe Thr Lys Tyr Phe Thr Glu
225   230   235   240

Ala Gly Leu Lys Glu Leu Ser Glu Tyr Val Arg Asn Gln Gln Thr Ile
                245   250   255

Gly Ala Arg Lys Glu Leu Gln Lys Glu Leu Gln Glu Gln Met Ser Arg
            260   265   270

Gly Asp Pro Phe Lys Asp Ile Ile Leu Tyr Val Lys Glu Glu Met Lys
        275   280   285

Lys Asn Asn Ile Pro Glu Pro Val Val Ile Gly Ile Val Trp Ser Ser
    290   295   300

Val Met Ser Thr Val Glu Trp Asn Lys Lys Glu Glu Leu Val Ala Glu
305   310   315   320

Gln Ala Ile Lys His Leu Lys Gln Tyr Ser Pro Leu Leu Ala Ala Phe
                325   330   335

Thr Thr Gln Gly Gln Ser Glu Leu Thr Leu Leu Leu Lys Ile Gln Glu
            340   345   350

Tyr Cys Tyr Asp Asn Ile His Phe Met Lys Ala Phe Gln Lys Ile Val
        355   360   365

Val Leu Phe Tyr Lys Ala Glu Val Leu Ser Glu Glu Pro Ile Leu Lys
    370   375   380

Trp Tyr Lys Asp Ala His Val Ala Lys Gly Lys Ser Val Phe Leu Glu
385   390   395   400

Gln Met Lys Lys Phe Val Glu Trp Leu Lys Asn Ala Glu Glu Glu Ser
                405   410   415

Glu Ser Glu Ala Glu Glu Gly Asp
            420

<210> 1329
<211> 558
<212> PRT
<213> Homo sapiens

<400> 1329

Trp Tyr Cys Ser Val Gly Leu Ala Ser Thr Ala Gly Glu Gln Ala Ala
1   5   10   15

Ala Val Ala Ala Ala Phe Ser Leu His Pro Asp Tyr Ala Met Leu Gly
            20   25   30

Phe Val Gly Arg Val Ala Ala Ala Pro Ala Ser Gly Ala Leu Arg Arg
        35   40   45

Leu Thr Pro Ser Ala Ser Leu Pro Pro Ala Gln Leu Leu Leu Arg Ala
    50   55   60

Ala Pro Thr Ala Val His Pro Val Arg Asp Tyr Ala Ala Gln Thr Ser
65   70   75   80

Pro Ser Pro Lys Ala Gly Ala Ala Thr Gly Arg Ile Val Ala Val Ile
                85   90   95

Gly Ala Val Val Asp Val Gln Phe Asp Glu Gly Leu Pro Pro Ile Leu
            100   105   110

Asn Ala Leu Glu Val Gln Gly Arg Glu Thr Arg Leu Val Leu Glu Val
        115   120   125

Ala Gln His Leu Gly Glu Ser Thr Val Arg Thr Ile Ala Met Asp Gly
    130   135   140

Thr Glu Gly Leu Val Arg Gly Gln Lys Val Leu Asp Ser Gly Ala Pro
145   150   155   160

Ile Lys Ile Pro Val Gly Pro Glu Thr Leu Gly Arg Ile Met Asn Val
                165   170   175

Ile Gly Glu Pro Ile Asp Glu Arg Gly Pro Ile Lys Thr Lys Gln Phe
            180   185   190

Ala Pro Ile His Ala Glu Ala Pro Glu Phe Met Glu Met Ser Val Glu
        195   200   205

Gln Glu Ile Leu Val Thr Gly Ile Lys Val Val Asp Leu Leu Ala Pro
    210   215   220

Tyr Ala Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly
225   230   235   240

Lys Thr Val Leu Ile Met Glu Leu Ile Asn Asn Val Ala Lys Ala His
                245   250   255

Gly Gly Tyr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly
            260   265   270

Asn Asp Leu Tyr His Glu Met Ile Glu Ser Gly Val Ile Asn Leu Lys
275 280 285

Asp Ala Thr Ser Lys Val Ala Leu Val Tyr Gly Gln Met Asn Glu Pro
290 295 300

Pro Gly Ala Arg Ala Arg Val Ala Leu Thr Gly Leu Thr Val Ala Glu
305 310 315 320

Tyr Phe Arg Asp Gln Glu Gly Gln Asp Val Leu Leu Phe Ile Asp Asn
325 330 335

Ile Phe Arg Phe Thr Gln Ala Gly Ser Glu Val Ser Ala Leu Leu Gly
340 345 350

Arg Ile Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala Thr Asp Met
355 360 365

Gly Thr Met Gln Glu Arg Ile Thr Thr Thr Lys Lys Gly Ser Ile Thr
370 375 380

Ser Val Gln Ala Ile Tyr Val Pro Ala Asp Asp Leu Thr Asp Pro Ala
385 390 395 400

Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Val Leu Ser Arg
405 410 415

Ala Ile Ala Glu Leu Gly Ile Tyr Pro Ala Val Asp Pro Leu Asp Ser
420 425 430

Thr Ser Arg Ile Met Asp Pro Asn Ile Val Gly Ser Glu His Tyr Asp
435 440 445

Val Ala Arg Gly Val Gln Lys Ile Leu Gln Asp Tyr Lys Ser Leu Gln
450 455 460

Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu Glu Asp Lys
465 470 475 480

Leu Thr Val Ser Arg Ala Arg Lys Ile Gln Arg Phe Leu Ser Gln Pro
485 490 495

Phe Gln Val Ala Glu Val Phe Thr Gly His Met Gly Lys Leu Val Pro
500 505 510

Leu Lys Glu Thr Ile Lys Gly Phe Gln Gln Ile Leu Ala Gly Glu Tyr
515 520 525

Asp His Leu Pro Glu Gln Ala Phe Tyr Met Val Gly Pro Ile Glu Glu
530 535 540

Ala Val Ala Lys Ala Asp Lys Leu Ala Glu Glu His Ser Ser
545 550 555

<210> 1330
<211> 134
<212> PRT
<213> Homo sapiens

<400> 1330
Thr Thr Pro Leu Ser Gln Ile Val Ala Arg Gly Leu Ile Ala Arg Gly
1 5 10 15

Val Pro Gly Ala Ile Val Asn Val Ser Ser Gln Cys Ser Gln Arg Ala
20 25 30

Val Thr Asn His Ser Val Tyr Cys Ser Thr Lys Gly Ala Leu Asp Met
35 40 45

Leu Thr Lys Val Met Ala Leu Glu Leu Gly Pro His Lys Ile Arg Val
50 55 60

Asn Ala Val Asn Pro Thr Val Val Met Thr Ser Met Gly Gln Ala Thr
65 70 75 80

Trp Ser Asp Pro His Lys Ala Lys Thr Met Leu Asn Arg Ile Pro Leu
85 90 95

Gly Lys Phe Ala Glu Val Glu His Val Val Asn Ala Ile Leu Phe Leu
100 105 110

Leu Ser Asp Arg Ser Gly Met Thr Thr Gly Ser Thr Leu Pro Val Glu
115 120 125

Gly Gly Phe Trp Ala Cys
130

<210> 1331
<211> 188
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (135)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (137)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1331
Ile Arg His Glu Pro Ser Arg Cys Arg Ser Arg Thr Ala Ala Val Cys
1   5   10   15

Ser Pro Pro Pro Cys Pro Pro Trp Arg Arg Pro Arg Gly Pro Trp Thr
            20   25   30

Ala Lys Ser Pro Pro Trp Pro Pro Ala Arg Pro Arg Trp Gln Trp Thr
        35   40   45

Arg Ala Leu Asn Ser Thr Ala Ala Pro Pro Arg Ser Pro Pro Ala Pro
    50   55   60

Cys Pro Cys Arg Pro Asn Ser Ala Arg Arg Lys Arg Arg Pro Pro Ala
65   70   75   80

Asn Cys Arg Ala Ser Ser Gly Trp Leu Ala Ala Trp Lys Pro Ser Arg
                85   90   95

Thr Gly Pro Ala Ala Arg Pro Arg Arg Pro Val Pro Asp Thr Ser Phe
            100   105   110

His Ser Ser Pro Val Gln Ala Ala Val His Phe Val Gly Tyr Lys Ile
        115   120   125

Asn His Gly Pro Ala Met Xaa Leu Xaa Phe Leu Leu Gln Leu Arg Leu
    130   135   140

Gly Arg Gly Pro Gly Leu Pro Arg Glu Asn Val Leu Glu Thr Ala Pro
145   150   155   160

Val Phe Leu Ala Trp Phe Ile Cys Pro Gly Ser Gly Ser Asp Ser Gly
                165   170   175

Gly Ser Glu Thr Ser Val Ala Leu Ser Tyr Trp Gly
            180   185

<210> 1332
<211> 237
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (5)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1332

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Asp Asp Arg Arg Xaa Asp Ala Glu Ala Asp Lys Met Ala Ala Ala Ala
 1               5                  10                  15

Val Gln Gly Gly Arg Ser Gly Gly Ser Gly Gly Cys Ser Gly Ala Gly
            20                  25                  30

Gly Ala Ser Asn Cys Gly Thr Gly Ser Gly Arg Ser Gly Leu Leu Asp
        35                  40                  45

Lys Trp Lys Ile Asp Asp Lys Pro Val Lys Ile Asp Lys Trp Asp Gly
    50                  55                  60

Ser Ala Val Lys Asn Ser Leu Asp Asp Ser Ala Lys Lys Val Leu Leu
65                  70                  75                  80

Glu Lys Tyr Lys Tyr Val Glu Asn Phe Gly Leu Ile Asp Gly Arg Leu
                85                  90                  95

Thr Ile Cys Thr Ile Ser Cys Phe Phe Ala Ile Val Ala Leu Ile Trp
            100                 105                 110

Asp Tyr Met His Pro Phe Pro Glu Ser Lys Pro Val Leu Ala Leu Cys
        115                 120                 125

Val Ile Ser Tyr Phe Val Met Met Gly Ile Leu Thr Ile Tyr Thr Ser
    130                 135                 140

Tyr Lys Glu Lys Ser Ile Phe Leu Val Ala His Arg Lys Asp Pro Thr
145                 150                 155                 160

Gly Met Asp Pro Asp Asp Ile Trp Gln Leu Ser Ser Ser Leu Lys Arg
                165                 170                 175

Phe Asp Asp Lys Tyr Thr Leu Lys Leu Thr Phe Ile Ser Gly Arg Thr
            180                 185                 190

Lys Gln Gln Arg Glu Ala Glu Phe Thr Lys Ser Ile Ala Lys Phe Phe
        195                 200                 205

Asp His Ser Gly Thr Leu Val Met Asp Ala Tyr Glu Pro Glu Ile Ser
    210                 215                 220

Arg Leu His Asp Ser Leu Ala Ile Glu Arg Lys Ile Lys
225                 230                 235
```

<210> 1333

<211> 56
<212> PRT
<213> Homo sapiens

<400> 1333
Thr Thr Ala Asn Pro Leu Lys Thr Arg Gly Leu Ala Leu Val Ala Gln
1   5   10   15

Pro Lys Val Ala Leu Gln Ile Phe Glu Arg Ala Thr Ala Thr Phe Leu
            20   25   30

Pro Ser Gln Leu Ser Leu Asp Phe Ser Glu Ser Gly Tyr Cys Tyr Pro
        35   40   45

Asn Val Cys Leu Tyr Glu Cys Ile
    50   55

<210> 1334
<211> 207
<212> PRT
<213> Homo sapiens

<400> 1334
Ser His Pro Ala Cys Ala Lys Val Glu Tyr Ala Tyr Ser Asp Asn Ser
1   5   10   15

Leu Asp Pro Asp Asp Glu Asp Ser Asp Tyr His Gln Glu Ala Tyr Lys
            20   25   30

Glu Ser Tyr Lys Asp Arg Arg Arg Arg Ala His Thr Gln Ala Glu Gln
        35   40   45

Lys Arg Arg Asp Ala Ile Lys Arg Gly Tyr Asp Asp Leu Gln Thr Ile
    50   55   60

Val Pro Thr Cys Gln Gln Gln Asp Phe Ser Ile Gly Ser Gln Lys Leu
65   70   75   80

Ser Lys Ala Ile Val Leu Gln Lys Thr Ile Asp Tyr Ile Gln Phe Leu
                85   90   95

His Lys Glu Lys Lys Lys Gln Glu Glu Glu Val Ser Thr Leu Arg Lys
            100   105   110

Asp Val Thr Ala Leu Lys Ile Met Lys Val Asn Tyr Glu Gln Ile Val
        115   120   125

Lys Ala His Gln Asp Asn Pro His Glu Gly Glu Asp Gln Val Ser Asp
    130   135   140

Gln Val Lys Phe Asn Val Phe Gln Gly Ile Met Asp Ser Leu Phe Gln
145 150 155 160

Ser Phe Asn Ala Ser Ile Ser Val Ala Ser Phe Gln Glu Leu Ser Ala
165 170 175

Cys Val Phe Ser Trp Ile Glu Glu His Cys Lys Pro Gln Thr Leu Arg
180 185 190

Glu Ile Val Ile Gly Val Leu His Gln Leu Lys Asn Gln Leu Tyr
195 200 205

<210> 1335
<211> 1005
<212> PRT
<213> Homo sapiens

<400> 1335
Arg Val Leu Gln Tyr Val Val Pro Glu Val Lys Asp Leu Tyr Asn Trp
1 5 10 15

Leu Glu Val Glu Phe Asn Pro Leu Lys Leu Cys Glu Arg Val Thr Lys
20 25 30

Val Leu Asn Trp Val Arg Glu Gln Pro Glu Lys Glu Pro Glu Leu Gln
35 40 45

Gln Tyr Val Pro Gln Leu Gln Asn Asn Thr Ile Leu Arg Leu Leu Gln
50 55 60

Gln Val Ser Gln Ile Tyr Gln Ser Ile Glu Phe Ser Arg Leu Thr Ser
65 70 75 80

Leu Val Pro Phe Val Asp Ala Phe Gln Leu Glu Arg Ala Ile Val Asp
85 90 95

Ala Ala Arg His Cys Asp Leu Gln Val Arg Ile Asp His Thr Ser Arg
100 105 110

Thr Leu Ser Phe Gly Ser Asp Leu Asn Tyr Ala Thr Arg Glu Asp Ala
115 120 125

Pro Ile Gly Pro His Leu Gln Ser Met Pro Ser Glu Gln Ile Arg Asn
130 135 140

Gln Leu Thr Ala Met Ser Ser Val Leu Ala Lys Ala Leu Glu Val Ile
145 150 155 160

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Lys Pro Ala His Ile Leu Gln Glu Lys Glu Glu Gln His Gln Leu Ala
                165                 170                 175

Val Thr Ala Tyr Leu Lys Asn Ser Arg Lys Glu His Gln Arg Ile Leu
            180                 185                 190

Ala Arg Arg Gln Thr Ile Glu Glu Arg Lys Glu Arg Leu Glu Ser Leu
        195                 200                 205

Asn Ile Gln Arg Glu Lys Glu Glu Leu Glu Gln Arg Glu Ala Glu Leu
    210                 215                 220

Gln Lys Val Arg Lys Ala Glu Glu Glu Arg Leu Arg Gln Glu Ala Lys
225                 230                 235                 240

Glu Arg Glu Lys Glu Arg Ile Leu Gln Glu His Glu Gln Ile Lys Lys
                245                 250                 255

Lys Thr Val Arg Glu Arg Leu Glu Gln Ile Lys Lys Thr Glu Leu Gly
            260                 265                 270

Ala Lys Ala Phe Lys Asp Ile Asp Ile Glu Asp Leu Glu Glu Leu Asp
        275                 280                 285

Pro Asp Phe Ile Met Ala Lys Gln Val Glu Gln Leu Glu Lys Glu Lys
    290                 295                 300

Lys Glu Leu Gln Glu Arg Leu Lys Asn Gln Glu Lys Lys Ile Asp Tyr
305                 310                 315                 320

Phe Glu Arg Ala Lys Arg Leu Glu Glu Ile Pro Leu Ile Lys Ser Ala
                325                 330                 335

Tyr Glu Glu Gln Arg Ile Lys Asp Met Asp Leu Trp Glu Gln Gln Glu
            340                 345                 350

Glu Glu Arg Ile Thr Thr Met Gln Leu Glu Arg Glu Lys Ala Leu Glu
        355                 360                 365

His Lys Asn Arg Met Ser Arg Met Leu Glu Asp Arg Asp Leu Phe Val
    370                 375                 380

Met Arg Leu Lys Ala Ala Arg Gln Ser Val Tyr Glu Glu Lys Leu Lys
385                 390                 395                 400

Gln Phe Glu Glu Arg Leu Ala Glu Glu Arg His Asn Arg Leu Glu Glu
                405                 410                 415

Arg Lys Arg Gln Arg Lys Glu Glu Arg Arg Ile Thr Tyr Tyr Arg Glu
            420                 425                 430
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Lys Glu Glu Glu Glu Gln Arg Arg Ala Glu Glu Gln Met Leu Lys Glu
        435                 440                 445

Arg Glu Glu Arg Glu Arg Ala Glu Arg Ala Lys Arg Glu Glu Glu Leu
    450                 455                 460

Arg Glu Tyr Gln Glu Arg Val Lys Lys Leu Glu Glu Val Glu Arg Lys
465                 470                 475                 480

Lys Arg Gln Arg Glu Leu Glu Ile Glu Glu Arg Glu Arg Arg Arg Glu
                485                 490                 495

Glu Glu Arg Arg Leu Gly Asp Ser Ser Leu Ser Arg Lys Asp Ser Arg
            500                 505                 510

Trp Gly Asp Arg Asp Ser Glu Gly Thr Trp Arg Lys Gly Pro Glu Ala
        515                 520                 525

Asp Ser Glu Trp Arg Arg Gly Pro Pro Glu Lys Glu Trp Arg Arg Gly
    530                 535                 540

Glu Gly Arg Asp Glu Asp Arg Ser His Arg Arg Asp Glu Glu Arg Pro
545                 550                 555                 560

Arg Arg Leu Gly Asp Asp Glu Asp Arg Glu Pro Ser Leu Arg Pro Asp
                565                 570                 575

Asp Asp Arg Val Pro Arg Arg Gly Met Asp Asp Asp Arg Gly Pro Arg
            580                 585                 590

Arg Gly Pro Glu Glu Asp Arg Phe Ser Arg Arg Gly Ala Asp Asp Asp
        595                 600                 605

Arg Pro Ser Trp Arg Asn Thr Asp Asp Asp Arg Pro Pro Arg Arg Ile
    610                 615                 620

Ala Asp Glu Asp Arg Gly Asn Trp Arg His Ala Asp Asp Asp Arg Pro
625                 630                 635                 640

Pro Arg Arg Gly Leu Asp Glu Asp Arg Gly Ser Trp Arg Thr Ala Asp
                645                 650                 655

Glu Asp Arg Gly Pro Arg Arg Gly Met Asp Asp Asp Arg Gly Pro Arg
            660                 665                 670

Arg Gly Gly Ala Asp Asp Glu Arg Ser Ser Trp Arg Asn Ala Asp Asp
        675                 680                 685

Asp Arg Gly Pro Arg Arg Gly Leu Asp Asp Asp Arg Gly Pro Arg Arg
    690                 695                 700
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Gly Met Asp Asp Asp Arg Gly Pro Arg Arg Gly Met Asp Asp Asp Arg
705 710 715 720

Gly Pro Arg Arg Gly Met Asp Asp Asp Arg Gly Pro Arg Arg Gly Leu
725 730 735

Asp Asp Asp Arg Gly Pro Trp Arg Asn Ala Asp Asp Asp Arg Ile Pro
740 745 750

Arg Arg Gly Ala Glu Asp Asp Arg Gly Pro Trp Arg Asn Met Asp Asp
755 760 765

Asp Arg Leu Ser Arg Arg Ala Asp Asp Asp Arg Phe Pro Arg Arg Gly
770 775 780

Asp Asp Ser Arg Pro Gly Pro Trp Arg Pro Leu Val Lys Pro Gly Gly
785 790 795 800

Trp Arg Glu Lys Glu Lys Ala Arg Glu Glu Ser Trp Gly Pro Pro Arg
805 810 815

Glu Ser Arg Pro Ser Glu Glu Arg Glu Trp Asp Arg Glu Lys Glu Arg
820 825 830

Asp Arg Asp Asn Gln Asp Arg Glu Glu Asn Asp Lys Asp Pro Glu Arg
835 840 845

Glu Arg Asp Arg Glu Arg Asp Val Asp Arg Glu Asp Arg Phe Arg Arg
850 855 860

Pro Arg Asp Glu Gly Gly Trp Arg Arg Gly Pro Ala Glu Glu Ser Ser
865 870 875 880

Ser Trp Arg Asp Ser Ser Arg Arg Asp Asp Arg Asp Arg Asp Asp Arg
885 890 895

Arg Arg Glu Arg Asp Asp Arg Arg Asp Leu Arg Glu Arg Arg Asp Leu
900 905 910

Arg Asp Asp Arg Asp Arg Arg Gly Pro Pro Leu Arg Ser Glu Arg Glu
915 920 925

Glu Val Ser Ser Trp Arg Arg Ala Asp Asp Arg Lys Asp Asp Arg Val
930 935 940

Glu Glu Arg Asp Pro Pro Arg Arg Val Pro Pro Pro Ala Leu Ser Arg
945 950 955 960

Asp Arg Glu Arg Asp Arg Asp Arg Glu Arg Glu Gly Glu Lys Glu Lys
965 970 975

Ala Ser Trp Arg Ala Glu Lys Asp Arg Glu Ser Leu Arg Arg Thr Lys
980 985 990

Asn Glu Thr Asp Glu Asp Gly Trp Thr Thr Val Arg Arg
995 1000 1005

<210> 1336
<211> 231
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (52)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (64)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (73)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (79)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (82)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (83)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (118)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1336
Ala Gly Ile His Pro Met Asn Ser Ile Ser Ser Leu Asp Arg Thr Arg
1 5 10 15

Met Met Thr Pro Phe Met Gly Ile Ser Pro Leu Pro Gly Gly Glu Arg
20 25 30

Phe Pro Tyr Pro Ser Phe His Trp Asp Pro Ile Arg Asp Pro Leu Arg
35 40 45

Asp Pro Tyr Xaa Glu Leu Asp Ile His Arg Arg Asp Pro Leu Gly Xaa
50 55 60

Asp Phe Leu Leu Arg Asn Asp Pro Xaa His Arg Leu Ser Thr Xaa Arg
65 70 75 80

Leu Xaa Xaa Ala Asp Arg Ser Phe Arg Asp Arg Glu Pro His Asp Tyr
85 90 95

Ser His His His His His His His His Pro Leu Ser Val Asp Pro Arg
100 105 110

Arg Glu His Glu Arg Xaa Gly His Leu Asp Glu Arg Glu Arg Leu His
115 120 125

Met Leu Arg Glu Asp Tyr Glu His Thr Arg Leu His Ser Val His Pro
130 135 140

Ala Ser Leu Asp Gly His Leu Pro His Pro Ser Leu Ile Thr Pro Gly
145 150 155 160

Leu Pro Ser Met His Tyr Pro Arg Ile Ser Pro Thr Ala Gly Asn Gln
165 170 175

Asn Gly Leu Leu Asn Lys Thr Pro Pro Thr Ala Ala Leu Ser Ala Pro
180 185 190

Pro Pro Leu Ile Ser Thr Leu Gly Gly Arg Pro Val Ser Pro Arg Arg
195 200 205

Thr Thr Pro Leu Ser Ala Glu Ile Arg Glu Arg Pro Pro Ser His Thr
210 215 220

Leu Lys Asp Ile Glu Ala Arg
225 230

<210> 1337
<211> 155
<212> PRT
<213> Homo sapiens

<400> 1337

Gly Val Glu Gly Leu Lys Asp Ala Gln Met Arg Asp Leu Leu Ser Pro
1 5 10 15

Pro Thr Asp Asn Arg Pro Gly Gln Met Asp Asn Arg Ser Lys Leu Arg
20 25 30

Asn Ile Val Glu Leu Arg Leu Ala Gly Leu Asp Ile Thr Asp Ala Ser
35 40 45

Leu Arg Leu Ile Ile Arg His Met Pro Leu Leu Ser Lys Leu His Leu
50 55 60

Ser Tyr Cys Asn His Val Thr Asp Gln Ser Ile Asn Leu Leu Thr Ala
65 70 75 80

Val Gly Thr Thr Thr Arg Asp Ser Leu Thr Glu Ile Asn Leu Ser Asp
85 90 95

Cys Asn Lys Val Thr Asp Gln Cys Leu Ser Phe Phe Lys Arg Cys Gly
100 105 110

Asn Ile Cys His Ile Asp Leu Arg Tyr Cys Lys Gln Val Thr Lys Glu
115 120 125

Gly Cys Glu Gln Phe Ile Ala Glu Met Ser Val Ser Val Gln Phe Gly
130 135 140

Gln Val Glu Glu Lys Leu Leu Gln Lys Leu Ser
145 150 155

<210> 1338
<211> 328
<212> PRT
<213> Homo sapiens

<400> 1338
Asn Asn Ser Gly Val Met Pro Glu Met Pro Glu Asp Met Glu Gln Glu
1 5 10 15

Glu Val Asn Ile Pro Asn Arg Arg Val Leu Val Thr Gly Ala Thr Gly
20 25 30

Leu Leu Gly Arg Ala Val His Lys Glu Phe Gln Gln Asn Asn Trp His
35 40 45

Ala Val Gly Cys Gly Phe Arg Arg Ala Arg Pro Lys Phe Glu Gln Val
50 55 60

Asn Leu Leu Asp Ser Asn Ala Val His His Ile Ile His Asp Phe Gln

```
 65                  70                  75                  80

Pro His Val Ile Val His Cys Ala Ala Glu Arg Arg Pro Asp Val Val
                85                  90                  95

Glu Asn Gln Pro Asp Ala Ala Ser Gln Leu Asn Val Asp Ala Ser Gly
            100                 105                 110

Asn Leu Ala Lys Glu Ala Ala Ala Val Gly Ala Phe Leu Ile Tyr Ile
        115                 120                 125

Ser Ser Asp Tyr Val Phe Asp Gly Thr Asn Pro Pro Tyr Arg Glu Glu
    130                 135                 140

Asp Ile Pro Ala Pro Leu Asn Leu Tyr Gly Lys Thr Lys Leu Asp Gly
145                 150                 155                 160

Glu Lys Ala Val Leu Glu Asn Asn Leu Gly Ala Ala Val Leu Arg Ile
                165                 170                 175

Pro Ile Leu Tyr Gly Glu Val Glu Lys Leu Glu Glu Ser Ala Val Thr
            180                 185                 190

Val Met Phe Asp Lys Val Gln Phe Ser Asn Lys Ser Ala Asn Met Asp
        195                 200                 205

His Trp Gln Gln Arg Phe Pro Thr His Val Lys Asp Val Ala Thr Val
    210                 215                 220

Cys Arg Gln Leu Ala Glu Lys Arg Met Leu Asp Pro Ser Ile Lys Gly
225                 230                 235                 240

Thr Phe His Trp Ser Gly Asn Glu Gln Met Thr Lys Tyr Glu Met Ala
                245                 250                 255

Cys Ala Ile Ala Asp Ala Phe Asn Leu Pro Ser Ser His Leu Arg Pro
            260                 265                 270

Ile Thr Asp Ser Pro Val Leu Gly Ala Gln Arg Pro Arg Asn Ala Gln
        275                 280                 285

Leu Asp Cys Ser Lys Leu Glu Thr Leu Gly Ile Gly Gln Arg Thr Pro
    290                 295                 300

Phe Arg Ile Gly Ile Lys Glu Ser Leu Trp Pro Phe Leu Ile Asp Lys
305                 310                 315                 320

Arg Trp Arg Gln Thr Val Phe His
                325
```

<210> 1339
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1339
Leu Xaa His Pro Phe Ala Val Thr Ser Tyr Gly Lys Asn Leu Tyr Phe
1 5 10 15

Thr Asp Trp Lys Met Asn Ser Val Val Ala Leu Asp Leu Ala Ile Ser
20 25 30

Lys Glu Thr Asp Ala Phe Gln Pro His Lys Gln Thr Arg Leu Tyr Gly
35 40 45

Ile Thr Thr Ala Leu Ser Gln Cys Pro Gln Ala Ile Thr Thr Ala Gln
50 55 60

<210> 1340
<211> 155
<212> PRT
<213> Homo sapiens

<400> 1340
Arg Lys Met Ala Val Glu Ser Arg Val Thr Gln Glu Glu Ile Lys Lys
1 5 10 15

Glu Pro Glu Lys Pro Ile Asp Arg Glu Lys Thr Cys Pro Leu Leu Leu
20 25 30

Arg Val Phe Thr Thr Asn Asn Gly Arg His His Arg Met Asp Glu Phe
35 40 45

Ser Arg Gly Asn Val Pro Ser Ser Glu Leu Gln Ile Tyr Thr Trp Met
50 55 60

Asp Ala Thr Leu Lys Glu Leu Thr Ser Leu Val Lys Glu Val Tyr Pro
65 70 75 80

Glu Ala Arg Lys Lys Gly Thr His Phe Asn Phe Ala Ile Val Phe Thr

85 90 95

Asp Val Lys Arg Pro Gly Tyr Arg Val Lys Glu Ile Gly Ser Thr Met
100 105 110

Ser Gly Arg Lys Gly Thr Asp Asp Ser Met Thr Leu Gln Ser Gln Lys
115 120 125

Phe Gln Ile Gly Asp Tyr Leu Asp Ile Ala Ile Thr Pro Pro Asn Arg
130 135 140

Ala Pro Pro Pro Ser Gly Arg Met Arg Pro Tyr
145 150 155

<210> 1341
<211> 72
<212> PRT
<213> Homo sapiens

<400> 1341
Ala Gln Leu Pro Ser Ser Ser Phe Leu Arg His Arg Gly Val Phe Leu
1 5 10 15

Thr Pro Leu Leu Ala Met Ser Ser His Lys Thr Phe Arg Ile Lys Arg
20 25 30

Phe Leu Ala Lys Lys Gln Lys Gln Asn Arg Pro Ile Pro Gln Trp Ile
35 40 45

Arg Met Lys Thr Gly Asn Lys Ile Arg Tyr Asn Ser Lys Arg Arg His
50 55 60

Trp Arg Arg Thr Lys Leu Gly Leu
65 70

<210> 1342
<211> 270
<212> PRT
<213> Homo sapiens

<400> 1342
Leu Lys Val Ala Gln Thr Asp Gly Val Asn Val Asp Met His Leu Lys
1 5 10 15

Gln Ile Glu Ile Lys Lys Phe Lys Tyr Gly Ile Glu Glu His Gly Lys
20 25 30

Val Lys Met Arg Gly Gly Leu Leu Arg Thr Tyr Ile Ile Ser Ile Leu
35 40 45

Phe Lys Ser Ile Phe Glu Val Ala Phe Leu Leu Ile Gln Trp Tyr Ile
50 55 60

Tyr Gly Phe Ser Leu Ser Ala Val Tyr Thr Cys Lys Arg Asp Pro Cys
65 70 75 80

Pro His Gln Val Asp Cys Phe Leu Ser Arg Pro Thr Glu Lys Thr Ile
85 90 95

Phe Ile Ile Phe Met Leu Val Val Ser Leu Val Ser Leu Ala Leu Asn
100 105 110

Ile Ile Glu Leu Phe Tyr Val Phe Phe Lys Gly Val Lys Asp Arg Val
115 120 125

Lys Gly Lys Ser Asp Pro Tyr His Ala Thr Ser Gly Ala Leu Ser Pro
130 135 140

Ala Lys Asp Cys Gly Ser Gln Lys Tyr Ala Tyr Phe Asn Gly Cys Ser
145 150 155 160

Ser Pro Thr Ala Pro Leu Ser Pro Met Ser Pro Pro Gly Tyr Lys Leu
165 170 175

Val Thr Gly Asp Arg Asn Asn Ser Ser Cys Arg Asn Tyr Asn Lys Gln
180 185 190

Ala Ser Glu Gln Asn Trp Ala Asn Tyr Ser Ala Glu Gln Asn Arg Met
195 200 205

Gly Gln Ala Gly Ser Thr Ile Ser Asn Ser His Ala Gln Pro Phe Asp
210 215 220

Phe Pro Asp Asp Asn Gln Asn Ser Lys Lys Leu Ala Ala Gly His Glu
225 230 235 240

Leu Gln Pro Leu Ala Ile Val Asp Gln Arg Pro Ser Ser Arg Ala Ser
245 250 255

Ser Arg Ala Ser Ser Arg Pro Arg Pro Asp Asp Leu Glu Ile
260 265 270

<210> 1343
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1343
Gln Glu Leu Arg Ser Pro Ser Arg Ser Pro Ser Pro Pro Pro Lys Ser
1 5 10 15

Pro Pro Trp Thr Thr Gly Gly Ser Leu Cys Glu Gln Leu Ala Phe Arg
20 25 30

Lys Pro Leu Ser Val Phe Lys Gln Lys Val Glu Gly Ala Thr Lys Gln
35 40 45

Ala Ala Val Arg Ala Ser Xaa Cys Arg Pro Leu Pro Cys Ser Ser Ser
50 55 60

Ser Phe Ala Ser Ala Ser Ser Val Met Phe Cys Leu Glu Phe Tyr Leu
65 70 75 80

Asp Phe Phe Ser Gly Tyr Phe Ser Val Phe Gln Pro Leu Leu
85 90

<210> 1344
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (118)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (122)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (123)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1344
Tyr Ser Thr Arg Ala Leu Trp Lys Pro Asn His Val His Val Cys Val
1 5 10 15

Cys Val Cys Ala Ser Phe Glu Pro Pro Ser Thr Ala Ala Ser Ser His
20 25 30

Asp Thr Lys Leu Leu Ile Ser Thr Phe Leu Trp Val Ala Gln Gly Leu
35 40 45

Ile Ala Ser His Ser Ile Thr Arg Ile Glu Ala Arg His Gly Gly Ala
50 55 60

Cys Leu Val Val Pro Ala Lys Leu Gly Arg Leu Glu Gly Arg Glu Gly
65 70 75 80

Ser Leu Trp Ser Pro Gly Arg Leu Glu Gly Trp Gln Trp Ser His Gly
85 90 95

Ser Gly Gly His Trp His Phe Gln Pro Gly Gly Gly Arg Val Glu Thr
100 105 110

Phe Val Leu Gln Lys Xaa Lys Lys Lys Xaa Xaa Gly Gly
115 120 125

<210> 1345
<211> 131
<212> PRT
<213> Homo sapiens

<400> 1345
Pro Arg Val Arg Arg Leu Arg Glu Asp Asp Arg Arg Gly Phe Leu Ser
1 5 10 15

Phe Arg Ala Asp Ser Ala His Ala Ser Met Val Asn Val Pro Lys Thr
20 25 30

Arg Arg Thr Phe Cys Lys Lys Cys Gly Lys His Gln Pro His Lys Val
35 40 45

Thr Gln Tyr Lys Lys Gly Lys Asp Ser Leu Tyr Ala Gln Gly Lys Arg
50 55 60

Arg Tyr Asp Arg Lys Gln Ser Gly Tyr Gly Gly Gln Thr Lys Pro Ile
65 70 75 80

Phe Arg Lys Lys Ala Lys Thr Thr Lys Lys Ile Val Leu Arg Leu Glu
85 90 95

Cys Val Glu Pro Asn Cys Arg Ser Lys Arg Met Leu Ala Ile Lys Arg
100 105 110

Cys Lys His Phe Glu Leu Gly Gly Asp Lys Lys Arg Lys Gly Gln Val

115 120 125

Ile Gln Phe
130

<210> 1346
<211> 75
<212> PRT
<213> Homo sapiens

<400> 1346
Asn Lys Arg Asn Cys Lys Phe Pro Leu Leu Lys Ile Thr Lys Ile Thr
1 5 10 15

Glu Thr Lys Glu Glu Ile Arg Ile Trp Gly Ile Val Leu Asn Asn Leu
20 25 30

Val Val Lys Lys Asn Asn Cys Ala Cys Leu Asp Leu Asn Lys Pro Pro
35 40 45

Ser Lys Cys Glu Gly Ser Ser Asn Phe Ser Lys His Met Lys Val Leu
50 55 60

Ile His Phe Asp Lys Gly Pro Leu Lys Lys Ser
65 70 75

<210> 1347
<211> 413
<212> PRT
<213> Homo sapiens

<400> 1347
Gly Val Ala Arg Ala Gln Pro Val Pro Ala Val Leu Ser Trp Leu Leu
1 5 10 15

Ala Leu Leu Arg Cys Ala Ala Thr Met Leu Ser Leu Arg Val Pro Leu
20 25 30

Ala Pro Ile Thr Asp Pro Gln Gln Leu Gln Leu Ser Pro Leu Lys Gly
35 40 45

Leu Ser Leu Val Asp Lys Glu Asn Thr Pro Pro Ala Leu Ser Gly Thr
50 55 60

Arg Val Leu Ala Ser Lys Thr Ala Arg Arg Ile Phe Gln Glu Pro Thr
65 70 75 80

```
Glu Pro Lys Thr Lys Ala Ala Ala Pro Gly Val Glu Asp Glu Pro Leu
                85                  90                  95

Leu Arg Glu Asn Pro Arg Arg Phe Val Ile Phe Pro Ile Glu Tyr His
            100                 105                 110

Asp Ile Trp Gln Met Tyr Lys Lys Ala Glu Ala Ser Phe Trp Thr Ala
        115                 120                 125

Glu Glu Val Asp Leu Ser Lys Asp Ile Gln His Trp Glu Ser Leu Lys
    130                 135                 140

Pro Glu Glu Arg Tyr Phe Ile Ser His Val Leu Ala Phe Phe Ala Ala
145                 150                 155                 160

Ser Asp Gly Ile Val Asn Glu Asn Leu Val Glu Arg Phe Ser Gln Glu
                165                 170                 175

Val Gln Ile Thr Glu Ala Arg Cys Phe Tyr Gly Phe Gln Ile Ala Met
            180                 185                 190

Glu Asn Ile His Ser Glu Met Tyr Ser Leu Leu Ile Asp Thr Tyr Ile
        195                 200                 205

Lys Asp Pro Lys Glu Arg Glu Phe Leu Phe Asn Ala Ile Glu Thr Met
    210                 215                 220

Pro Cys Val Lys Lys Lys Ala Asp Trp Ala Leu Arg Trp Ile Gly Asp
225                 230                 235                 240

Lys Glu Ala Thr Tyr Gly Glu Arg Val Val Ala Phe Ala Ala Val Glu
                245                 250                 255

Gly Ile Phe Phe Ser Gly Ser Phe Ala Ser Ile Phe Trp Leu Lys Lys
            260                 265                 270

Arg Gly Leu Met Pro Gly Leu Thr Phe Ser Asn Glu Leu Ile Ser Arg
        275                 280                 285

Asp Glu Gly Leu His Cys Asp Phe Ala Cys Leu Met Phe Lys His Leu
    290                 295                 300

Val His Lys Pro Ser Glu Glu Arg Val Arg Glu Ile Ile Ile Asn Ala
305                 310                 315                 320

Val Arg Ile Glu Gln Glu Phe Leu Thr Glu Ala Leu Pro Val Lys Leu
                325                 330                 335

Ile Gly Met Asn Cys Thr Leu Met Lys Gln Tyr Ile Glu Phe Val Ala
            340                 345                 350
```

Asp Arg Leu Met Leu Glu Leu Gly Phe Ser Lys Val Phe Arg Val Glu
355 360 365

Asn Pro Phe Asp Phe Met Glu Asn Ile Ser Leu Glu Gly Lys Thr Asn
370 375 380

Phe Phe Glu Lys Arg Val Gly Glu Tyr Gln Arg Met Gly Val Met Ser
385 390 395 400

Ser Pro Thr Glu Asn Ser Phe Thr Leu Asp Ala Asp Phe
405 410

<210> 1348
<211> 243
<212> PRT
<213> Homo sapiens

<400> 1348
Thr Gly Asn Lys Met Gln Asp Pro Asn Ala Asp Thr Glu Trp Asn Asp
1 5 10 15

Ile Leu Arg Lys Lys Gly Ile Leu Pro Pro Lys Glu Ser Leu Lys Glu
20 25 30

Leu Glu Glu Glu Ala Glu Glu Glu Gln Arg Ile Leu Gln Gln Ser Val
35 40 45

Val Lys Thr Tyr Glu Asp Met Thr Leu Glu Glu Leu Glu Asp His Glu
50 55 60

Asp Glu Phe Asn Glu Glu Asp Glu Arg Ala Ile Glu Met Tyr Arg Arg
65 70 75 80

Arg Arg Leu Ala Glu Trp Lys Ala Thr Lys Leu Lys Asn Lys Phe Gly
85 90 95

Glu Val Leu Glu Ile Ser Gly Lys Asp Tyr Val Gln Glu Val Thr Lys
100 105 110

Ala Gly Glu Gly Leu Trp Val Ile Leu His Leu Tyr Lys Gln Gly Ile
115 120 125

Pro Leu Cys Ala Leu Ile Asn Gln His Leu Ser Gly Leu Ala Arg Lys
130 135 140

Phe Pro Asp Val Lys Phe Ile Lys Ala Ile Ser Thr Thr Cys Ile Pro
145 150 155 160

Asn Tyr Pro Asp Arg Asn Leu Pro Thr Ile Phe Val Tyr Leu Glu Gly

165 170 175

Asp Ile Lys Ala Gln Phe Ile Gly Pro Leu Val Phe Gly Gly Met Asn
180 185 190

Leu Thr Arg Asp Glu Leu Glu Trp Lys Leu Ser Glu Ser Gly Ala Ile
195 200 205

Met Thr Asp Leu Glu Glu Asn Pro Lys Lys Pro Ile Glu Asp Val Leu
210 215 220

Leu Ser Ser Val Arg Arg Ser Val Leu Met Lys Arg Asp Ser Asp Ser
225 230 235 240

Glu Gly Asp

<210> 1349
<211> 326
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (137)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (142)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1349
Arg Met Ala Thr Pro Leu Pro Pro Pro Ser Pro Arg His Leu Arg Leu
1 5 10 15

Leu Arg Leu Leu Leu Ser Gly Leu Val Leu Gly Ala Ala Leu Arg Gly
20 25 30

Ala Ala Ala Gly His Pro Asp Val Ala Ala Cys Pro Gly Ser Leu Asp
35 40 45

Cys Ala Leu Lys Arg Arg Ala Arg Cys Pro Pro Gly Ala His Ala Cys
50 55 60

Gly Pro Cys Leu Gln Pro Phe Gln Glu Asp Gln Gln Gly Leu Cys Val
65 70 75 80

Pro Arg Met Arg Arg Pro Pro Gly Gly Gly Arg Pro Gln Pro Arg Leu

```
                85                  90                  95

Glu Asp Glu Ile Asp Phe Leu Ala Gln Glu Leu Ala Arg Lys Glu Ser
            100                 105                 110

Gly His Ser Thr Pro Pro Leu Pro Lys Asp Arg Gln Arg Leu Pro Glu
        115                 120                 125

Pro Ala Thr Leu Gly Phe Ser Ala Xaa Gly Gln Gly Leu Xaa Leu Gly
    130                 135                 140

Leu Pro Ser Thr Pro Gly Thr Pro Thr Pro Thr Pro His Thr Ser Leu
145                 150                 155                 160

Gly Ser Pro Val Ser Ser Asp Pro Val His Met Ser Pro Leu Glu Pro
                165                 170                 175

Arg Gly Gly Gln Gly Asp Gly Leu Ala Leu Val Leu Ile Leu Ala Phe
            180                 185                 190

Cys Val Ala Gly Ala Ala Ala Leu Ser Val Ala Ser Leu Cys Trp Cys
        195                 200                 205

Arg Leu Gln Arg Glu Ile Arg Leu Thr Gln Lys Ala Asp Tyr Ala Thr
    210                 215                 220

Ala Lys Ala Pro Gly Ser Pro Ala Ala Pro Arg Ile Ser Pro Gly Asp
225                 230                 235                 240

Gln Arg Leu Ala Gln Ser Ala Glu Met Tyr His Tyr Gln His Gln Arg
                245                 250                 255

Gln Gln Met Leu Cys Leu Glu Arg His Lys Glu Pro Pro Lys Glu Leu
            260                 265                 270

Asp Thr Ala Ser Ser Asp Glu Glu Asn Glu Asp Gly Asp Phe Thr Val
        275                 280                 285

Tyr Glu Cys Pro Gly Leu Ala Pro Thr Gly Glu Met Glu Val Arg Asn
    290                 295                 300

Pro Leu Phe Asp His Ala Ala Leu Ser Ala Pro Leu Pro Ala Pro Ser
305                 310                 315                 320

Ser Pro Pro Ala Leu Pro
                325


<210> 1350
<211> 62
```

<212> PRT
<213> Homo sapiens

<400> 1350
Val Lys Ser Asp Thr Pro Pro Cys Val Ser Lys Asn Leu Val Pro Pro
1 5 10 15

Leu His Thr Ser Leu Thr Leu Asn Ile Phe His Trp Ile Leu Asp Arg
20 25 30

Ala Lys Gly Arg Thr Gly Ala Ser Gly Gly Pro Trp Leu Phe Lys Ser
35 40 45

Trp Ile Ile Cys Asp Ser Asn His Lys Phe Leu Ala Asn Phe
50 55 60

<210> 1351
<211> 312
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (299)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1351
Glu Pro Arg Pro Gly Cys Gly Asn Lys Met Ala Gly Lys Lys Asn Val
1 5 10 15

Leu Ser Ser Leu Ala Val Tyr Ala Glu Asp Ser Glu Pro Glu Ser Asp
20 25 30

Gly Glu Ala Gly Ile Glu Ala Val Gly Ser Ala Ala Glu Glu Lys Gly
35 40 45

Gly Leu Val Ser Asp Ala Tyr Gly Glu Asp Asp Phe Ser Arg Leu Gly
50 55 60

Gly Asp Glu Asp Gly Tyr Glu Glu Glu Glu Asp Glu Asn Ser Arg Gln
65 70 75 80

Ser Glu Asp Asp Asp Ser Glu Thr Glu Lys Pro Glu Ala Asp Asp Pro
85 90 95

Lys Asp Asn Thr Glu Ala Glu Lys Arg Asp Pro Gln Glu Leu Val Ala
100 105 110

Ser Phe Ser Glu Arg Val Arg Asn Met Ser Pro Asp Glu Ile Lys Ile

```
        115                 120                 125

Pro Pro Glu Pro Pro Gly Arg Cys Ser Asn His Leu Gln Asp Lys Ile
    130                 135                 140

Gln Lys Leu Tyr Glu Arg Lys Ile Lys Glu Gly Met Asp Met Asn Tyr
145                 150                 155                 160

Ile Ile Gln Arg Lys Lys Glu Phe Arg Asn Pro Ser Ile Tyr Glu Lys
                165                 170                 175

Leu Ile Gln Phe Cys Ala Ile Asp Glu Leu Gly Thr Asn Tyr Pro Lys
            180                 185                 190

Asp Met Phe Asp Pro His Gly Trp Ser Glu Asp Ser Tyr Tyr Glu Ala
        195                 200                 205

Leu Ala Lys Ala Gln Lys Ile Glu Met Asp Lys Leu Glu Lys Ala Lys
    210                 215                 220

Lys Glu Arg Thr Lys Ile Glu Phe Val Thr Gly Thr Lys Lys Gly Thr
225                 230                 235                 240

Thr Thr Asn Ala Thr Ser Thr Thr Thr Thr Thr Ala Ser Thr Ala Val
                245                 250                 255

Ala Asp Ala Gln Lys Arg Lys Ser Lys Trp Asp Ser Ala Ile Pro Val
            260                 265                 270

Thr Thr Ile Ser Pro Ala His His Pro His His His Ser His Pro Ala
        275                 280                 285

Ser Cys Cys His Gly His His Gln Arg Gln Xaa Ser Lys Asp His Arg
    290                 295                 300

His Leu Cys Cys Gly Ala Pro Leu
305                 310
```

<210> 1352
<211> 259
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1352

```
Leu Leu Asp Ser Leu Lys Xaa Asp Tyr Ala Gly Lys Pro Gln Pro Pro
 1               5                  10                  15

Ile Lys Ser Glu Arg Arg Asn Pro Pro Ser Tyr Ala Met Ala Gly Lys
            20                  25                  30

Lys Val Leu Ile Val Tyr Ala His Gln Glu Pro Lys Ser Phe Asn Gly
        35                  40                  45

Ser Leu Lys Asn Val Ala Val Asp Glu Leu Ser Arg Gln Gly Cys Thr
    50                  55                  60

Val Thr Val Ser Asp Leu Tyr Ala Met Asn Phe Glu Pro Arg Ala Thr
65                  70                  75                  80

Asp Lys Asp Ile Thr Gly Thr Leu Ser Asn Pro Glu Val Phe Asn Tyr
                85                  90                  95

Gly Val Glu Thr His Glu Ala Tyr Lys Gln Arg Ser Leu Ala Ser Asp
            100                 105                 110

Ile Thr Asp Glu Gln Lys Lys Val Arg Glu Ala Asp Leu Val Ile Phe
        115                 120                 125

Gln Phe Pro Leu Tyr Trp Phe Ser Val Pro Ala Ile Leu Lys Gly Trp
    130                 135                 140

Met Asp Arg Val Leu Cys Gln Gly Phe Ala Phe Asp Ile Pro Gly Phe
145                 150                 155                 160

Tyr Asp Ser Gly Leu Leu Gln Gly Lys Leu Ala Leu Leu Ser Val Thr
                165                 170                 175

Thr Gly Gly Thr Ala Glu Met Tyr Thr Lys Thr Gly Val Asn Gly Asp
            180                 185                 190

Ser Arg Tyr Phe Leu Trp Pro Leu Gln His Gly Thr Leu His Phe Cys
        195                 200                 205

Gly Phe Lys Val Leu Ala Pro Gln Ile Ser Phe Ala Pro Glu Ile Ala
    210                 215                 220

Ser Glu Glu Glu Arg Lys Gly Met Val Ala Ala Trp Ser Gln Arg Leu
225                 230                 235                 240

Gln Thr Ile Trp Lys Glu Glu Pro Ile Pro Cys Thr Ala His Trp His
                245                 250                 255

Phe Gly Gln
```

<210> 1353
<211> 72
<212> PRT
<213> Homo sapiens

<400> 1353
Asp Leu Ala Ser Glu Glu His Phe Phe Ser Val Lys Phe Leu Tyr Leu
1 5 10 15

Lys Ile Gln Lys Tyr Phe Arg Ile Leu Leu Ile Leu Ser Pro Val Phe
20 25 30

Thr Ser Phe Trp Lys Thr Cys Ile Thr Met Ser Leu Glu Lys Gly Gln
35 40 45

Arg Lys Ala Phe His Val Lys Ile Arg Ser Leu Ala Ile Ser Asn Pro
50 55 60

Val Leu Phe Ser Leu His Phe Phe
65 70

<210> 1354
<211> 301
<212> PRT
<213> Homo sapiens

<400> 1354
Lys Arg Arg Arg Arg Leu Glu Gln Arg Gln Gln Pro Asp Glu Gln Arg
1 5 10 15

Arg Arg Ser Gly Ala Met Val Lys Met Ala Ala Ala Gly Gly Gly Gly
20 25 30

Gly Gly Gly Arg Tyr Tyr Gly Gly Gly Ser Glu Gly Gly Arg Ala Pro
35 40 45

Lys Arg Leu Lys Thr Asp Asn Ala Gly Asp Gln His Gly Gly Gly Gly
50 55 60

Gly Gly Gly Gly Gly Ala Gly Ala Ala Gly Gly Gly Gly Gly Gly Glu
65 70 75 80

Asn Tyr Asp Asp Pro His Lys Thr Pro Ala Ser Pro Val Val His Ile
85 90 95

Arg Gly Leu Ile Asp Gly Val Val Glu Ala Asp Leu Val Glu Ala Leu
100 105 110

```
Gln Glu Phe Gly Pro Ile Ser Tyr Val Val Val Met Pro Lys Lys Arg
        115                 120                 125

Gln Ala Leu Val Glu Phe Glu Asp Val Leu Gly Ala Cys Asn Ala Val
    130                 135                 140

Asn Tyr Ala Ala Asp Asn Gln Ile Tyr Ile Ala Gly His Pro Ala Phe
145                 150                 155                 160

Val Asn Tyr Ser Thr Ser Gln Lys Ile Ser Arg Pro Gly Asp Ser Asp
                165                 170                 175

Asp Ser Arg Ser Val Asn Ser Val Leu Leu Phe Thr Ile Leu Asn Pro
            180                 185                 190

Ile Tyr Ser Ile Thr Thr Asp Val Leu Tyr Thr Ile Cys Asn Pro Cys
        195                 200                 205

Gly Pro Val Gln Arg Ile Val Ile Phe Arg Lys Asn Gly Val Gln Ala
    210                 215                 220

Met Val Glu Phe Asp Ser Val Gln Ser Ala Gln Arg Ala Lys Ala Ser
225                 230                 235                 240

Leu Asn Gly Ala Asp Ile Tyr Ser Gly Cys Cys Thr Leu Lys Ile Glu
                245                 250                 255

Tyr Ala Lys Pro Thr Arg Leu Asn Val Phe Lys Asn Asp Gln Asp Thr
            260                 265                 270

Trp Asp Tyr Thr Asn Pro Asn Leu Ser Gly Gln Gly Asn Leu Asp Asp
        275                 280                 285

His Phe Val Leu Asn Ile Pro Ala Leu Leu Ser Leu Asp
    290                 295                 300
```

<210> 1355
<211> 466
<212> PRT
<213> Homo sapiens

<400> 1355

```
Asn Thr Val Met Gly Arg Lys Lys Lys Lys Gln Leu Lys Pro Trp Cys
  1               5                  10                  15

Trp Tyr Cys Asn Arg Asp Phe Asp Asp Glu Lys Ile Leu Ile Gln His
             20                  25                  30
```

```
Gln Lys Ala Lys His Phe Lys Cys His Ile Cys His Lys Lys Leu Tyr
        35                  40                  45

Thr Gly Pro Gly Leu Ala Ile His Cys Met Gln Val His Lys Glu Thr
    50                  55                  60

Ile Asp Ala Val Pro Asn Ala Ile Pro Gly Arg Thr Asp Ile Glu Leu
65                  70                  75                  80

Glu Ile Tyr Gly Met Glu Gly Ile Pro Glu Lys Asp Met Asp Glu Arg
                85                  90                  95

Arg Arg Leu Leu Glu Gln Lys Thr Gln Glu Ser Gln Lys Lys Lys Gln
            100                 105                 110

Gln Asp Asp Ser Asp Glu Tyr Asp Asp Asp Asp Ser Ala Ala Ser Thr
        115                 120                 125

Ser Phe Gln Pro Gln Pro Val Gln Pro Gln Gln Gly Tyr Ile Pro Pro
    130                 135                 140

Met Ala Gln Pro Gly Leu Pro Pro Val Pro Gly Ala Pro Gly Met Pro
145                 150                 155                 160

Pro Gly Ile Pro Pro Leu Met Pro Gly Val Pro Pro Leu Met Pro Gly
                165                 170                 175

Met Pro Pro Val Met Pro Gly Met Pro Pro Gly Leu His His Gln Arg
            180                 185                 190

Lys Tyr Thr Gln Ser Phe Cys Gly Glu Asn Ile Met Met Pro Met Gly
        195                 200                 205

Gly Met Met Pro Pro Gly Pro Gly Ile Pro Pro Leu Met Pro Gly Met
    210                 215                 220

Pro Pro Gly Met Pro Pro Pro Val Pro Arg Pro Gly Ile Pro Pro Met
225                 230                 235                 240

Thr Gln Ala Gln Ala Val Ser Ala Pro Gly Ile Leu Asn Arg Pro Pro
                245                 250                 255

Ala Pro Thr Ala Thr Val Pro Ala Pro Gln Pro Pro Val Thr Lys Pro
            260                 265                 270

Leu Phe Pro Ser Ala Gly Gln Ala Gln Ala Ala Val Gln Gly Pro Val
        275                 280                 285

Gly Thr Asp Phe Lys Pro Leu Asn Ser Thr Pro Ala Thr Thr Thr Glu
    290                 295                 300
```

Pro Pro Lys Pro Thr Phe Pro Ala Tyr Thr Gln Ser Thr Ala Ser Thr
305 310 315 320

Thr Ser Thr Thr Asn Ser Thr Ala Ala Lys Pro Ala Ala Ser Ile Thr
325 330 335

Ser Lys Pro Ala Thr Leu Thr Thr Thr Ser Ala Thr Ser Lys Leu Ile
340 345 350

His Pro Asp Glu Asp Ile Ser Leu Glu Glu Arg Arg Ala Gln Leu Pro
355 360 365

Lys Tyr Gln Arg Asn Leu Pro Arg Pro Gly Gln Ala Pro Ile Gly Asn
370 375 380

Pro Pro Val Gly Pro Ile Gly Gly Met Met Pro Pro Gln Pro Gly Ile
385 390 395 400

Pro Gln Gln Gln Gly Met Arg Pro Pro Met Pro Pro His Gly Gln Tyr
405 410 415

Gly Gly His His Gln Gly Met Pro Gly Tyr Leu Pro Gly Ala Met Pro
420 425 430

Pro Tyr Gly Gln Gly Pro Pro Met Val Pro Pro Tyr Gln Gly Gly Pro
435 440 445

Pro Arg Pro Pro Met Gly Met Arg Pro Pro Val Met Ser Gln Gly Gly
450 455 460

Arg Tyr
465

<210> 1356
<211> 85
<212> PRT
<213> Homo sapiens

<400> 1356
Leu Ser Asp Asp Gln Ser Leu Leu Ile Ile Leu Leu Leu Lys Gly Leu
1 5 10 15

Leu Thr Asn Leu Ser Phe Thr Pro Cys Gly Pro Cys Tyr Trp Tyr Thr
20 25 30

Gln Tyr Val Leu Thr Glu Asp Met Asp Phe Ile Cys Ser Ser Ala Gly
35 40 45

Ile Gly Lys Leu Asp Leu Phe Ser Met Ile Gln Asn Ser Pro Ile Arg

50 55 60

Arg Leu Glu Lys Glu Glu Leu Tyr Ser Ser Leu Cys Tyr Phe Leu Leu
65 70 75 80

Pro Phe Leu Phe Leu
85

<210> 1357
<211> 580
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (526)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1357
Asp Ser Xaa Thr Phe Asp Asp Leu Ala Val Asp Phe Thr Pro Glu Glu
1 5 10 15

Trp Thr Leu Leu Asp Pro Thr Gln Arg Asn Leu Tyr Arg Asp Val Met
20 25 30

Leu Glu Asn Tyr Lys Asn Leu Ala Thr Val Gly Tyr Gln Leu Phe Lys
35 40 45

Pro Ser Leu Ile Ser Trp Leu Glu Gln Glu Glu Ser Arg Thr Val Gln
50 55 60

Arg Gly Asp Phe Gln Ala Ser Glu Trp Lys Val Gln Leu Lys Thr Lys
65 70 75 80

Glu Leu Ala Leu Gln Gln Asp Val Leu Gly Glu Pro Thr Ser Ser Gly
85 90 95

Ile Gln Met Ile Gly Ser His Asn Gly Gly Glu Val Ser Asp Val Lys
100 105 110

Gln Cys Gly Asp Val Ser Ser Glu His Ser Cys Leu Lys Thr His Val
115 120 125

Arg Thr Gln Asn Ser Glu Asn Thr Phe Glu Cys Tyr Leu Tyr Gly Val

130 135 140

Asp Phe Leu Thr Leu His Lys Lys Thr Ser Thr Gly Glu Gln Arg Ser
145 150 155 160

Val Phe Ser Gln Cys Gly Lys Ala Phe Ser Leu Asn Pro Asp Val Val
165 170 175

Cys Gln Arg Thr Cys Thr Gly Glu Lys Ala Phe Asp Cys Ser Asp Ser
180 185 190

Gly Lys Ser Phe Ile Asn His Ser His Leu Gln Gly His Leu Arg Thr
195 200 205

His Asn Gly Glu Ser Leu His Glu Trp Lys Glu Cys Gly Arg Gly Phe
210 215 220

Ile His Ser Thr Asp Leu Ala Val Arg Ile Gln Thr His Arg Ser Glu
225 230 235 240

Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Gly Phe Arg Tyr Ser Ala
245 250 255

Tyr Leu Asn Ile His Met Gly Thr His Thr Gly Asp Asn Pro Tyr Glu
260 265 270

Cys Lys Glu Cys Gly Lys Ala Phe Thr Arg Ser Cys Gln Leu Thr Gln
275 280 285

His Arg Lys Thr His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Asp Cys
290 295 300

Gly Arg Ala Phe Thr Val Ser Ser Cys Leu Ser Gln His Met Lys Ile
305 310 315 320

His Val Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Ile Ala Phe
325 330 335

Thr Arg Ser Ser Gln Leu Thr Glu His Leu Lys Thr His Thr Ala Lys
340 345 350

Asp Pro Phe Glu Cys Lys Ile Cys Gly Lys Ser Phe Arg Asn Ser Ser
355 360 365

Cys Leu Ser Asp His Phe Arg Ile His Thr Gly Ile Lys Pro Tyr Lys
370 375 380

Cys Lys Asp Cys Gly Lys Ala Phe Thr Gln Asn Ser Asp Leu Thr Lys
385 390 395 400

His Ala Arg Thr His Ser Gly Glu Arg Pro Tyr Glu Cys Lys Glu Cys

```
                405                 410                 415

Gly Lys Ala Phe Ala Arg Ser Ser Arg Leu Ser Glu His Thr Arg Thr
            420                 425                 430

His Thr Gly Glu Lys Pro Phe Glu Cys Val Lys Cys Gly Lys Ala Phe
        435                 440                 445

Ala Ile Ser Ser Asn Leu Ser Gly His Leu Arg Ile His Thr Gly Glu
    450                 455                 460

Lys Pro Phe Glu Cys Leu Glu Cys Gly Lys Ala Phe Thr His Ser Ser
465                 470                 475                 480

Ser Leu Asn Asn His Met Arg Thr His Ser Ala Lys Lys Pro Phe Thr
                485                 490                 495

Cys Met Glu Cys Gly Lys Ala Phe Lys Phe Pro Thr Cys Val Asn Leu
            500                 505                 510

His Met Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Xaa Gln Cys
        515                 520                 525

Gly Lys Ser Phe Ser Tyr Ser Asn Ser Phe Gln Leu His Glu Arg Thr
    530                 535                 540

His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe
545                 550                 555                 560

Ser Ser Ser Ser Ser Phe Arg Asn His Glu Arg Arg His Ala Asp Glu
                565                 570                 575

Arg Leu Ser Ala
            580
```

```
<210> 1358
<211> 612
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (134)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (445)
<223> Xaa equals any of the naturally occurring L-amino acids
```

<400> 1358

```
Glu Val Pro Glu Ala His Arg Ala Ser Pro Arg Glu Gly Thr Ser Gly
 1               5                  10                  15

Gly Glu Arg Leu Gln Asp Leu Val Lys Ser Lys Met Ser Glu Thr Ser
            20                  25                  30

Arg Thr Ala Phe Gly Gly Arg Arg Ala Val Pro Pro Asn Asn Ser Asn
        35                  40                  45

Ala Ala Glu Asp Asp Leu Pro Thr Val Glu Leu Gln Gly Val Val Pro
    50                  55                  60

Arg Gly Val Asn Leu Gln Asp Asp Ala Val Tyr Leu Asp Asn Glu Lys
65                  70                  75                  80

Glu Arg Glu Glu Tyr Val Leu Asn Asp Ile Gly Val Ile Phe Tyr Gly
                85                  90                  95

Glu Val Asn Asp Ile Lys Thr Arg Ser Trp Ser Tyr Gly Gln Phe Glu
            100                 105                 110

Asp Gly Ile Leu Asp Thr Cys Leu Tyr Val Met Asp Arg Ala Gln Met
        115                 120                 125

Asp Leu Ser Gly Arg Xaa Asn Pro Ile Lys Val Ser Arg Val Gly Ser
    130                 135                 140

Ala Met Val Asn Ala Lys Asp Asp Glu Gly Val Leu Val Gly Ser Trp
145                 150                 155                 160

Asp Asn Ile Tyr Ala Tyr Gly Val Pro Pro Ser Ala Trp Thr Gly Ser
                165                 170                 175

Val Asp Ile Leu Leu Glu Tyr Arg Ser Ser Glu Asn Pro Val Arg Tyr
            180                 185                 190

Gly Gln Cys Trp Val Phe Ala Gly Val Phe Asn Thr Phe Leu Arg Cys
        195                 200                 205

Leu Gly Ile Pro Ala Arg Ile Val Thr Asn Tyr Phe Ser Ala His Asp
    210                 215                 220

Asn Asp Ala Asn Leu Gln Met Asp Ile Phe Leu Glu Glu Asp Gly Asn
225                 230                 235                 240

Val Asn Ser Lys Leu Thr Lys Asp Ser Val Trp Asn Tyr His Cys Trp
                245                 250                 255

Asn Glu Ala Trp Met Thr Arg Pro Asp Leu Pro Val Gly Phe Gly Gly
```

```
            260                 265                 270

Trp Gln Ala Val Asp Ser Thr Pro Gln Glu Asn Ser Asp Gly Met Tyr
        275                 280                 285

Arg Cys Gly Pro Ala Ser Val Gln Ala Ile Lys His Gly His Val Cys
    290                 295                 300

Phe Gln Phe Asp Ala Pro Phe Val Phe Ala Glu Val Asn Ser Asp Leu
305                 310                 315                 320

Ile Tyr Ile Thr Ala Lys Lys Asp Gly Thr His Val Val Glu Asn Val
                325                 330                 335

Asp Ala Thr His Ile Gly Lys Leu Ile Val Thr Lys Gln Ile Gly Gly
            340                 345                 350

Asp Gly Met Met Asp Ile Thr Asp Thr Tyr Lys Phe Gln Glu Gly Gln
        355                 360                 365

Glu Glu Glu Arg Leu Ala Leu Glu Thr Ala Leu Met Tyr Gly Ala Lys
    370                 375                 380

Lys Pro Leu Asn Thr Glu Gly Val Met Lys Ser Arg Ser Asn Val Asp
385                 390                 395                 400

Met Asp Phe Glu Val Glu Asn Ala Val Leu Gly Lys Asp Phe Lys Leu
                405                 410                 415

Ser Ile Thr Phe Arg Asn Asn Ser His Asn Arg Tyr Thr Ile Thr Ala
            420                 425                 430

Tyr Leu Ser Ala Asn Ile Thr Phe Tyr Thr Gly Val Xaa Lys Ala Glu
        435                 440                 445

Phe Lys Lys Glu Thr Phe Asp Val Thr Leu Glu Pro Leu Ser Phe Lys
    450                 455                 460

Lys Glu Ala Val Leu Ile Gln Ala Gly Glu Tyr Met Gly Gln Leu Leu
465                 470                 475                 480

Glu Gln Ala Ser Leu His Phe Phe Val Thr Ala Arg Ile Asn Glu Thr
                485                 490                 495

Arg Asp Val Leu Ala Lys Gln Lys Ser Thr Val Leu Thr Ile Pro Glu
            500                 505                 510

Ile Ile Ile Lys Val Arg Gly Thr Gln Val Val Gly Ser Asp Met Thr
        515                 520                 525

Val Thr Val Glu Phe Thr Asn Pro Leu Lys Glu Thr Leu Arg Asn Val
```

530 535 540

Trp Val His Leu Asp Gly Pro Gly Val Thr Arg Pro Met Lys Lys Met
545 550 555 560

Phe Arg Glu Ile Arg Pro Asn Ser Thr Val Gln Trp Glu Glu Val Cys
565 570 575

Arg Pro Trp Val Ser Gly His Arg Lys Leu Ile Ala Ser Met Ser Ser
580 585 590

Asp Ser Leu Arg His Val Tyr Gly Glu Leu Asp Val Gln Ile Gln Arg
595 600 605

Arg Pro Ser Met
610

<210> 1359
<211> 56
<212> PRT
<213> Homo sapiens

<400> 1359
Leu Ser Cys Ile Val Leu Leu Arg Gln Ser Ser Val Lys Leu Tyr Gln
1 5 10 15

Leu Arg Leu Val Ser Ser Asp Phe His Trp Gly Ile Arg Val Leu Ala
20 25 30

Gly Leu Asn Leu Leu Leu Val Gly Ser Val Phe Leu Met Asn Lys Ser
35 40 45

His Ser Thr Glu Leu Gln Val Ile
50 55

<210> 1360
<211> 415
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (368)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (374)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (379)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (381)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (384)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (385)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (386)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (389)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (397)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (404)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (405)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (409)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1360
Gly Gly Gly Gly Glu Lys Met Ala Asp Asp Pro Ser Ala Ala Asp Arg
1 5 10 15

Asn Val Glu Ile Trp Lys Ile Lys Lys Leu Ile Lys Ser Leu Glu Ala
20 25 30

Ala Arg Gly Asn Gly Thr Ser Met Ile Ser Leu Ile Ile Pro Pro Lys
35 40 45

Asp Gln Ile Ser Arg Val Ala Lys Met Leu Ala Asp Glu Phe Gly Thr
50 55 60

Ala Ser Asn Ile Lys Ser Arg Val Asn Arg Leu Ser Val Leu Gly Ala
65 70 75 80

Ile Thr Ser Val Gln Gln Arg Leu Lys Leu Tyr Asn Lys Val Pro Pro
85 90 95

Asn Gly Leu Val Val Tyr Cys Gly Thr Ile Val Thr Glu Glu Gly Lys
100 105 110

Glu Lys Lys Val Asn Ile Asp Phe Glu Pro Phe Lys Pro Ile Asn Thr
115 120 125

Ser Leu Tyr Leu Cys Asp Asn Lys Phe His Thr Glu Ala Leu Thr Ala
130 135 140

Leu Leu Ser Asp Asp Ser Lys Phe Gly Phe Ile Val Ile Asp Gly Ser
145 150 155 160

Gly Ala Leu Phe Gly Thr Leu Gln Gly Asn Thr Arg Glu Val Leu His
165 170 175

Lys Phe Thr Val Asp Leu Pro Lys Lys His Gly Arg Gly Gly Gln Ser
180 185 190

Ala Leu Arg Phe Ala Arg Leu Arg Met Glu Lys Arg His Asn Tyr Val
195 200 205

Arg Lys Val Ala Glu Thr Ala Val Gln Leu Phe Ile Ser Gly Asp Lys
210 215 220

Val Asn Val Ala Gly Leu Val Leu Ala Gly Ser Ala Asp Phe Lys Thr
225 230 235 240

Glu Leu Ser Gln Ser Asp Met Phe Asp Gln Arg Leu Gln Ser Lys Val
245 250 255

Leu Lys Leu Val Asp Ile Ser Tyr Gly Gly Glu Asn Gly Phe Asn Gln
260 265 270

Ala Ile Glu Leu Ser Thr Glu Val Leu Ser Asn Val Lys Phe Ile Gln
275 280 285

Glu Lys Lys Leu Ile Gly Arg Tyr Phe Asp Glu Ile Ser Gln Asp Thr
290 295 300

Gly Lys Tyr Cys Phe Gly Val Glu Asp Thr Leu Lys Ala Leu Glu Met
305 310 315 320

Gly Ala Val Glu Ile Leu Ile Val Tyr Glu Asn Leu Asp Ile Met Arg
325 330 335

Tyr Val Leu His Cys Gln Gly Thr Glu Glu Glu Lys Ile Leu Tyr Leu
340 345 350

Thr Pro Glu Gln Glu Lys Asp Lys Ser His Phe Thr Asp Lys Glu Xaa
355 360 365

Arg Thr Gly Thr Met Xaa Leu Ser Arg Ala Xaa Pro Xaa Leu Glu Xaa
370 375 380

Xaa Xaa Asn Asn Xaa Lys Lys Leu Gly Leu Pro Trp Xaa Ile Gly Pro
385 390 395 400

Ile Asn Ser Xaa Xaa Arg Gly Gln Xaa Trp Lys Arg Ile Gly Gly
405 410 415

<210> 1361
<211> 119
<212> PRT
<213> Homo sapiens

<400> 1361
His Ala Ser Ala Asp Ala Trp Ala Asp Ala Trp Val Ala Gly Ser Asp
1 5 10 15

Phe Ile Lys Thr Ser Thr Gly Lys Glu Thr Val Asn Ala Thr Phe Pro
20 25 30

Val Ala Ile Val Met Leu Arg Ala Ile Arg Asp Phe Phe Trp Lys Thr
35 40 45

Gly Asn Lys Ile Gly Phe Lys Pro Ala Gly Gly Ile Arg Ser Ala Lys
50 55 60

Asp Ser Leu Ala Trp Leu Ser Leu Val Lys Glu Glu Leu Gly Asp Glu

```
 65                  70                  75                  80

Trp Leu Lys Pro Glu Leu Phe Arg Ile Gly Ala Ser Thr Leu Leu Ser
                85                  90                  95

Asp Ile Glu Arg Gln Ile Tyr His His Val Thr Gly Arg Tyr Ala Ala
            100                 105                 110

Tyr His Asp Leu Pro Met Ser
        115



<210> 1362
<211> 282
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (34)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1362
Gly Arg Val Gly Gly Arg Val Gly Gly Arg Val Gly Phe Thr Ala Lys
  1               5                  10                  15

Val Trp Asp Ala Val Ser Gly Asp Glu Leu Met Thr Leu Ala His Lys
             20                  25                  30

His Xaa Xaa Lys Thr Val Asp Phe Thr Gln Asp Ser Asn Tyr Leu Leu
         35                  40                  45

Thr Gly Gly Gln Asp Lys Leu Leu Arg Ile Tyr Asp Leu Asn Lys Pro
     50                  55                  60

Glu Ala Glu Pro Lys Glu Ile Ser Gly His Thr Ser Gly Ile Lys Lys
 65                  70                  75                  80

Ala Leu Trp Cys Ser Glu Asp Lys Gln Ile Leu Ser Ala Asp Asp Lys
                85                  90                  95

Thr Val Arg Leu Trp Asp His Ala Thr Met Thr Glu Val Lys Ser Leu
            100                 105                 110

Asn Phe Asn Met Ser Val Ser Ser Met Glu Tyr Ile Pro Glu Gly Glu
```

115 120 125

Ile Leu Val Ile Thr Tyr Gly Arg Ser Ile Ala Phe His Ser Ala Val
130 135 140

Ser Leu Asp Pro Ile Lys Ser Phe Glu Ala Pro Ala Thr Ile Asn Ser
145 150 155 160

Ala Ser Leu His Pro Glu Lys Glu Phe Leu Val Ala Gly Gly Glu Asp
165 170 175

Phe Lys Leu Tyr Lys Tyr Asp Tyr Asn Ser Gly Glu Glu Leu Glu Ser
180 185 190

Tyr Lys Gly His Phe Gly Pro Ile His Cys Val Arg Phe Ser Pro Asp
195 200 205

Gly Glu Leu Tyr Ala Ser Gly Ser Glu Asp Gly Thr Leu Arg Leu Trp
210 215 220

Gln Thr Val Val Gly Lys Thr Tyr Gly Leu Trp Lys Cys Val Leu Pro
225 230 235 240

Glu Glu Asp Ser Gly Glu Leu Ala Lys Pro Lys Ile Gly Phe Pro Glu
245 250 255

Thr Thr Glu Glu Glu Leu Glu Glu Ile Ala Ser Glu Asn Ser Asp Cys
260 265 270

Ile Phe Pro Ser Ala Pro Asp Val Lys Ala
275 280

<210> 1363
<211> 334
<212> PRT
<213> Homo sapiens

<400> 1363
Thr Pro Arg Thr Pro Glu Pro His Lys Pro Gly Leu Ala Met Lys Pro
1 5 10 15

Gly Phe Ser Pro Arg Gly Gly Gly Phe Gly Gly Arg Gly Gly Phe Gly
20 25 30

Asp Arg Gly Gly Arg Gly Gly Arg Gly Gly Phe Gly Gly Gly Arg Gly
35 40 45

Arg Gly Gly Gly Phe Arg Gly Arg Gly Arg Gly Gly Gly Gly Gly Gly
50 55 60

```
Gly Gly Gly Gly Gly Gly Gly Arg Gly Gly Gly Gly Phe His Ser Gly
 65                 70                  75                  80

Gly Asn Arg Gly Arg Gly Arg Gly Gly Lys Arg Gly Asn Gln Ser Gly
                85                  90                  95

Lys Asn Val Met Val Glu Pro His Arg His Glu Gly Val Phe Ile Cys
            100                 105                 110

Arg Gly Lys Glu Asp Ala Leu Val Thr Lys Asn Leu Val Pro Gly Glu
        115                 120                 125

Ser Val Tyr Gly Glu Lys Arg Val Ser Ile Ser Glu Gly Asp Asp Lys
    130                 135                 140

Ile Glu Tyr Arg Ala Trp Asn Pro Phe Arg Ser Lys Leu Ala Ala Ala
145                 150                 155                 160

Ile Leu Gly Gly Val Asp Gln Ile His Ile Lys Pro Gly Ala Lys Val
                165                 170                 175

Leu Tyr Leu Gly Ala Ala Ser Gly Thr Thr Val Ser His Val Ser Asp
            180                 185                 190

Ile Val Gly Pro Asp Gly Leu Val Tyr Ala Val Glu Phe Ser His Arg
        195                 200                 205

Ser Gly Arg Asp Leu Ile Asn Leu Ala Lys Lys Arg Thr Asn Ile Ile
    210                 215                 220

Pro Val Ile Glu Asp Ala Arg His Pro His Lys Tyr Arg Met Leu Ile
225                 230                 235                 240

Ala Met Val Asp Val Ile Phe Ala Asp Val Ala Gln Pro Asp Gln Thr
                245                 250                 255

Arg Ile Val Ala Leu Asn Ala His Thr Phe Leu Arg Asn Gly Gly His
            260                 265                 270

Phe Val Ile Ser Ile Lys Ala Asn Cys Ile Asp Ser Thr Ala Ser Ala
        275                 280                 285

Glu Ala Val Phe Ala Ser Glu Val Lys Lys Met Gln Gln Glu Asn Met
    290                 295                 300

Lys Pro Gln Glu Gln Leu Thr Leu Glu Pro Tyr Glu Arg Asp His Ala
305                 310                 315                 320

Val Val Val Gly Val Tyr Arg Pro Pro Pro Lys Val Lys Asn
                325                 330
```

<210> 1364
<211> 602
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (356)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1364
```
Pro Gly Ala Glu Lys Ser Gly Arg Ala Ala Glu Arg Pro Gly Arg Gly
  1               5                  10                  15

Pro Gly Arg Gly Ala His Ser Arg Pro Thr Ala Pro Arg Glu Arg Ala
             20                  25                  30

Pro Arg Ser Pro Ala Pro Ser Pro Pro Gly Met Gly Arg Ala Ala Ala
         35                  40                  45

Ala Glu Ala Pro Ala Trp Pro Gly Arg Thr Arg Pro Glu Ala Glu Gly
     50                  55                  60

Arg Ala Arg Ala Gln Leu Pro Gly His Gln Ile Gly Ala Arg Arg Ala
 65                  70                  75                  80

Gly Gly Pro Arg Ala Gly Leu Glu Met Ser Trp Pro Arg Arg Leu Leu
                 85                  90                  95

Leu Arg Tyr Leu Phe Pro Ala Leu Leu Leu His Gly Leu Gly Glu Gly
            100                 105                 110

Ser Ala Leu Leu His Pro Asp Ser Arg Ser His Pro Arg Ser Leu Glu
        115                 120                 125

Lys Ser Ala Trp Arg Ala Phe Lys Glu Ser Gln Cys His His Met Leu
    130                 135                 140

Lys His Leu His Asn Gly Ala Arg Ile Thr Val Gln Met Pro Pro Thr
145                 150                 155                 160

Ile Glu Gly His Trp Val Ser Thr Gly Cys Glu Val Arg Ser Gly Pro
                165                 170                 175

Glu Phe Ile Thr Arg Ser Tyr Arg Phe Tyr His Asn Asn Thr Phe Lys
            180                 185                 190

Ala Tyr Gln Phe Tyr Tyr Gly Ser Asn Arg Cys Thr Asn Pro Thr Tyr
```

195 200 205

Thr Leu Ile Ile Arg Gly Lys Ile Arg Leu Arg Gln Ala Ser Trp Ile
210 215 220

Ile Arg Gly Gly Thr Glu Ala Asp Tyr Gln Leu His Asn Val Gln Val
225 230 235 240

Ile Cys His Thr Glu Ala Val Ala Glu Lys Leu Gly Gln Gln Val Asn
245 250 255

Arg Thr Cys Pro Gly Phe Leu Ala Asp Gly Gly Pro Trp Val Gln Asp
260 265 270

Val Ala Tyr Asp Leu Trp Arg Glu Glu Asn Gly Cys Glu Cys Thr Lys
275 280 285

Ala Val Asn Phe Ala Met His Glu Leu Gln Leu Ile Arg Val Glu Lys
290 295 300

Gln Tyr Leu His His Asn Leu Asp His Leu Val Glu Glu Leu Phe Leu
305 310 315 320

Gly Asp Ile His Thr Asp Ala Thr Gln Arg Met Phe Tyr Arg Pro Ser
325 330 335

Ser Tyr Gln Pro Pro Leu Gln Asn Ala Lys Asn His Asp His Ala Cys
340 345 350

Ile Ala Cys Xaa Ile Ile Tyr Arg Ser Asp Glu His His Pro Pro Ile
355 360 365

Leu Pro Pro Lys Ala Asp Leu Thr Ile Gly Leu His Gly Glu Trp Val
370 375 380

Ser Gln Arg Cys Glu Val Arg Pro Glu Val Leu Phe Leu Thr Arg His
385 390 395 400

Phe Ile Phe His Asp Asn Asn Asn Thr Trp Glu Gly His Tyr Tyr His
405 410 415

Tyr Ser Asp Pro Val Cys Lys His Pro Thr Phe Ser Ile Tyr Ala Arg
420 425 430

Gly Arg Tyr Ser Arg Gly Val Leu Ser Ser Arg Val Met Gly Gly Thr
435 440 445

Glu Phe Val Phe Lys Val Asn His Met Lys Val Thr Pro Met Asp Ala
450 455 460

Ala Thr Ala Ser Leu Leu Asn Val Phe Asn Gly Asn Glu Cys Gly Ala

```
465                 470                 475                 480

Glu Gly Ser Trp Gln Val Gly Ile Gln Gln Asp Val Thr His Thr Asn
                485                 490                 495

Gly Cys Val Ala Leu Gly Ile Lys Leu Pro His Thr Glu Tyr Glu Ile
            500                 505                 510

Phe Lys Met Glu Gln Asp Ala Arg Gly Arg Tyr Leu Leu Phe Asn Gly
        515                 520                 525

Gln Arg Pro Ser Asp Gly Ser Ser Pro Asp Arg Pro Glu Lys Arg Ala
    530                 535                 540

Thr Ser Tyr Gln Met Pro Leu Val Gln Cys Ala Ser Ser Ser Pro Arg
545                 550                 555                 560

Ala Glu Asp Leu Ala Glu Asp Ser Gly Ser Ser Leu Tyr Gly Arg Ala
                565                 570                 575

Pro Gly Arg His Thr Trp Ser Leu Leu Leu Ala Ala Leu Ala Cys Leu
            580                 585                 590

Val Pro Leu Leu His Trp Asn Ile Arg Arg
        595                 600
```

<210> 1365
<211> 158
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (40)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (78)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (98)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (141)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (142)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1365
Ser Asn Ser Gly Tyr Pro Phe Trp Thr Pro Ser Met Leu Trp Lys Leu
1   5   10   15

Cys Thr Phe Thr Leu Leu Asn Lys Ala Xaa Ser Phe Phe Ser Leu Ser
            20   25   30

Val His Val Ser Phe Thr His Xaa Gly Gln Leu Pro His His Phe Phe
        35   40   45

Gly Val Ala Trp Gln Glu Pro Gln Val Leu His Leu Gly Glu Pro Asp
    50   55   60

Arg Arg Leu Gln Lys Arg Ile Lys Ala Ile Lys Leu Gln Xaa Ile Leu
65   70   75   80

Gln Met Glu Pro Gln Met Ser Ser Ala His Gly Phe Tyr Arg Gly Pro
                85   90   95

Leu Xaa Gln Pro Ala Gly Pro Ser Ile Thr Leu Glu Asn Ser Pro Leu
            100   105   110

Glu Asp Thr Lys Leu Gln Gly Pro Phe Phe Thr Pro Asn Gln Gln Glu
        115   120   125

Val Ala Arg Thr Asp Cys His Xaa Val Pro Asn Ser Xaa Xaa Gly Cys
    130   135   140

Pro Val Leu Glu Ala Gly Phe Arg Gly Gly Ala Gln Leu Gly
145   150   155

<210> 1366

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<211> 466
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (12)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (205)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (220)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (347)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1366
Ser Thr Arg Xaa Arg Glu Gly Asn Ser His Ser Xaa Gly His Lys Thr
  1               5                  10                  15

Ile Gln Gly Ser Leu Gly Arg Leu Ser Ser Ala Val Pro Gly Ser Gly
             20                  25                  30

Ala Glu Leu Ser Pro Val Pro Asn Thr Asp Gly Thr Met Asn Ser Gly
         35                  40                  45

His Ser Phe Ser Gln Thr Pro Ser Ala Ser Phe His Gly Ala Gly Gly
     50                  55                  60

Gly Trp Gly Arg Pro Arg Ser Phe Pro Arg Ala Pro Thr Val His Gly
 65                  70                  75                  80

Gly Ala Gly Gly Ala Arg Ile Ser Leu Ser Phe Thr Thr Arg Ser Cys
                 85                  90                  95

Pro Pro Pro Gly Gly Ser Trp Gly Ser Gly Arg Ser Ser Pro Leu Leu
            100                 105                 110
```

Gly Gly Asn Gly Lys Ala Thr Met Gln Asn Leu Asn Asp Arg Leu Ala
115 120 125

Ser Tyr Leu Glu Lys Val Arg Ala Leu Glu Glu Ala Asn Met Lys Leu
130 135 140

Glu Ser Arg Ile Leu Lys Trp His Gln Gln Arg Asp Pro Gly Ser Lys
145 150 155 160

Lys Asp Tyr Ser Gln Tyr Glu Glu Asn Ile Thr His Leu Gln Glu Gln
165 170 175

Ile Val Asp Gly Lys Met Thr Asn Ala Gln Ile Ile Leu Leu Ile Asp
180 185 190

Asn Ala Arg Met Ala Val Asp Asp Phe Asn Leu Lys Xaa Glu Asn Glu
195 200 205

His Ser Phe Lys Lys Asp Leu Glu Ile Glu Val Xaa Gly Leu Arg Arg
210 215 220

Thr Leu Asp Asn Leu Thr Ile Val Thr Thr Asp Leu Glu Gln Glu Val
225 230 235 240

Glu Gly Met Arg Lys Glu Leu Ile Leu Met Lys Lys His His Glu Gln
245 250 255

Glu Met Glu Lys His His Val Pro Ser Asp Phe Asn Val Asn Val Lys
260 265 270

Val Asp Thr Gly Pro Arg Glu Asp Leu Ile Lys Val Leu Glu Asp Met
275 280 285

Arg Gln Glu Tyr Glu Leu Ile Ile Lys Lys Lys His Arg Asp Leu Asp
290 295 300

Thr Trp Tyr Lys Glu Gln Ser Ala Ala Met Ser Gln Glu Ala Ala Ser
305 310 315 320

Pro Ala Thr Val Gln Ser Arg Gln Gly Asp Ile His Glu Leu Lys Arg
325 330 335

Thr Phe Gln Ala Leu Glu Ile Asp Leu Gln Xaa Gln Tyr Ser Thr Lys
340 345 350

Ser Ala Leu Glu Asn Met Leu Ser Glu Thr Gln Ser Arg Tyr Ser Cys
355 360 365

Lys Leu Gln Asp Met Gln Glu Ile Ile Ser His Tyr Glu Glu Glu Leu
370 375 380

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Thr Gln Leu Arg His Glu Leu Glu Arg Gln Asn Asn Glu Tyr Gln Val
385                 390                 395                 400

Leu Leu Gly Ile Lys Thr His Leu Glu Lys Glu Ile Thr Thr Tyr Arg
                405                 410                 415

Arg Leu Leu Glu Gly Glu Ser Glu Gly Thr Arg Glu Glu Ser Lys Ser
            420                 425                 430

Ser Met Lys Val Ser Ala Thr Pro Lys Ile Lys Ala Ile Thr Gln Glu
        435                 440                 445

Thr Ile Asn Gly Arg Leu Val Leu Cys Gln Val Asn Glu Ile Gln Lys
    450                 455                 460

His Ala
465



<210> 1367
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (138)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (141)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (142)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (143)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<221> SITE
<222> (152)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1367
Leu Arg Phe Ala Ser Pro Gly Pro Gly Ala Gly Arg Ala Arg Asp Ser
1   5   10   15

Gln Arg Lys Trp Arg Arg Leu Arg Ala Arg Pro Leu Leu Gly Pro Gly
            20   25   30

Gln Gly Trp Ser Trp Ala Gly Ile Pro Ser Ser Ala Ala Ala Gln Arg
        35   40   45

Ala Gly Pro Pro Ala Gly Ala Leu Glu Ala Leu Ser Pro Gly Gly Ala
    50   55   60

Arg Ala His Ala Glu Arg Arg Gly Glu Met Arg Ala Thr Pro Leu Ala
65   70   75   80

Ala Pro Ala Gly Ser Leu Ser Arg Lys Lys Arg Leu Glu Leu Asp Asp
                85   90   95

Asn Leu Asp Thr Glu Arg Pro Val Gln Lys Arg Ala Arg Ser Gly Pro
            100   105   110

Gln Pro Arg Leu Pro Pro Cys Leu Leu Pro Leu Ser Pro Pro Thr Ala
        115   120   125

Pro Asp Arg Ala Thr Ala Val Xaa Thr Xaa Ser Arg Xaa Xaa Xaa Tyr
    130   135   140

Val Leu Leu Glu Ala Arg Arg Xaa Ala
145   150

<210> 1368
<211> 399
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1368

```
Ser Asp Asn Xaa Thr Asn Gly Cys Gly Leu Glu Ser Xaa Gly Asn Thr
 1               5                  10                  15

Val Thr Pro Val Asn Val Asn Glu Val Lys Pro Ile Asn Lys Gly Glu
            20                  25                  30

Glu Gln Ile Gly Phe Glu Leu Val Glu Lys Leu Phe Gln Gly Gln Leu
        35                  40                  45

Val Leu Arg Thr Arg Cys Leu Glu Cys Glu Ser Leu Thr Glu Arg Arg
    50                  55                  60

Glu Asp Phe Gln Asp Ile Ser Val Pro Val Gln Glu Asp Glu Leu Ser
65                  70                  75                  80

Lys Val Glu Glu Ser Ser Glu Ile Ser Pro Glu Pro Lys Thr Glu Met
                85                  90                  95

Lys Thr Leu Arg Trp Ala Ile Ser Gln Phe Ala Ser Val Glu Arg Ile
            100                 105                 110

Val Gly Glu Asp Lys Tyr Phe Cys Glu Asn Cys His His Tyr Thr Glu
        115                 120                 125

Ala Glu Arg Ser Leu Leu Phe Asp Lys Met Pro Glu Val Ile Thr Ile
    130                 135                 140

His Leu Lys Cys Phe Ala Ala Ser Gly Leu Glu Phe Asp Cys Tyr Gly
145                 150                 155                 160

Gly Gly Leu Ser Lys Ile Asn Thr Pro Leu Leu Thr Pro Leu Lys Leu
                165                 170                 175

Ser Leu Glu Glu Trp Ser Thr Lys Pro Thr Asn Asp Ser Tyr Gly Leu
            180                 185                 190

Phe Ala Val Val Met His Ser Gly Ile Thr Ile Ser Ser Gly His Tyr
        195                 200                 205

Thr Ala Ser Val Lys Val Thr Asp Leu Asn Ser Leu Glu Leu Asp Lys
    210                 215                 220

Gly Asn Phe Val Val Asp Gln Met Cys Glu Ile Gly Lys Pro Glu Pro
225                 230                 235                 240

Leu Asn Glu Glu Glu Ala Arg Gly Val Val Glu Asn Tyr Asn Asp Glu
                245                 250                 255

Glu Val Ser Ile Arg Val Gly Gly Asn Thr Gln Pro Ser Lys Val Leu
```

```
        260                 265                 270

Asn Lys Lys Asn Val Glu Ala Ile Gly Leu Leu Gly Gly Gln Lys Ser
    275                 280                 285

Lys Ala Asp Tyr Glu Leu Tyr Asn Lys Ala Ser Asn Pro Asp Lys Val
    290                 295                 300

Ala Ser Thr Ala Phe Ala Glu Asn Arg Asn Ser Glu Thr Ser Asp Thr
305                 310                 315                 320

Thr Gly Thr His Glu Ser Asp Arg Asn Lys Glu Ser Ser Asp Gln Thr
                325                 330                 335

Gly Ile Asn Ile Ser Gly Phe Glu Asn Lys Ile Ser Tyr Val Val Gln
            340                 345                 350

Ser Leu Lys Glu Tyr Glu Gly Lys Trp Leu Leu Phe Asp Asp Ser Glu
        355                 360                 365

Val Lys Val Thr Glu Glu Lys Asp Phe Leu Asn Ser Leu Ser Pro Ser
    370                 375                 380

Thr Ser Pro Thr Ser Thr Pro Tyr Leu Leu Phe Tyr Lys Lys Leu
385                 390                 395


<210> 1369
<211> 260
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1369
Val Phe Xaa Ser Phe Phe Ala Glu Lys Glu Gln Gln Glu Ala Ile Glu
  1               5                  10                  15

His Ile Asp Glu Val Gln Asn Glu Ile Asp Arg Leu Asn Glu Gln Ala
             20                  25                  30

Ser Glu Glu Ile Leu Lys Val Glu Gln Lys Tyr Asn Lys Leu Arg Gln
         35                  40                  45

Pro Phe Phe Gln Lys Arg Ser Glu Leu Ile Ala Lys Ile Pro Asn Phe
     50                  55                  60
```

Trp Val Thr Thr Phe Val Asn His Pro Gln Val Ser Ala Leu Leu Gly
65 70 75 80

Glu Glu Asp Glu Glu Ala Leu His Tyr Leu Thr Arg Val Glu Val Thr
85 90 95

Glu Phe Glu Asp Ile Lys Ser Gly Tyr Arg Ile Asp Phe Tyr Phe Asp
100 105 110

Glu Asn Pro Tyr Phe Glu Asn Lys Val Leu Ser Lys Glu Phe His Leu
115 120 125

Asn Glu Ser Gly Asp Pro Ser Ser Lys Ser Thr Glu Ile Lys Trp Lys
130 135 140

Ser Gly Lys Asp Leu Thr Lys Arg Ser Ser Gln Thr Gln Asn Lys Ala
145 150 155 160

Ser Arg Lys Arg Gln His Glu Glu Pro Glu Ser Phe Phe Thr Trp Phe
165 170 175

Thr Asp His Ser Asp Ala Gly Ala Asp Glu Leu Gly Glu Val Ile Lys
180 185 190

Asp Asp Ile Trp Pro Asn Pro Leu Gln Tyr Tyr Leu Val Pro Asp Met
195 200 205

Asp Asp Glu Glu Gly Glu Gly Glu Glu Asp Asp Asp Asp Asp Glu Glu
210 215 220

Glu Glu Gly Leu Glu Asp Ile Asp Glu Glu Gly Asp Glu Asp Glu Gly
225 230 235 240

Glu Glu Asp Glu Asp Asp Asp Glu Gly Glu Glu Gly Glu Glu Asp Glu
245 250 255

Gly Glu Asp Asp
260

<210> 1370
<211> 155
<212> PRT
<213> Homo sapiens

<400> 1370
Lys Gly Glu Ala Ala Ala Phe Ser Ala Thr Phe Pro Ile Ala Arg Gln
1 5 10 15

Glu Phe Leu Ser Val Thr Thr Ile Ala Val Met Ser Gly Arg Gly Lys

20 25 30

Gln Gly Gly Lys Ala Arg Ala Lys Ala Lys Ser Arg Ser Ser Arg Ala
35 40 45

Gly Leu Gln Phe Pro Val Gly Glu Cys Ile Ala Leu Arg Lys Gly Asn
50 55 60

Tyr Ala Glu Arg Val Gly Ala Gly Ala Pro Val Tyr Met Ala Ala Val
65 70 75 80

Leu Glu Tyr Leu Thr Ala Glu Ile Leu Glu Leu Ala Gly Asn Ala Ala
85 90 95

Arg Asp Asn Lys Lys Thr Arg Ile Ile Pro Arg His Leu Gln Leu Ala
100 105 110

Ile Arg Asn Asp Glu Glu Leu Asn Lys Leu Leu Gly Lys Val Thr Ile
115 120 125

Ala Gln Gly Gly Val Leu Pro Asn Ile Gln Ala Val Leu Leu Pro Lys
130 135 140

Lys Thr Glu Ser His His Lys Ala Lys Gly Lys
145 150 155

<210> 1371
<211> 140
<212> PRT
<213> Homo sapiens

<400> 1371
Phe Pro Gly Arg Thr His Ala Leu Cys Arg Gly Ala Ala Ser Arg Gly
1 5 10 15

Leu Leu Cys Lys Trp Ala Pro Trp Pro Ser Ala Pro Val Pro Ala Thr
20 25 30

Arg Asp Arg Ala Pro Arg Pro Ala Arg Gly Arg Arg Pro Asp Pro Thr
35 40 45

Ser Gln Gln Ala Lys Ala Trp Arg Pro Ser Pro Pro Ala Ala Arg Ser
50 55 60

Trp Pro Pro Thr Thr Thr Thr Gly Ala Ala Trp Val Pro Leu Pro Ala
65 70 75 80

Thr Ala Pro Ala Ala Val Pro Ser Ala Pro Gly Lys Pro Phe Pro Thr
85 90 95

Pro Gln Val Ser Pro Arg Leu Thr Arg Val Ile Gly Gly Pro Ala Ser
            100   105   110

Phe Ser Gly Ser Pro Pro Ser Arg Ser Trp Pro Arg Cys Trp Ser Pro
        115   120   125

Gln Ser Thr Arg Asn Leu Pro Arg Pro Pro Ala Ala
    130   135   140

<210> 1372
<211> 150
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (126)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (127)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (128)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (135)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (142)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (147)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1372
Pro Trp Thr Leu Gly Gly Pro Glu Leu Asp Ala Met Gly Gly Cys Ala
  1   5   10   15

Gly Ser Arg Arg Arg Phe Ser Asp Ser Glu Gly Glu Glu Thr Val Pro
20 25 30

Glu Pro Arg Leu Pro Leu Leu Asp His Gln Gly Ala His Trp Lys Asn
35 40 45

Ala Val Gly Phe Trp Leu Leu Gly Leu Cys Asn Asn Phe Ser Tyr Val
50 55 60

Val Met Leu Ser Ala Ala His Asp Ile Leu Ser His Lys Arg Thr Ser
65 70 75 80

Gly Asn Gln Ser His Val Asp Pro Gly Pro Thr Pro Ile Pro His Asn
85 90 95

Ser Ser Ser Arg Phe Asp Cys Asn Ser Val Ser Thr Ala Ala Val Leu
100 105 110

Leu Ala Asp Ile Leu Pro Thr Leu Val Ile Lys Leu Leu Xaa Xaa Xaa
115 120 125

Gly Leu His Leu Leu Pro Xaa Thr Val Glu Asp Ala Val Xaa Leu Cys
130 135 140

Ala Leu Xaa Gly Thr Ala
145 150

<210> 1373
<211> 128
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (21)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (121)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1373
Arg His Ser Arg Val Asp Pro Arg Val Arg Ala Arg Phe Arg Arg Arg
1 5 10 15

Arg Ala Phe Ala Xaa Leu Gly Trp Ser Ser Gly Arg Val Ser Arg Pro
20 25 30

Glu His Val Asp Ala His Pro Pro Leu Ser Leu Met Glu Val Val Thr
35 40 45

Phe Gly Asp Val Ala Val His Phe Ser Arg Glu Glu Trp Gln Cys Leu
50 55 60

Asp Pro Gly Gln Arg Ala Leu Tyr Arg Glu Val Met Leu Glu Asn His
65 70 75 80

Ser Ser Val Ala Gly Leu Ala Gly Phe Leu Val Phe Lys Pro Glu Leu
85 90 95

Ile Ser Arg Leu Glu Gln Gly Glu Glu Pro Trp Val Leu Asp Leu Gln
100 105 110

Gly Ala Glu Gly Thr Glu Ala Pro Xaa Thr Ser Lys Thr Gly Glu Ala
115 120 125

<210> 1374
<211> 398
<212> PRT
<213> Homo sapiens

<400> 1374
Ser Ser Trp Leu Arg Ser Arg Ser Gly Met Gln Thr Asp Leu Gln Asn
1 5 10 15

Leu Gly Asn Asp Ser Gly Asp His Ser Asp His Met His Tyr Tyr Gln
20 25 30

Gly Lys Lys Tyr Phe Arg Asp Arg Arg Gly Gly Gly Arg Asn Ser Asp
35 40 45

Trp Ser Ser Asp Thr Asn Arg Gln Gly Gln Gln Ser Ser Ser Asp Cys
50 55 60

Tyr Ile Tyr Asp Ser Ala Thr Gly Tyr Tyr Tyr Asp Pro Leu Ala Gly
65 70 75 80

Thr Tyr Tyr Asp Pro Asn Thr Gln Gln Glu Val Tyr Val Pro Gln Asp
85 90 95

Pro Gly Leu Pro Glu Glu Glu Glu Ile Lys Glu Lys Lys Pro Thr Ser
100 105 110

Gln Gly Lys Ser Ser Ser Lys Lys Glu Met Ser Lys Arg Asp Gly Lys

115 120 125

Glu Lys Lys Asp Arg Gly Val Thr Arg Phe Gln Glu Asn Ala Ser Glu
130 135 140

Gly Lys Ala Pro Ala Glu Asp Val Phe Lys Lys Pro Leu Pro Pro Thr
145 150 155 160

Val Lys Lys Glu Glu Ser Pro Pro Pro Pro Lys Val Val Asn Pro Leu
165 170 175

Ile Gly Leu Leu Gly Glu Tyr Gly Gly Asp Ser Asp Tyr Glu Glu Glu
180 185 190

Glu Glu Glu Glu Gln Thr Pro Pro Pro Gln Pro Arg Thr Ala Gln Pro
195 200 205

Gln Lys Arg Glu Glu Gln Thr Lys Lys Glu Asn Glu Glu Asp Lys Leu
210 215 220

Thr Asp Trp Asn Lys Leu Ala Cys Leu Leu Cys Arg Arg Gln Phe Pro
225 230 235 240

Asn Lys Glu Val Leu Ile Lys His Gln Gln Leu Ser Asp Leu His Lys
245 250 255

Gln Asn Leu Glu Ile His Arg Lys Ile Lys Gln Ser Glu Gln Glu Leu
260 265 270

Ala Tyr Leu Glu Arg Arg Glu Arg Glu Gly Lys Phe Lys Gly Arg Gly
275 280 285

Asn Asp Arg Arg Glu Lys Leu Gln Ser Phe Asp Ser Pro Glu Arg Lys
290 295 300

Arg Ile Lys Tyr Ser Arg Glu Thr Asp Ser Asp Arg Lys Leu Val Asp
305 310 315 320

Lys Glu Asp Ile Asp Thr Ser Ser Lys Gly Gly Cys Val Gln Gln Ala
325 330 335

Thr Gly Trp Arg Lys Gly Thr Gly Leu Gly Tyr Gly His Pro Gly Leu
340 345 350

Ala Ser Ser Glu Glu Ala Glu Gly Arg Met Arg Gly Pro Ser Val Gly
355 360 365

Ala Ser Gly Arg Thr Ser Lys Arg Gln Ser Asn Glu Thr Tyr Arg Asp
370 375 380

Ala Val Arg Arg Val Met Phe Ala Arg Tyr Lys Glu Leu Asp

385 390 395

<210> 1375
<211> 167
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (157)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (161)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (163)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1375
His Arg Gly Lys Arg Tyr Thr Asp Ser Thr Val Arg Asn Ser Arg Val
1 5 10 15

Asp Pro Arg Val Arg Ser Ala Lys Pro Glu Ser Cys Pro Phe Ser Leu
20 25 30

Pro Gly Gln His Glu Leu His His Ser Leu His Leu Leu His Gln Leu
35 40 45

Pro Val Pro Gly Leu Cys Pro Gly Ala Gln Leu Arg Arg Pro Ala Gly
50 55 60

Gln Gln Arg Gly Gln Arg Leu Cys Arg Arg Trp Gly Leu Trp Phe Pro
65 70 75 80

Asp Leu Arg Val Pro Leu His Gln Leu Gln Gly Arg His Gly Val Arg
85 90 95

Gly Pro Gly His Arg Asp Ser Arg Gly Ser Gly Arg Asn Gly Ser Ile
100 105 110

Gln Asn Glu Lys Glu Thr Met Gln Lys Leu Asn Asp Arg Leu Ala Ser
115 120 125

Tyr Leu Asp Lys Met Lys Glu Pro Gly Asp Arg Glu Thr Gly Gly Trp
130 135 140

Lys Ala Lys Thr Arg Glu His Phe Gly Glu Glu Gly Xaa Gln Val Arg
145 150 155 160

Xaa Trp Xaa Pro Leu Ile Gln
165

<210> 1376
<211> 448
<212> PRT
<213> Homo sapiens

<400> 1376
Leu Pro Asp Val Glu Lys Leu Gly Arg Arg Arg Gly Arg Lys Met Asp
1 5 10 15

Ser Val Glu Lys Gly Ala Ala Thr Ser Val Ser Asn Pro Arg Gly Arg
20 25 30

Pro Ser Arg Gly Arg Pro Pro Lys Leu Gln Arg Asn Ser Arg Gly Gly
35 40 45

Gln Gly Arg Gly Val Glu Lys Pro Pro His Leu Ala Ala Leu Ile Leu
50 55 60

Ala Arg Gly Gly Ser Lys Gly Ile Pro Leu Lys Asn Ile Lys His Leu
65 70 75 80

Ala Gly Val Pro Leu Ile Gly Trp Val Leu Arg Ala Ala Leu Asp Ser
85 90 95

Gly Ala Phe Gln Ser Val Trp Val Ser Thr Asp His Asp Glu Ile Glu
100 105 110

Asn Val Ala Lys Gln Phe Gly Ala Gln Val His Arg Arg Ser Ser Glu
115 120 125

Val Ser Lys Asp Ser Ser Thr Ser Leu Asp Ala Ile Ile Glu Phe Leu
130 135 140

Asn Tyr His Asn Glu Val Asp Ile Val Gly Asn Ile Gln Ala Thr Ser
145 150 155 160

Pro Cys Leu His Pro Thr Asp Leu Gln Lys Val Ala Glu Met Ile Arg
165 170 175

Glu Glu Gly Tyr Asp Ser Val Phe Ser Val Val Arg Arg His Gln Phe
180 185 190

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Arg Trp Ser Glu Ile Gln Lys Gly Val Arg Glu Val Thr Glu Pro Leu
        195                 200                 205

Asn Leu Asn Pro Ala Lys Arg Pro Arg Arg Gln Asp Trp Asp Gly Glu
    210                 215                 220

Leu Tyr Glu Asn Gly Ser Phe Tyr Phe Ala Lys Arg His Leu Ile Glu
225                 230                 235                 240

Met Gly Tyr Leu Gln Gly Gly Lys Met Ala Tyr Tyr Glu Met Arg Ala
                245                 250                 255

Glu His Ser Val Asp Ile Asp Val Asp Ile Asp Trp Pro Ile Ala Glu
            260                 265                 270

Gln Arg Val Leu Arg Tyr Gly Tyr Phe Gly Lys Glu Lys Leu Lys Glu
        275                 280                 285

Ile Lys Leu Leu Val Cys Asn Ile Asp Gly Cys Leu Thr Asn Gly His
    290                 295                 300

Ile Tyr Val Ser Gly Asp Gln Lys Glu Ile Ile Ser Tyr Asp Val Lys
305                 310                 315                 320

Asp Ala Ile Gly Ile Ser Leu Leu Lys Lys Ser Gly Ile Glu Val Arg
                325                 330                 335

Leu Ile Ser Glu Arg Ala Cys Ser Lys Gln Thr Leu Ser Ser Leu Lys
            340                 345                 350

Leu Asp Cys Lys Met Glu Val Ser Val Ser Asp Lys Leu Ala Val Val
        355                 360                 365

Asp Glu Trp Arg Lys Glu Met Gly Leu Cys Trp Lys Glu Val Ala Tyr
    370                 375                 380

Leu Gly Asn Glu Val Ser Asp Glu Glu Cys Leu Lys Arg Val Gly Leu
385                 390                 395                 400

Ser Gly Ala Pro Ala Asp Ala Cys Ser Thr Ala Gln Lys Ala Val Gly
                405                 410                 415

Tyr Ile Cys Lys Cys Asn Gly Gly Arg Gly Ala Ile Arg Glu Phe Ala
            420                 425                 430

Glu His Ile Cys Leu Leu Met Glu Lys Val Asn Asn Ser Cys Gln Lys
        435                 440                 445
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<210> 1377
<211> 469
<212> PRT
<213> Homo sapiens

<400> 1377
Gly Gly Pro Ala Lys Met Ala Ala Ser Cys Leu Val Leu Leu Ala Leu
1 5 10 15

Cys Leu Leu Leu Pro Leu Leu Leu Leu Gly Gly Trp Lys Arg Trp Arg
20 25 30

Arg Gly Arg Ala Ala Arg His Val Val Ala Val Val Leu Gly Asp Val
35 40 45

Gly Arg Ser Pro Arg Met Gln Tyr His Ala Leu Ser Leu Ala Met His
50 55 60

Gly Phe Ser Val Thr Leu Leu Gly Phe Cys Asn Ser Lys Pro His Asp
65 70 75 80

Glu Leu Leu Gln Asn Asn Arg Ile Gln Ile Val Gly Leu Thr Glu Leu
85 90 95

Gln Ser Leu Ala Val Gly Pro Arg Val Phe Gln Tyr Gly Val Lys Val
100 105 110

Val Leu Gln Ala Met Tyr Leu Leu Trp Lys Leu Met Trp Arg Glu Pro
115 120 125

Gly Ala Tyr Ile Phe Leu Gln Asn Pro Pro Gly Leu Pro Ser Ile Ala
130 135 140

Val Cys Trp Phe Val Gly Cys Leu Cys Gly Ser Lys Leu Val Ile Asp
145 150 155 160

Trp His Asn Tyr Gly Tyr Ser Ile Met Gly Leu Val His Gly Pro Asn
165 170 175

His Pro Leu Val Leu Leu Ala Lys Trp Tyr Glu Lys Phe Phe Gly Arg
180 185 190

Leu Ser His Leu Asn Leu Cys Val Thr Asn Ala Met Arg Glu Asp Leu
195 200 205

Ala Asp Asn Trp His Ile Arg Ala Val Thr Val Tyr Asp Lys Pro Ala
210 215 220

Ser Phe Phe Lys Glu Thr Pro Leu Asp Leu Gln His Arg Leu Phe Met

225 230 235 240

Lys Leu Gly Ser Met His Ser Pro Phe Arg Ala Arg Ser Glu Pro Glu
245 250 255

Asp Pro Val Thr Glu Arg Ser Ala Phe Thr Glu Arg Asp Ala Gly Ser
260 265 270

Gly Leu Val Thr Arg Leu Arg Glu Arg Pro Ala Leu Leu Val Ser Ser
275 280 285

Thr Ser Trp Thr Glu Asp Glu Asp Phe Ser Ile Leu Leu Ala Ala Leu
290 295 300

Glu Lys Phe Glu Gln Leu Thr Leu Asp Gly His Asn Leu Pro Ser Leu
305 310 315 320

Val Cys Val Ile Thr Gly Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg
325 330 335

Leu Ile His Gln Lys His Phe Gln His Ile Gln Val Cys Thr Pro Trp
340 345 350

Leu Glu Ala Glu Asp Tyr Pro Leu Leu Leu Gly Ser Ala Asp Leu Gly
355 360 365

Val Cys Leu His Thr Ser Ser Ser Gly Leu Asp Leu Pro Met Lys Val
370 375 380

Val Asp Met Phe Gly Cys Cys Leu Pro Val Cys Ala Val Asn Phe Lys
385 390 395 400

Cys Leu His Glu Leu Val Lys His Glu Glu Asn Gly Leu Val Phe Glu
405 410 415

Asp Ser Glu Glu Leu Ala Ala Gln Leu Gln Met Leu Phe Ser Asn Phe
420 425 430

Pro Asp Pro Ala Gly Lys Leu Asn Gln Phe Arg Lys Asn Leu Arg Glu
435 440 445

Ser Gln Gln Leu Arg Trp Asp Glu Ser Trp Val Gln Thr Val Leu Pro
450 455 460

Leu Val Met Asp Thr
465

<210> 1378
<211> 314

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<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (93)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1378
Glu Lys Ala Ala Gly Ala Gly Lys Ser His Leu Ala Ile Val Gln Lys
  1               5                  10                  15

Val Asn Asn Glu Gly Glu Gly Asp Pro Phe Tyr Glu Val Leu Gly Leu
             20                  25                  30

Val Thr Leu Glu Asp Val Ile Glu Glu Ile Ile Lys Ser Glu Ile Leu
         35                  40                  45

Asp Glu Ser Asp Met Tyr Thr Asp Asn Arg Ser Arg Lys Arg Val Ser
     50                  55                  60

Glu Lys Asn Lys Arg Asp Phe Ser Ala Phe Lys Asp Ala Asp Asn Glu
 65                  70                  75                  80

Leu Lys Val Lys Ile Ser Pro Gln Leu Leu Leu Ala Xaa His Arg Phe
                 85                  90                  95

Leu Ala Thr Glu Val Ser Gln Phe Ser Pro Ser Leu Ile Ser Glu Lys
            100                 105                 110

Ile Leu Leu Arg Leu Leu Lys Tyr Pro Asp Val Ile Gln Glu Leu Lys
        115                 120                 125

Phe Asp Glu His Asn Lys Tyr Tyr Ala Arg His Tyr Leu Tyr Thr Arg
    130                 135                 140

Asn Lys Pro Ala Asp Tyr Phe Ile Leu Ile Leu Gln Gly Lys Val Glu
145                 150                 155                 160

Val Glu Ala Gly Lys Glu Asn Met Lys Phe Glu Thr Gly Ala Phe Ser
                165                 170                 175

Tyr Tyr Gly Thr Met Ala Leu Thr Ser Val Pro Ser Asp Arg Ser Pro
            180                 185                 190

Ala His Pro Thr Pro Leu Ser Arg Ser Ala Ser Leu Ser Tyr Pro Asp
        195                 200                 205

Arg Thr Asp Val Ser Thr Ala Ala Thr Leu Ala Gly Ser Ser Asn Gln
    210                 215                 220
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Phe Gly Ser Ser Val Leu Gly Gln Tyr Ile Ser Asp Phe Ser Val Arg
225 230 235 240

Ala Leu Val Asp Leu Gln Tyr Ile Lys Ile Thr Arg Gln Gln Tyr Gln
245 250 255

Asn Gly Leu Leu Ala Ser Arg Met Glu Asn Ser Pro Gln Phe Pro Ile
260 265 270

Asp Gly Cys Thr Thr His Met Glu Asn Leu Ala Glu Lys Ser Glu Leu
275 280 285

Pro Val Val Asp Glu Thr Thr Thr Leu Leu Asn Glu Arg Asn Ser Leu
290 295 300

Leu His Lys Ala Ser His Glu Asn Ala Ile
305 310

<210> 1379
<211> 131
<212> PRT
<213> Homo sapiens

<400> 1379
Ser Cys Pro Val Leu Lys Met Phe Pro Glu Gln Gln Lys Glu Glu Phe
1 5 10 15

Val Ser Val Trp Val Arg Asp Pro Arg Ile Gln Lys Glu Asp Phe Trp
20 25 30

His Ser Tyr Ile Asp Tyr Glu Ile Cys Ile His Thr Asn Ser Met Cys
35 40 45

Phe Thr Met Lys Thr Ser Cys Val Arg Arg Arg Tyr Arg Glu Phe Val
50 55 60

Trp Leu Arg Gln Arg Leu Gln Ser Asn Ala Leu Leu Val Gln Leu Pro
65 70 75 80

Glu Leu Pro Ser Lys Asn Leu Phe Phe Asn Met Asn Asn Arg Gln His
85 90 95

Val Asp Gln Arg Arg Gln Gly Leu Gly Asn Phe Leu Arg Lys Val Leu
100 105 110

Gln Met His Phe Cys Phe Gln Ile Ala Ala Phe Thr Ser Ser Leu Gln
115 120 125

Ser His Leu

130

<210> 1380
<211> 219
<212> PRT
<213> Homo sapiens

<400> 1380
Pro Gly Ala Ala Trp Ser Arg Pro Asp Leu Arg Gly Cys Cys Thr Gly
1 5 10 15

Pro Gln Pro Ala Leu Arg Met Leu Val Leu Pro Ser Pro Cys Pro Gln
20 25 30

Pro Leu Ala Phe Ser Ser Val Glu Thr Met Glu Gly Pro Pro Arg Arg
35 40 45

Thr Cys Arg Ser Pro Glu Pro Gly Pro Ser Ser Ser Ile Gly Ser Pro
50 55 60

Gln Ala Ser Ser Pro Pro Arg Pro Asn His Tyr Leu Leu Ile Asp Thr
65 70 75 80

Gln Gly Val Pro Tyr Thr Val Leu Val Asp Glu Glu Ser Gln Arg Glu
85 90 95

Pro Gly Ala Ser Gly Ala Pro Gly Gln Lys Lys Cys Tyr Ser Cys Pro
100 105 110

Val Cys Ser Arg Val Phe Glu Tyr Met Ser Tyr Leu Gln Arg His Ser
115 120 125

Ile Thr His Ser Glu Val Lys Pro Phe Glu Cys Asp Ile Cys Gly Lys
130 135 140

Ala Phe Lys Arg Ala Ser His Leu Ala Arg His His Ser Ile His Leu
145 150 155 160

Ala Gly Gly Gly Arg Pro His Gly Cys Pro Leu Cys Pro Arg Arg Phe
165 170 175

Arg Asp Ala Gly Glu Leu Ala Gln His Ser Arg Val His Ser Gly Glu
180 185 190

Arg Pro Phe Gln Cys Pro His Cys Pro Arg Arg Phe Met Glu Gln Asn
195 200 205

Thr Leu Gln Lys His Thr Arg Trp Lys His Pro
210 215

<210> 1381
<211> 275
<212> PRT
<213> Homo sapiens

<400> 1381
Gly Val Ala Leu Phe Lys Ser Ala Ala Gly Asp Gln Pro Thr Ala Ala
1   5   10   15

Cys Ile Cys Ile Gln Arg Gln Val Pro Pro Val Pro Ala Ala Arg Ala
            20   25   30

Pro Gln Ser Arg Thr Arg Ser Ala Gln Ala Lys Leu Ala Leu Thr Met
        35   40   45

Pro Val Lys Gly Gly Thr Lys Cys Ile Lys Tyr Leu Leu Phe Gly Phe
    50   55   60

Asn Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly Leu
65   70   75   80

Trp Leu Arg Phe Asp Ser Gln Thr Lys Ser Ile Phe Glu Gln Glu Thr
                85   90   95

Asn Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile Gly
            100   105   110

Ala Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly Ala
        115   120   125

Val Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu Leu
    130   135   140

Val Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser His
145   150   155   160

Lys Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr Tyr
                165   170   175

Asn Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys Ala
            180   185   190

Ile His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu Gln
        195   200   205

Phe Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe Thr
    210   215   220

Val Lys Ser Cys Pro Asp Ala Ile Lys Glu Val Phe Asp Asn Lys Phe
225 230 235 240

His Ile Ile Gly Ala Val Gly Ile Gly Ile Ala Val Val Met Ile Phe
245 250 255

Gly Met Ile Phe Ser Met Ile Leu Cys Cys Ala Ile Arg Arg Asn Arg
260 265 270

Glu Met Val
275

<210> 1382
<211> 766
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (123)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1382
Pro Cys Trp Glu Leu Val Gly Pro Pro Gly Trp Gln Xaa Ile Arg Ala
1 5 10 15

Xaa Pro Ala Thr Val His Arg Ala Glu Ile Leu Ser Phe Pro Arg Ser
20 25 30

Lys Thr Ser Glu Pro Ala Lys Arg Gly Arg Thr Ala Ser Ala Ala Met
35 40 45

Ala Leu Lys Asp Tyr Ala Leu Glu Lys Glu Lys Val Lys Lys Phe Leu
50 55 60

Gln Glu Phe Tyr Gln Asp Asp Glu Leu Gly Lys Lys Gln Phe Lys Tyr
65 70 75 80

Gly Asn Gln Leu Val Arg Leu Ala His Arg Glu Gln Val Ala Leu Tyr

```
                85                  90                  95

Val Asp Leu Asp Asp Val Ala Glu Asp Asp Pro Glu Leu Val Asp Ser
            100                 105                 110

Ile Cys Glu Asn Ala Arg Arg Tyr Ala Lys Xaa Phe Ala Asp Ala Val
        115                 120                 125

Gln Glu Leu Leu Pro Gln Tyr Lys Glu Arg Glu Val Val Asn Lys Asp
    130                 135                 140

Val Leu Asp Val Tyr Ile Glu His Arg Leu Met Met Glu Gln Arg Ser
145                 150                 155                 160

Arg Asp Pro Gly Met Val Arg Ser Pro Gln Asn Gln Tyr Pro Ala Glu
                165                 170                 175

Leu Met Arg Arg Phe Glu Leu Tyr Phe Gln Gly Pro Ser Ser Asn Lys
            180                 185                 190

Pro Arg Val Ile Arg Glu Val Arg Ala Asp Ser Val Gly Lys Leu Val
        195                 200                 205

Thr Val Arg Gly Ile Val Thr Arg Val Ser Glu Val Lys Pro Lys Met
    210                 215                 220

Val Val Ala Thr Tyr Thr Cys Asp Gln Cys Gly Ala Glu Thr Tyr Gln
225                 230                 235                 240

Pro Ile Gln Ser Pro Thr Phe Met Pro Leu Ile Met Cys Pro Ser Gln
                245                 250                 255

Glu Cys Gln Thr Asn Arg Ser Gly Gly Arg Leu Tyr Leu Gln Thr Arg
            260                 265                 270

Gly Ser Arg Phe Ile Lys Phe Gln Glu Met Lys Met Gln Glu His Ser
        275                 280                 285

Asp Gln Val Pro Val Gly Asn Ile Pro Arg Ser Ile Thr Val Leu Val
    290                 295                 300

Glu Gly Glu Asn Thr Arg Ile Ala Gln Pro Gly Asp His Val Ser Val
305                 310                 315                 320

Thr Gly Ile Phe Leu Pro Ile Leu Arg Thr Gly Phe Arg Gln Val Val
                325                 330                 335

Gln Gly Leu Leu Ser Glu Thr Tyr Leu Glu Ala His Arg Ile Val Lys
            340                 345                 350

Met Asn Lys Ser Glu Asp Asp Glu Ser Gly Ala Gly Glu Leu Thr Arg
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355 360 365

Glu Glu Leu Arg Gln Ile Ala Glu Glu Asp Phe Tyr Glu Lys Leu Ala
370 375 380

Ala Ser Ile Ala Pro Glu Ile Tyr Gly His Glu Asp Val Lys Lys Ala
385 390 395 400

Leu Leu Leu Leu Leu Val Gly Gly Val Asp Gln Ser Pro Arg Gly Met
405 410 415

Lys Ile Arg Gly Asn Ile Asn Ile Cys Leu Met Gly Asp Pro Gly Val
420 425 430

Ala Lys Ser Gln Leu Leu Ser Tyr Ile Asp Arg Leu Ala Pro Arg Ser
435 440 445

Gln Tyr Thr Thr Gly Arg Gly Ser Ser Gly Val Gly Leu Thr Ala Ala
450 455 460

Val Leu Arg Asp Ser Val Ser Gly Glu Leu Thr Leu Glu Gly Gly Ala
465 470 475 480

Leu Val Leu Ala Asp Gln Gly Val Cys Cys Ile Asp Glu Phe Asp Lys
485 490 495

Met Ala Glu Ala Asp Arg Thr Ala Ile His Glu Val Met Glu Gln Gln
500 505 510

Thr Ile Ser Ile Ala Lys Ala Gly Ile Leu Thr Thr Leu Asn Ala Arg
515 520 525

Cys Ser Ile Leu Ala Ala Ala Asn Pro Ala Tyr Gly Arg Tyr Asn Pro
530 535 540

Arg Arg Ser Leu Glu Gln Asn Ile Gln Leu Pro Ala Ala Leu Leu Ser
545 550 555 560

Arg Phe Asp Leu Leu Trp Leu Ile Gln Asp Arg Pro Asp Arg Asp Asn
565 570 575

Asp Leu Arg Leu Ala Gln His Ile Thr Tyr Val His Gln His Ser Arg
580 585 590

Gln Pro Pro Ser Gln Phe Glu Pro Leu Asp Met Lys Leu Met Arg Arg
595 600 605

Tyr Ile Ala Met Cys Arg Glu Lys Gln Pro Met Val Pro Glu Ser Leu
610 615 620

Ala Asp Tyr Ile Thr Ala Ala Tyr Val Glu Met Arg Arg Glu Ala Trp

625 630 635 640

Ala Ser Lys Asp Ala Thr Tyr Thr Ser Ala Arg Thr Leu Leu Ala Ile
645 650 655

Leu Arg Leu Ser Thr Ala Leu Ala Arg Leu Arg Met Val Asp Val Val
660 665 670

Glu Lys Glu Asp Val Asn Glu Ala Ile Arg Leu Met Glu Met Ser Lys
675 680 685

Asp Ser Leu Leu Gly Asp Lys Gly Gln Thr Ala Arg Thr Gln Arg Pro
690 695 700

Ala Asp Val Ile Phe Ala Thr Val Arg Glu Leu Val Ser Gly Gly Arg
705 710 715 720

Ser Val Arg Phe Ser Glu Ala Glu Gln Arg Cys Val Ser Arg Gly Phe
725 730 735

Thr Pro Ala Gln Phe Gln Ala Ala Leu Asp Glu Tyr Glu Glu Leu Asn
740 745 750

Val Trp Gln Val Asn Ala Ser Arg Thr Arg Ile Thr Phe Val
755 760 765

<210> 1383
<211> 296
<212> PRT
<213> Homo sapiens

<400> 1383
Phe Arg Pro Gly Ser Pro Arg Gln Pro Arg Ala Gln Pro Ile Ser Ala
1 5 10 15

Pro Asp Cys Thr Arg Ala Met Val Gly Arg Arg Ala Leu Ile Val Leu
20 25 30

Ala His Ser Glu Arg Thr Ser Phe Asn Tyr Ala Met Lys Glu Ala Ala
35 40 45

Ala Ala Ala Leu Lys Lys Lys Gly Trp Glu Val Val Glu Ser Asp Leu
50 55 60

Tyr Ala Met Asn Phe Asn Pro Ile Ile Ser Arg Lys Asp Ile Thr Gly
65 70 75 80

Lys Leu Lys Asp Pro Ala Asn Phe Gln Tyr Pro Ala Glu Ser Val Leu
85 90 95

Ala Tyr Lys Glu Gly His Leu Ser Pro Asp Ile Val Ala Glu Gln Lys
100 105 110

Lys Leu Glu Ala Ala Asp Leu Val Ile Phe Gln Phe Pro Leu Gln Trp
115 120 125

Phe Gly Val Pro Ala Ile Leu Lys Gly Trp Phe Glu Arg Val Phe Ile
130 135 140

Gly Glu Phe Ala Tyr Thr Tyr Ala Ala Met Tyr Asp Lys Gly Pro Phe
145 150 155 160

Arg Ser Lys Lys Ala Val Leu Ser Ile Thr Thr Gly Gly Ser Gly Ser
165 170 175

Met Tyr Ser Leu Gln Gly Ile His Gly Asp Met Asn Val Ile Leu Trp
180 185 190

Pro Ile Gln Ser Gly Ile Leu His Phe Cys Gly Phe Gln Val Leu Glu
195 200 205

Pro Gln Leu Thr Tyr Ser Ile Gly His Thr Pro Ala Asp Ala Arg Ile
210 215 220

Gln Ile Leu Glu Gly Trp Lys Lys Arg Leu Glu Asn Ile Trp Asp Glu
225 230 235 240

Thr Pro Leu Tyr Phe Ala Pro Ser Ser Leu Phe Asp Leu Asn Phe Gln
245 250 255

Ala Gly Phe Leu Met Lys Lys Glu Val Gln Asp Glu Glu Lys Asn Lys
260 265 270

Lys Phe Gly Leu Ser Val Gly His His Leu Gly Lys Ser Ile Pro Thr
275 280 285

Asp Asn Gln Ile Lys Ala Arg Lys
290 295

<210> 1384
<211> 165
<212> PRT
<213> Homo sapiens

<400> 1384
Asp Pro Arg Thr Met Asn Leu Ala Ile Ser Ile Ala Leu Leu Leu Thr
1 5 10 15

Val Leu Gln Val Ser Arg Gly Gln Lys Val Thr Ser Leu Thr Ala Cys
20 25 30

Leu Val Asp Gln Ser Leu Arg Leu Asp Cys Arg His Glu Asn Thr Ser
35 40 45

Ser Ser Pro Ile Gln Tyr Glu Phe Ser Leu Thr Arg Glu Thr Lys Lys
50 55 60

His Val Leu Phe Gly Thr Val Gly Val Pro Glu His Thr Tyr Arg Ser
65 70 75 80

Arg Thr Asn Phe Thr Ser Lys Tyr Asn Met Lys Val Leu Tyr Leu Ser
85 90 95

Ala Phe Thr Ser Lys Asp Glu Gly Thr Tyr Thr Cys Ala Leu His His
100 105 110

Ser Gly His Ser Pro Pro Ile Ser Ser Gln Asn Val Thr Val Leu Arg
115 120 125

Asp Lys Leu Val Lys Cys Glu Gly Ile Ser Leu Leu Ala Gln Asn Thr
130 135 140

Ser Trp Leu Leu Leu Leu Leu Leu Ser Leu Ser Leu Leu Gln Ala Thr
145 150 155 160

Asp Phe Met Ser Leu
165

<210> 1385
<211> 399
<212> PRT
<213> Homo sapiens

<400> 1385
His Glu Arg Thr Pro Ser Arg Pro Gln Pro Asp Thr Pro Arg Gly Pro
1 5 10 15

Pro Val Ser Arg Gly Cys Ser Pro Arg His Gly Thr Gly Pro Arg Leu
20 25 30

Thr Met Ala Ala Ala Arg His Ser Thr Leu Asp Phe Met Leu Gly Ala
35 40 45

Lys Ala Asp Gly Glu Thr Ile Leu Lys Gly Leu Gln Ser Ile Phe Gln
50 55 60

Glu Gln Gly Met Ala Glu Ser Val His Thr Trp Gln Asp His Gly Tyr

65 70 75 80

Leu Ala Thr Tyr Thr Asn Lys Asn Gly Ser Phe Ala Asn Leu Arg Ile
85 90 95

Tyr Pro His Gly Leu Val Leu Leu Asp Leu Gln Ser Tyr Asp Gly Asp
100 105 110

Ala Gln Gly Lys Glu Glu Ile Asp Ser Ile Leu Asn Lys Val Glu Glu
115 120 125

Arg Met Lys Glu Leu Ser Gln Asp Ser Thr Gly Arg Val Lys Arg Leu
130 135 140

Pro Pro Ile Val Arg Gly Gly Ala Ile Asp Arg Tyr Trp Pro Thr Ala
145 150 155 160

Asp Gly Arg Leu Val Glu Tyr Asp Ile Asp Glu Val Val Tyr Asp Glu
165 170 175

Asp Ser Pro Tyr Gln Asn Ile Lys Ile Leu His Ser Lys Gln Phe Gly
180 185 190

Asn Ile Leu Ile Leu Ser Gly Asp Val Asn Leu Ala Glu Ser Asp Leu
195 200 205

Ala Tyr Thr Arg Ala Ile Met Gly Ser Gly Lys Glu Asp Tyr Thr Gly
210 215 220

Lys Asp Val Leu Ile Leu Gly Gly Gly Asp Gly Gly Ile Leu Cys Glu
225 230 235 240

Ile Val Lys Leu Lys Pro Lys Met Val Thr Met Val Glu Ile Asp Gln
245 250 255

Met Val Ile Asp Gly Cys Lys Lys Tyr Met Arg Lys Thr Cys Gly Asp
260 265 270

Val Leu Asp Asn Leu Lys Gly Asp Cys Tyr Gln Val Leu Ile Glu Asp
275 280 285

Cys Ile Pro Val Leu Lys Arg Tyr Ala Lys Glu Gly Arg Glu Phe Asp
290 295 300

Tyr Val Ile Asn Asp Leu Thr Ala Val Pro Ile Ser Thr Ser Pro Glu
305 310 315 320

Glu Asp Ser Thr Trp Glu Phe Leu Arg Leu Ile Leu Asp Leu Ser Met
325 330 335

Lys Val Leu Lys Gln Asp Gly Lys Tyr Phe Thr Gln Gly Asn Cys Val

340 345 350

Asn Leu Thr Glu Ala Leu Ser Leu Tyr Glu Glu Gln Leu Gly Arg Leu
355 360 365

Tyr Cys Pro Val Glu Phe Ser Lys Glu Ile Val Cys Val Pro Ser Tyr
370 375 380

Leu Glu Leu Trp Val Phe Tyr Thr Val Trp Lys Lys Ala Lys Pro
385 390 395

<210> 1386
<211> 287
<212> PRT
<213> Homo sapiens

<400> 1386
Phe Asp Cys Arg Asp Val Ala Phe Thr Val Gly Glu Gly Glu Asp His
1 5 10 15

Asp Ile Pro Ile Gly Ile Asp Lys Ala Leu Glu Lys Met Gln Arg Glu
20 25 30

Glu Gln Cys Ile Leu Tyr Leu Gly Pro Arg Tyr Gly Phe Gly Glu Ala
35 40 45

Gly Lys Pro Lys Phe Gly Ile Glu Pro Asn Ala Glu Leu Ile Tyr Glu
50 55 60

Val Thr Leu Lys Ser Phe Glu Lys Ala Lys Glu Ser Trp Glu Met Asp
65 70 75 80

Thr Lys Glu Lys Leu Glu Gln Ala Ala Ile Val Lys Glu Lys Gly Thr
85 90 95

Val Tyr Phe Lys Gly Gly Lys Tyr Met Gln Ala Val Ile Gln Tyr Gly
100 105 110

Lys Ile Val Ser Trp Leu Glu Met Glu Tyr Gly Leu Ser Glu Lys Glu
115 120 125

Ser Lys Ala Ser Glu Ser Phe Leu Leu Ala Ala Phe Leu Asn Leu Ala
130 135 140

Met Cys Tyr Leu Lys Leu Arg Glu Tyr Thr Lys Ala Val Glu Cys Cys
145 150 155 160

Asp Lys Ala Leu Gly Leu Asp Ser Ala Asn Glu Lys Gly Leu Tyr Arg
165 170 175

Arg Gly Glu Ala Gln Leu Leu Met Asn Glu Phe Glu Ser Ala Lys Gly
180 185 190

Asp Phe Glu Lys Val Leu Glu Val Asn Pro Gln Asn Lys Ala Ala Arg
195 200 205

Leu Gln Ile Ser Met Cys Gln Lys Lys Ala Lys Glu His Asn Glu Arg
210 215 220

Asp Arg Arg Tyr Thr Pro Thr Cys Ser Arg Ser Leu Gln Ser Arg Met
225 230 235 240

Pro Arg Lys Arg Pro Ile Lys Gln Trp Ala Arg Arg Leu Gln Lys Gly
245 250 255

Ser Leu Met Lys Lys Glu Gln Thr Val Lys Gln Trp Lys Lys Arg Asn
260 265 270

Leu Arg Ala Thr Tyr Asp Ala Thr Pro Arg Arg Glu Glu Ser Gln
275 280 285

<210> 1387
<211> 206
<212> PRT
<213> Homo sapiens

<400> 1387
Arg Leu Pro Ile Arg Gln Ser Ala Ala Asp Gly Leu Arg Ala Arg Pro
1 5 10 15

Leu Gly Ser Asn Thr Ala Pro Ala Leu Arg Val Met Val Gln Ala Trp
20 25 30

Tyr Met Asp Asp Ala Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp
35 40 45

Pro Gly Arg Pro Val Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu
50 55 60

Tyr Trp Lys Leu Asp Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu
65 70 75 80

Lys Ile Arg Arg Glu Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile
85 90 95

Cys Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr
100 105 110

Glu Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly
115 120 125

Ser Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile
130 135 140

Phe Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His
145 150 155 160

Arg Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe
165 170 175

Val Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe
180 185 190

Glu Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala
195 200 205

<210> 1388
<211> 394
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1388
Phe His Xaa Ala Ala His Tyr Ser Leu Pro Asp Gly Arg His Gly Arg
1 5 10 15

Leu Asp Ser Pro Thr Phe His Leu Thr Leu His Tyr Pro Thr Glu His
20 25 30

Val Gln Phe Trp Val Gly Ser Pro Ser Thr Pro Ala Gly Trp Val Arg
35 40 45

Glu Gly Asp Thr Val Gln Leu Leu Cys Arg Gly Asp Gly Ser Pro Ser
50 55 60

Pro Glu Tyr Thr Leu Phe Arg Leu Gln Asp Glu Gln Glu Glu Val Leu
65 70 75 80

Asn Val Asn Leu Glu Gly Asn Leu Thr Leu Glu Gly Val Thr Arg Gly
85 90 95

Gln Ser Gly Thr Tyr Gly Cys Arg Val Glu Asp Tyr Asp Ala Ala Asp
100 105 110

```
Asp Val Gln Leu Ser Lys Thr Leu Glu Leu Arg Val Ala Tyr Leu Asp
        115                 120                 125

Pro Leu Glu Leu Ser Glu Gly Lys Val Leu Ser Leu Pro Leu Asn Ser
    130                 135                 140

Ser Ala Val Val Asn Cys Ser Val His Gly Leu Pro Thr Pro Ala Leu
145                 150                 155                 160

Arg Trp Thr Lys Asp Ser Thr Pro Leu Gly Asp Gly Pro Met Leu Ser
                165                 170                 175

Leu Ser Ser Ile Thr Phe Asp Ser Asn Gly Thr Tyr Val Cys Glu Ala
            180                 185                 190

Ser Leu Pro Thr Val Pro Val Leu Ser Arg Thr Gln Asn Phe Thr Leu
        195                 200                 205

Leu Val Gln Gly Ser Pro Glu Leu Lys Thr Ala Glu Ile Glu Pro Lys
    210                 215                 220

Ala Asp Gly Ser Trp Arg Glu Gly Asp Glu Val Thr Leu Ile Cys Ser
225                 230                 235                 240

Ala Arg Gly His Pro Asp Pro Lys Leu Ser Trp Ser Gln Leu Gly Gly
                245                 250                 255

Ser Pro Ala Glu Pro Ile Pro Gly Arg Gln Gly Trp Val Ser Ser Ser
            260                 265                 270

Leu Thr Leu Lys Val Thr Ser Ala Leu Ser Arg Asp Gly Ile Ser Cys
        275                 280                 285

Glu Ala Ser Asn Pro His Gly Asn Lys Arg His Val Phe His Phe Gly
    290                 295                 300

Thr Val Ser Pro Gln Thr Ser Gln Ala Gly Val Ala Val Met Ala Val
305                 310                 315                 320

Ala Val Ser Val Gly Leu Leu Leu Leu Val Val Ala Val Phe Tyr Cys
                325                 330                 335

Val Arg Arg Lys Gly Gly Pro Cys Cys Arg Gln Arg Arg Glu Lys Gly
            340                 345                 350

Ala Pro Pro Pro Gly Glu Pro Gly Leu Ser His Ser Gly Ser Glu Gln
        355                 360                 365

Pro Glu Gln Thr Gly Leu Leu Met Gly Gly Ala Ser Gly Gly Ala Arg
    370                 375                 380
```

Gly Gly Ser Gly Gly Phe Gly Asp Glu Cys
385 390

<210> 1389
<211> 264
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1389
Val Gly Cys Arg Trp Ser Arg Val Gly Pro Gln Asn Pro Arg Val Xaa
1 5 10 15

Leu Pro Pro Pro Thr Leu Ala Met Phe Leu Thr Arg Ser Glu Tyr Asp
20 25 30

Arg Gly Val Asn Thr Phe Ser Pro Glu Gly Arg Leu Phe Gln Val Glu
35 40 45

Tyr Ala Ile Glu Ala Ile Lys Leu Gly Ser Thr Ala Ile Gly Ile Gln
50 55 60

Thr Ser Glu Gly Val Cys Leu Ala Val Glu Lys Arg Ile Thr Ser Pro
65 70 75 80

Leu Met Glu Pro Ser Ser Ile Glu Lys Ile Val Glu Ile Asp Ala His
85 90 95

Ile Gly Cys Ala Met Ser Gly Leu Ile Ala Asp Ala Lys Thr Leu Ile
100 105 110

Asp Lys Ala Arg Val Glu Thr Gln Asn His Trp Phe Thr Tyr Asn Glu
115 120 125

Thr Met Thr Val Glu Ser Val Thr Gln Ala Val Ser Asn Leu Ala Leu
130 135 140

Gln Phe Gly Glu Glu Asp Ala Asp Pro Gly Ala Met Ser Arg Pro Phe
145 150 155 160

Gly Val Ala Leu Leu Phe Gly Gly Val Asp Glu Lys Gly Pro Gln Leu
165 170 175

Phe His Met Asp Pro Ser Gly Thr Phe Val Gln Cys Asp Ala Arg Ala

180 185 190

Ile Gly Ser Ala Ser Glu Gly Ala Gln Ser Ser Leu Gln Glu Val Tyr
195 200 205

His Lys Ser Met Thr Leu Lys Glu Ala Ile Lys Ser Ser Leu Ile Ile
210 215 220

Leu Lys Gln Val Met Glu Glu Lys Leu Asn Ala Thr Asn Ile Glu Leu
225 230 235 240

Ala Thr Val Gln Pro Gly Gln Asn Phe His Met Phe Thr Lys Glu Glu
245 250 255

Leu Glu Glu Val Ile Lys Asp Ile
260

<210> 1390
<211> 178
<212> PRT
<213> Homo sapiens

<400> 1390
Gln Lys Leu Glu Leu His Arg Gly Gly Gly Arg Ser Arg Thr Ser Gly
1 5 10 15

Ser Pro Gly Leu Phe Gly Leu Ser Ala Arg Arg Leu Leu Ala Ala Ala
20 25 30

Ala Thr Arg Gly Leu Pro Ala Ala Arg Val Arg Trp Glu Ser Ser Phe
35 40 45

Ser Arg Thr Val Val Ala Pro Ser Ala Val Ala Gly Lys Arg Pro Pro
50 55 60

Glu Pro Thr Thr Pro Trp Gln Glu Asp Pro Glu Pro Glu Asp Glu Asn
65 70 75 80

Leu Tyr Glu Lys Asn Pro Asp Ser His Gly Tyr Asp Lys Asp Pro Val
85 90 95

Leu Asp Val Trp Asn Met Arg Leu Val Phe Phe Phe Gly Val Ser Ile
100 105 110

Ile Leu Val Leu Gly Ser Thr Phe Val Ala Tyr Leu Pro Asp Tyr Arg
115 120 125

Cys Thr Gly Cys Pro Arg Ala Trp Asp Gly Met Lys Glu Trp Ser Arg
130 135 140

Arg Glu Ala Glu Arg Leu Val Lys Tyr Arg Glu Ala Asn Gly Leu Pro
145 150 155 160

Ile Met Glu Ser Asn Cys Phe Asp Pro Ser Lys Ile Gln Leu Pro Glu
165 170 175

Asp Glu

<210> 1391
<211> 133
<212> PRT
<213> Homo sapiens

<400> 1391
Val Ile Ile Thr Ser Ile Asn Gln Lys Ile Phe His Pro Leu Arg Ala
1 5 10 15

Leu Lys Leu Ser Thr Ser Ala Thr Phe Leu Ile Leu Val Leu Gly Gly
20 25 30

His Val Tyr Gly Leu Phe Asn Phe His Val Pro Tyr Cys Pro Leu Pro
35 40 45

Ala Val Ala Lys Ala Ser Cys Phe Ser Pro Thr Glu Glu Thr Val Leu
50 55 60

Cys His Asp Asp Arg Ala Leu Leu Gly Leu Val Phe Leu Val Phe Pro
65 70 75 80

Phe Trp Gln Cys Gly Leu Gln Glu Leu Asp Val Tyr Ala Gln Gly Ile
85 90 95

Glu Phe Thr Leu Lys Leu Gly Asn Gly Val Phe Asn Leu Cys Ser Cys
100 105 110

Leu Phe Ile Leu Leu Phe Ile Phe Cys His Pro Ala Leu Tyr Trp Ala
115 120 125

Asn Asn Glu Ile Lys
130

<210> 1392
<211> 401
<212> PRT
<213> Homo sapiens

<400> 1392

Asn Thr Val Leu Lys Lys Met Asp Glu Glu Pro Glu Arg Thr Lys Arg
1 5 10 15

Trp Glu Gly Gly Tyr Glu Arg Thr Trp Glu Ile Leu Lys Glu Asp Glu
20 25 30

Ser Gly Ser Leu Lys Ala Thr Ile Glu Asp Ile Leu Phe Lys Ala Lys
35 40 45

Arg Lys Arg Val Phe Glu His His Gly Gln Val Arg Leu Gly Met Met
50 55 60

Arg His Leu Tyr Val Val Val Asp Gly Ser Arg Thr Met Glu Asp Gln
65 70 75 80

Asp Leu Lys Pro Asn Arg Leu Thr Cys Thr Leu Lys Leu Leu Glu Tyr
85 90 95

Phe Val Glu Glu Tyr Phe Asp Gln Asn Pro Ile Ser Gln Ile Gly Ile
100 105 110

Ile Val Thr Lys Ser Lys Arg Ala Glu Lys Leu Thr Glu Leu Ser Gly
115 120 125

Asn Pro Arg Lys His Ile Thr Ser Leu Lys Lys Ala Val Asp Met Thr
130 135 140

Cys His Gly Glu Pro Ser Leu Tyr Asn Ser Leu Ser Ile Ala Met Gln
145 150 155 160

Thr Leu Lys His Met Pro Gly His Thr Ser Arg Glu Val Leu Ile Ile
165 170 175

Phe Ser Ser Leu Thr Thr Cys Asp Pro Ser Asn Ile Tyr Asp Leu Ile
180 185 190

Lys Thr Leu Lys Ala Ala Lys Ile Arg Val Ser Val Ile Gly Leu Ser
195 200 205

Ala Glu Val Arg Val Cys Thr Val Leu Ala Arg Glu Thr Gly Gly Thr
210 215 220

Tyr His Val Ile Leu Asp Glu Ser His Tyr Lys Glu Leu Leu Thr His
225 230 235 240

His Val Ser Pro Pro Pro Ala Ser Ser Ser Ser Glu Cys Ser Leu Ile
245 250 255

Arg Met Gly Phe Pro Gln His Thr Ile Ala Ser Leu Ser Asp Gln Asp

260 265 270

Ala Lys Pro Ser Phe Ser Met Ala His Leu Asp Gly Asn Thr Glu Pro
275 280 285

Gly Leu Thr Leu Gly Gly Tyr Phe Cys Pro Gln Cys Arg Ala Lys Tyr
290 295 300

Cys Glu Leu Pro Val Glu Cys Lys Ile Cys Gly Leu Thr Leu Val Ser
305 310 315 320

Ala Pro His Leu Ala Arg Ser Tyr His His Leu Phe Pro Leu Asp Ala
325 330 335

Phe Gln Glu Ile Pro Leu Glu Glu Tyr Asn Gly Glu Arg Phe Cys Tyr
340 345 350

Gly Cys Gln Gly Glu Leu Lys Asp Gln His Val Tyr Val Cys Ala Val
355 360 365

Cys Gln Asn Val Phe Cys Val Asp Cys Asp Val Phe Val His Asp Ser
370 375 380

Leu His Cys Cys Pro Gly Cys Ile His Lys Ile Pro Ala Pro Ser Gly
385 390 395 400

Val

<210> 1393
<211> 318
<212> PRT
<213> Homo sapiens

<400> 1393
Pro Glu Gly Leu Pro Arg Phe Asn Asn Asn Phe Met Ala Pro Gly Ser
1 5 10 15

Ala Ser Ser Pro Ser Pro Ser Phe Pro Ala Ser Arg Pro Trp Ala Ala
20 25 30

Val Gly Thr Met Ala Ala Ala Ala Ala Ala Gly Pro Ser Pro Gly Ser
35 40 45

Gly Pro Gly Asp Ser Pro Glu Gly Pro Glu Gly Glu Ala Pro Glu Arg
50 55 60

Arg Arg Lys Ala His Gly Met Leu Lys Leu Tyr Tyr Gly Leu Ser Glu
65 70 75 80

```
Gly Glu Ala Ala Gly Arg Pro Ala Gly Pro Asp Pro Leu Asp Pro Thr
                85                  90                  95

Asp Leu Asn Gly Ala His Phe Asp Pro Glu Val Tyr Leu Asp Lys Leu
            100                 105                 110

Arg Arg Glu Cys Pro Leu Ala Gln Leu Met Asp Ser Glu Thr Asp Met
        115                 120                 125

Val Arg Gln Ile Arg Ala Leu Asp Ser Asp Met Gln Thr Leu Val Tyr
    130                 135                 140

Glu Asn Tyr Asn Lys Phe Ile Ser Ala Thr Asp Thr Ile Arg Lys Met
145                 150                 155                 160

Lys Asn Asp Phe Arg Lys Met Glu Asp Glu Met Asp Arg Leu Ala Thr
                165                 170                 175

Asn Met Ala Val Ile Thr Asp Phe Ser Ala Arg Ile Ser Ala Thr Leu
            180                 185                 190

Gln Asp Arg His Glu Arg Ile Thr Lys Leu Ala Gly Val His Ala Leu
        195                 200                 205

Leu Arg Lys Leu Gln Phe Leu Phe Glu Leu Pro Ser Arg Leu Thr Lys
    210                 215                 220

Cys Val Glu Leu Gly Ala Tyr Gly Gln Ala Val Arg Tyr Gln Gly Arg
225                 230                 235                 240

Ala Gln Ala Val Leu Gln Gln Tyr Gln His Leu Pro Ser Phe Arg Ala
                245                 250                 255

Ile Gln Asp Asp Cys Gln Val Ile Thr Ala Arg Leu Ala Gln Gln Leu
            260                 265                 270

Arg Gln Arg Phe Arg Glu Gly Gly Ser Gly Ala Pro Glu Gln Ala Glu
        275                 280                 285

Cys Val Glu Leu Leu Leu Ala Leu Gly Glu Pro Ala Glu Glu Leu Cys
    290                 295                 300

Glu Glu Phe Trp Arg Thr Pro Ala Ala Gly Trp Arg Arg Ser
305                 310                 315
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<210> 1394
<211> 1285
<212> PRT

<213> Homo sapiens

<400> 1394

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Phe Ser Phe Pro Leu Ser Ser Glu Pro Phe Gln Gly Ser Tyr Lys Val
  1               5                  10                  15

Val Val Gln Lys Lys Ser Gly Gly Arg Thr Glu His Pro Phe Thr Val
             20                  25                  30

Glu Glu Phe Val Leu Pro Lys Phe Glu Val Gln Val Thr Val Pro Lys
         35                  40                  45

Ile Ile Thr Ile Leu Glu Glu Glu Met Asn Val Ser Val Cys Gly Leu
     50                  55                  60

Tyr Thr Tyr Gly Lys Pro Val Pro Gly His Val Thr Val Ser Ile Cys
 65                  70                  75                  80

Arg Lys Tyr Ser Asp Ala Ser Asp Cys His Gly Glu Asp Ser Gln Ala
                 85                  90                  95

Phe Cys Glu Lys Phe Ser Gly Gln Leu Asn Ser His Gly Cys Phe Tyr
            100                 105                 110

Gln Gln Val Lys Thr Lys Val Phe Gln Leu Lys Arg Lys Glu Tyr Glu
        115                 120                 125

Met Lys Leu His Thr Glu Ala Gln Ile Gln Glu Glu Gly Thr Val Val
    130                 135                 140

Glu Leu Thr Gly Arg Gln Ser Ser Glu Ile Thr Arg Thr Ile Thr Lys
145                 150                 155                 160

Leu Ser Phe Val Lys Val Asp Ser His Phe Arg Gln Gly Ile Pro Phe
                165                 170                 175

Phe Gly Gln Val Arg Leu Val Asp Gly Lys Gly Val Pro Ile Pro Asn
            180                 185                 190

Lys Val Ile Phe Ile Arg Gly Asn Glu Ala Asn Tyr Tyr Ser Asn Ala
        195                 200                 205

Thr Thr Asp Glu His Gly Leu Val Gln Phe Ser Ile Asn Thr Thr Asn
    210                 215                 220

Val Met Gly Thr Ser Leu Thr Val Arg Val Asn Tyr Lys Asp Arg Ser
225                 230                 235                 240

Pro Cys Tyr Gly Tyr Gln Trp Val Ser Glu Glu His Glu Glu Ala His
                245                 250                 255
```

His Thr Ala Tyr Leu Val Phe Ser Pro Ser Lys Ser Phe Val His Leu
260 265 270

Glu Pro Met Ser His Glu Leu Pro Cys Gly His Thr Gln Thr Val Gln
275 280 285

Ala His Tyr Ile Leu Asn Gly Gly Thr Leu Leu Gly Leu Lys Lys Leu
290 295 300

Ser Phe Tyr Tyr Leu Ile Met Ala Lys Gly Gly Ile Val Arg Thr Gly
305 310 315 320

Thr His Gly Leu Leu Val Lys Gln Glu Asp Met Lys Gly His Phe Ser
325 330 335

Ile Ser Ile Pro Val Lys Ser Asp Ile Ala Pro Val Ala Arg Leu Leu
340 345 350

Ile Tyr Ala Val Leu Pro Thr Gly Asp Val Ile Gly Asp Ser Ala Lys
355 360 365

Tyr Asp Val Glu Asn Cys Leu Ala Asn Lys Val Asp Leu Ser Phe Ser
370 375 380

Pro Ser Gln Ser Leu Pro Ala Ser His Ala His Leu Arg Val Thr Ala
385 390 395 400

Ala Pro Gln Ser Val Cys Ala Leu Arg Ala Val Asp Gln Ser Val Leu
405 410 415

Leu Met Lys Pro Asp Ala Glu Leu Ser Ala Ser Ser Val Tyr Asn Leu
420 425 430

Leu Pro Glu Lys Asp Leu Thr Gly Phe Pro Gly Pro Leu Asn Asp Gln
435 440 445

Asp Asp Glu Asp Cys Ile Asn Arg His Asn Val Tyr Ile Asn Gly Ile
450 455 460

Thr Tyr Thr Pro Val Ser Ser Thr Asn Glu Lys Asp Met Tyr Ser Phe
465 470 475 480

Leu Glu Asp Met Gly Leu Lys Ala Phe Thr Asn Ser Lys Ile Arg Lys
485 490 495

Pro Lys Met Cys Pro Gln Leu Gln Gln Tyr Glu Met His Gly Pro Glu
500 505 510

Gly Leu Arg Val Gly Phe Tyr Glu Ser Asp Val Met Gly Arg Gly His
515 520 525

```
Ala Arg Leu Val His Val Glu Glu Pro His Thr Glu Thr Val Arg Lys
    530                 535                 540

Tyr Phe Pro Glu Thr Trp Ile Trp Asp Leu Val Val Val Asn Ser Ala
545                 550                 555                 560

Gly Val Ala Glu Val Gly Val Thr Val Pro Asp Thr Ile Thr Glu Trp
                565                 570                 575

Lys Ala Gly Ala Phe Cys Leu Ser Glu Asp Ala Gly Leu Gly Ile Ser
            580                 585                 590

Ser Thr Ala Ser Leu Arg Ala Phe Gln Pro Phe Phe Val Glu Leu Thr
        595                 600                 605

Met Pro Tyr Ser Val Ile Arg Gly Glu Ala Phe Thr Leu Lys Ala Thr
    610                 615                 620

Val Leu Asn Tyr Leu Pro Lys Cys Ile Arg Val Ser Val Gln Leu Glu
625                 630                 635                 640

Ala Ser Pro Ala Phe Leu Ala Val Pro Val Glu Lys Glu Gln Ala Pro
                645                 650                 655

His Cys Ile Cys Ala Asn Gly Arg Gln Thr Val Ser Trp Ala Val Thr
            660                 665                 670

Pro Lys Ser Leu Gly Asn Val Asn Phe Thr Val Ser Ala Glu Ala Leu
        675                 680                 685

Glu Ser Gln Glu Leu Cys Gly Thr Glu Val Pro Ser Val Pro Glu His
    690                 695                 700

Gly Arg Lys Asp Thr Val Ile Lys Pro Leu Leu Val Glu Pro Glu Gly
705                 710                 715                 720

Leu Glu Lys Glu Thr Thr Phe Asn Ser Leu Leu Cys Pro Ser Gly Gly
                725                 730                 735

Glu Val Ser Glu Glu Leu Ser Leu Lys Leu Pro Pro Asn Val Val Glu
            740                 745                 750

Glu Ser Ala Arg Ala Ser Val Ser Val Leu Gly Asp Ile Leu Gly Ser
        755                 760                 765

Ala Met Gln Asn Thr Gln Asn Leu Leu Gln Met Pro Tyr Gly Cys Gly
    770                 775                 780

Glu Gln Asn Met Val Leu Phe Ala Pro Asn Ile Tyr Val Leu Asp Tyr
785                 790                 795                 800
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Leu Asn Glu Thr Gln Gln Leu Thr Pro Glu Ile Lys Ser Lys Ala Ile
805 810 815

Gly Tyr Leu Asn Thr Gly Tyr Gln Arg Gln Leu Asn Tyr Lys His Tyr
820 825 830

Asp Gly Ser Tyr Ser Thr Phe Gly Glu Arg Tyr Gly Arg Asn Gln Gly
835 840 845

Asn Thr Trp Leu Thr Ala Phe Val Leu Lys Thr Phe Ala Gln Ala Arg
850 855 860

Ala Tyr Ile Phe Ile Asp Glu Ala His Ile Thr Gln Ala Leu Ile Trp
865 870 875 880

Leu Ser Gln Arg Gln Lys Asp Asn Gly Cys Phe Arg Ser Ser Gly Ser
885 890 895

Leu Leu Asn Asn Ala Ile Lys Gly Gly Val Glu Asp Glu Val Thr Leu
900 905 910

Ser Ala Tyr Ile Thr Ile Ala Leu Leu Glu Ile Pro Leu Thr Val Thr
915 920 925

His Pro Val Val Arg Asn Ala Leu Phe Cys Leu Glu Ser Ala Trp Lys
930 935 940

Thr Ala Gln Glu Gly Asp His Gly Ser His Val Tyr Thr Lys Ala Leu
945 950 955 960

Leu Ala Tyr Ala Phe Ala Leu Ala Gly Asn Gln Asp Lys Arg Lys Glu
965 970 975

Val Leu Lys Ser Leu Asn Glu Glu Ala Val Lys Lys Asp Asn Ser Val
980 985 990

His Trp Glu Arg Pro Gln Lys Pro Lys Ala Pro Val Gly His Phe Tyr
995 1000 1005

Glu Pro Gln Ala Pro Ser Ala Glu Val Glu Met Thr Ser Tyr Val Leu
1010 1015 1020

Leu Ala Tyr Leu Thr Ala Gln Pro Ala Pro Thr Ser Glu Asp Leu Thr
025 1030 1035 1040

Ser Ala Thr Asn Ile Val Lys Trp Ile Thr Lys Gln Gln Asn Ala Gln
1045 1050 1055

Gly Gly Phe Ser Ser Thr Gln Asp Thr Val Val Ala Leu His Ala Leu
1060 1065 1070

Ser Lys Tyr Gly Ala Ala Thr Phe Thr Arg Thr Gly Lys Ala Ala Gln
1075 1080 1085

Val Thr Ile Gln Ser Ser Gly Thr Phe Ser Ser Lys Phe Gln Val Asp
1090 1095 1100

Asn Asn Asn Arg Leu Leu Leu Gln Gln Val Ser Leu Pro Glu Leu Pro
105 1110 1115 1120

Gly Glu Tyr Ser Met Lys Val Thr Gly Glu Gly Cys Val Tyr Leu Gln
1125 1130 1135

Thr Ser Leu Lys Tyr Asn Ile Leu Pro Glu Lys Glu Glu Phe Pro Phe
1140 1145 1150

Ala Leu Gly Val Gln Thr Leu Pro Gln Thr Cys Asp Glu Pro Lys Ala
1155 1160 1165

His Thr Ser Phe Gln Ile Ser Leu Ser Val Ser Tyr Thr Gly Ser Arg
1170 1175 1180

Ser Ala Ser Asn Met Ala Ile Val Asp Val Lys Met Val Ser Gly Phe
185 1190 1195 1200

Ile Pro Leu Lys Pro Thr Val Lys Met Leu Glu Arg Ser Asn His Val
1205 1210 1215

Ser Arg Thr Glu Val Ser Ser Asn His Val Leu Ile Tyr Leu Asp Lys
1220 1225 1230

Val Ser Asn Gln Thr Leu Ser Leu Phe Phe Thr Val Leu Gln Asp Val
1235 1240 1245

Pro Val Arg Asp Leu Lys Pro Ala Ile Val Lys Val Tyr Asp Tyr Tyr
1250 1255 1260

Glu Thr Asp Glu Phe Ala Ile Ala Glu Tyr Asn Ala Pro Cys Ser Lys
265 1270 1275 1280

Asp Leu Gly Asn Ala
1285

<210> 1395
<211> 75
<212> PRT
<213> Homo sapiens

<400> 1395
Ile Thr Lys Asn Ile Tyr Ser Asp Leu Lys Asp Leu Ser Ala Lys Asn

1 5 10 15

Gln Ser Ile Ser Cys Pro Ser Ile Ile Val His Ala Cys Leu Leu Leu
20 25 30

Phe Thr Cys Ser Ser Ala Gln Thr Val Ser Asn Leu Gly Thr Pro Phe
35 40 45

Gly Ala Asp Lys Tyr Ser Ser Ala Phe Ser Pro Gln Ile Tyr Asn Asp
50 55 60

Phe Asn Ile Pro Lys Asn Ile Gly Ile Ser Glu
65 70 75

<210> 1396
<211> 920
<212> PRT
<213> Homo sapiens

<400> 1396
Arg Thr Arg Gly Ile His Gly Glu Met Arg Leu Phe Val Ser Asp Gly
1 5 10 15

Val Pro Gly Cys Leu Pro Val Leu Ala Ala Ala Gly Arg Ala Arg Gly
20 25 30

Arg Ala Glu Val Leu Ile Ser Thr Val Gly Pro Glu Asp Cys Val Val
35 40 45

Pro Phe Leu Thr Arg Pro Lys Val Pro Val Leu Gln Leu Asp Ser Gly
50 55 60

Asn Tyr Leu Phe Ser Thr Ser Ala Ile Cys Arg Tyr Phe Phe Leu Leu
65 70 75 80

Ser Gly Trp Glu Gln Asp Asp Leu Thr Asn Gln Trp Leu Glu Trp Glu
85 90 95

Ala Thr Glu Leu Gln Pro Ala Leu Ser Ala Ala Leu Tyr Tyr Leu Val
100 105 110

Val Gln Gly Lys Lys Gly Glu Asp Val Leu Gly Ser Val Arg Arg Ala
115 120 125

Leu Thr His Ile Asp His Ser Leu Ser Arg Gln Asn Cys Pro Phe Leu
130 135 140

Ala Gly Glu Thr Glu Ser Leu Ala Asp Ile Val Leu Trp Gly Ala Leu
145 150 155 160

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Tyr Pro Leu Leu Gln Asp Pro Ala Tyr Leu Pro Glu Glu Leu Ser Ala
                165                 170                 175

Leu His Ser Trp Phe Gln Thr Leu Ser Thr Gln Glu Pro Cys Gln Arg
            180                 185                 190

Ala Ala Glu Thr Val Leu Lys Gln Gln Gly Val Leu Ala Leu Arg Pro
        195                 200                 205

Tyr Leu Gln Lys Gln Pro Gln Pro Ser Pro Ala Glu Gly Arg Ala Val
    210                 215                 220

Thr Asn Glu Pro Glu Glu Glu Glu Leu Ala Thr Leu Ser Glu Glu Glu
225                 230                 235                 240

Ile Ala Met Ala Val Thr Ala Trp Glu Lys Gly Leu Glu Ser Leu Pro
                245                 250                 255

Pro Leu Arg Pro Gln Gln Asn Pro Val Leu Pro Val Ala Gly Glu Arg
            260                 265                 270

Asn Val Leu Ile Thr Ser Ala Leu Pro Tyr Val Asn Asn Val Pro His
        275                 280                 285

Leu Gly Asn Ile Ile Gly Cys Val Leu Ser Ala Asp Val Phe Ala Arg
    290                 295                 300

Tyr Ser Arg Leu Arg Gln Trp Asn Thr Leu Tyr Leu Cys Gly Thr Asp
305                 310                 315                 320

Glu Tyr Gly Thr Ala Thr Glu Thr Lys Ala Leu Glu Glu Gly Leu Thr
                325                 330                 335

Pro Gln Glu Ile Cys Asp Lys Tyr His Ile Ile His Ala Asp Ile Tyr
            340                 345                 350

Arg Trp Phe Asn Ile Ser Phe Asp Ile Phe Gly Arg Thr Thr Thr Pro
        355                 360                 365

Gln Gln Thr Lys Ile Thr Gln Asp Ile Phe Gln Gln Leu Leu Lys Arg
    370                 375                 380

Gly Phe Val Leu Gln Asp Thr Val Glu Gln Leu Arg Cys Glu His Cys
385                 390                 395                 400

Ala Arg Phe Leu Ala Asp Arg Phe Val Glu Gly Val Cys Pro Phe Cys
                405                 410                 415

Gly Tyr Glu Glu Ala Arg Gly Asp Gln Cys Asp Lys Cys Gly Lys Leu
            420                 425                 430
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```
Ile Asn Ala Val Glu Leu Lys Lys Pro Gln Cys Lys Val Cys Arg Ser
        435                 440                 445

Cys Pro Val Val Gln Ser Ser Gln His Leu Phe Leu Asp Leu Pro Lys
    450                 455                 460

Leu Glu Lys Arg Leu Glu Glu Trp Leu Gly Arg Thr Leu Pro Gly Ser
465                 470                 475                 480

Asp Trp Thr Pro Asn Ala Gln Phe Ile Thr Arg Ser Trp Leu Arg Asp
                485                 490                 495

Gly Leu Lys Pro Arg Cys Ile Thr Arg Asp Leu Lys Trp Gly Thr Pro
            500                 505                 510

Val Pro Leu Glu Gly Phe Glu Asp Lys Val Phe Tyr Val Trp Phe Asp
        515                 520                 525

Ala Thr Ile Gly Tyr Leu Ser Ile Thr Ala Asn Tyr Thr Asp Gln Trp
    530                 535                 540

Glu Arg Trp Trp Lys Asn Pro Glu Gln Val Asp Leu Tyr Gln Phe Met
545                 550                 555                 560

Ala Lys Asp Asn Val Pro Phe His Ser Leu Val Phe Pro Cys Ser Ala
                565                 570                 575

Leu Gly Ala Glu Asp Asn Tyr Thr Leu Val Ser His Leu Ile Ala Thr
            580                 585                 590

Glu Tyr Leu Asn Tyr Glu Asp Gly Lys Phe Ser Lys Ser Arg Gly Val
        595                 600                 605

Gly Val Phe Gly Asp Met Ala Gln Asp Thr Gly Ile Pro Ala Asp Ile
    610                 615                 620

Trp Arg Phe Tyr Leu Leu Tyr Ile Arg Pro Glu Gly Gln Asp Ser Ala
625                 630                 635                 640

Phe Ser Trp Thr Asp Leu Leu Leu Lys Asn Asn Ser Glu Leu Leu Asn
                645                 650                 655

Asn Leu Gly Asn Phe Ile Asn Arg Ala Gly Met Phe Val Ser Lys Phe
            660                 665                 670

Phe Gly Gly Tyr Val Pro Glu Met Val Leu Thr Pro Asp Asp Gln Arg
        675                 680                 685

Leu Leu Ala His Val Thr Leu Glu Leu Gln His Tyr His Gln Leu Leu
    690                 695                 700
```

Glu Lys Val Arg Ile Arg Asp Ala Leu Arg Ser Ile Leu Thr Ile Ser
705 710 715 720

Arg His Gly Asn Gln Tyr Ile Gln Val Asn Glu Pro Trp Lys Arg Ile
725 730 735

Lys Gly Ser Glu Ala Asp Arg Gln Arg Ala Gly Thr Val Thr Gly Leu
740 745 750

Ala Val Asn Ile Ala Ala Leu Leu Ser Val Met Leu Gln Pro Tyr Met
755 760 765

Pro Thr Val Ser Ala Thr Ile Gln Ala Gln Leu Gln Leu Pro Pro Pro
770 775 780

Ala Cys Ser Ile Leu Leu Thr Asn Phe Leu Cys Thr Leu Pro Ala Gly
785 790 795 800

His Gln Ile Gly Thr Val Ser Pro Leu Phe Gln Lys Leu Glu Asn Asp
805 810 815

Gln Ile Glu Ser Leu Arg Gln Arg Phe Gly Gly Gly Gln Ala Lys Thr
820 825 830

Ser Pro Lys Pro Ala Val Val Glu Thr Val Thr Thr Ala Lys Pro Gln
835 840 845

Gln Ile Gln Ala Leu Met Asp Glu Val Thr Lys Gln Gly Asn Ile Val
850 855 860

Arg Glu Leu Lys Ala Gln Lys Ala Asp Lys Asn Glu Val Ala Ala Glu
865 870 875 880

Val Ala Lys Leu Leu Asp Leu Lys Lys Gln Leu Ala Val Ala Glu Gly
885 890 895

Asn Pro Leu Lys Pro Leu Lys Ala Arg Arg Lys Ser Lys Arg Pro Trp
900 905 910

Leu Ile Glu Ser His Phe Asn Arg
915 920

<210> 1397
<211> 476
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (127)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1397
Lys Met Ala Ala Leu Thr Thr Leu Phe Lys Tyr Ile Asp Glu Asn Gln
1 5 10 15

Asp Arg Tyr Ile Lys Lys Leu Ala Lys Trp Val Ala Ile Gln Ser Val
20 25 30

Ser Ala Trp Pro Glu Lys Arg Gly Glu Ile Arg Arg Met Met Glu Val
35 40 45

Ala Ala Ala Asp Val Lys Gln Leu Gly Gly Ser Val Glu Leu Val Asp
50 55 60

Ile Gly Lys Gln Lys Leu Pro Asp Gly Ser Glu Ile Pro Leu Pro Pro
65 70 75 80

Ile Leu Leu Gly Arg Leu Gly Ser Asp Pro Gln Lys Lys Thr Val Cys
85 90 95

Ile Tyr Gly His Leu Asp Val Gln Pro Ala Ala Leu Glu Asp Gly Trp
100 105 110

Asp Ser Glu Pro Phe Thr Leu Val Glu Arg Asp Gly Lys Leu Xaa Gly
115 120 125

Arg Gly Ser Thr Asp Asp Lys Gly Pro Val Ala Gly Trp Ile Asn Ala
130 135 140

Leu Glu Ala Tyr Gln Lys Thr Gly Gln Glu Ile Pro Val Asn Val Arg
145 150 155 160

Phe Cys Leu Glu Gly Met Glu Glu Ser Gly Ser Glu Gly Leu Asp Glu
165 170 175

Leu Ile Phe Ala Arg Lys Asp Thr Phe Phe Lys Asp Val Asp Tyr Val
180 185 190

Cys Ile Ser Asp Asn Tyr Trp Leu Gly Lys Lys Lys Pro Cys Ile Thr
195 200 205

Tyr Gly Leu Arg Gly Ile Cys Tyr Phe Phe Ile Glu Val Glu Cys Ser
210 215 220

Asn Lys Asp Leu His Ser Gly Val Tyr Gly Gly Ser Val His Glu Ala
225 230 235 240

Met Thr Asp Leu Ile Leu Leu Met Gly Ser Leu Val Asp Lys Arg Gly

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                245                 250                 255

Asn Ile Leu Ile Pro Gly Ile Asn Glu Ala Val Ala Ala Val Thr Glu
            260                 265                 270

Glu Glu His Lys Leu Tyr Asp Asp Ile Asp Phe Asp Ile Glu Glu Phe
        275                 280                 285

Ala Lys Asp Val Gly Ala Gln Ile Leu Leu His Ser His Lys Lys Asp
    290                 295                 300

Ile Leu Met His Arg Trp Arg Tyr Pro Ser Leu Ser Leu His Gly Ile
305                 310                 315                 320

Glu Gly Ala Phe Ser Gly Ser Gly Ala Lys Thr Val Ile Pro Arg Lys
                325                 330                 335

Val Val Gly Lys Phe Ser Ile Arg Leu Val Pro Asn Met Thr Pro Glu
            340                 345                 350

Val Val Gly Glu Gln Val Thr Ser Tyr Leu Thr Lys Lys Phe Ala Glu
        355                 360                 365

Leu Arg Ser Pro Asn Glu Phe Lys Val Tyr Met Gly His Gly Gly Lys
    370                 375                 380

Pro Trp Val Ser Asp Phe Ser His Pro His Tyr Leu Ala Gly Arg Arg
385                 390                 395                 400

Ala Met Lys Thr Val Phe Gly Val Glu Pro Asp Leu Thr Arg Glu Gly
                405                 410                 415

Gly Ser Ile Pro Val Thr Leu Thr Phe Gln Glu Ala Thr Gly Lys Asn
            420                 425                 430

Val Met Leu Leu Pro Val Gly Ser Ala Asp Asp Gly Ala His Ser Gln
        435                 440                 445

Asn Glu Lys Leu Asn Arg Tyr Asn Tyr Ile Glu Gly Thr Lys Met Leu
    450                 455                 460

Ala Ala Tyr Leu Tyr Glu Val Ser Gln Leu Lys Asp
465                 470                 475
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<210> 1398
<211> 187
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1398
Leu His Leu Xaa Pro Thr Ser Ile Ser Ser Ser Ser Ser Cys Ser Val
1 5 10 15

Ser Ser Val Val Ser Gln Arg Leu Thr Glu Ser Pro Cys Ala Leu Val
20 25 30

Ala Ser Gln Tyr Gly Trp Ser Gly Asn Met Glu Arg Ile Met Lys Ala
35 40 45

Gln Ala Tyr Gln Thr Gly Lys Asp Ile Ser Thr Asn Tyr Tyr Ala Ser
50 55 60

Gln Lys Lys Thr Phe Glu Ile Asn Pro Arg His Pro Leu Ile Arg Asp
65 70 75 80

Met Leu Arg Arg Ile Lys Glu Asp Glu Asp Asp Lys Thr Val Leu Asp
85 90 95

Leu Ala Val Val Leu Phe Glu Thr Ala Thr Leu Arg Ser Gly Tyr Leu
100 105 110

Leu Pro Asp Thr Lys Ala Tyr Gly Asp Arg Ile Glu Arg Met Leu Arg
115 120 125

Leu Ser Leu Asn Ile Asp Pro Asp Ala Lys Val Glu Glu Glu Pro Glu
130 135 140

Glu Glu Pro Glu Glu Thr Ala Glu Asp Thr Thr Glu Asp Thr Glu Gln
145 150 155 160

Asp Glu Asp Glu Glu Met Asp Val Gly Thr Asp Glu Glu Glu Glu Thr
165 170 175

Ala Lys Glu Ser Thr Ala Glu Lys Asp Glu Leu
180 185

<210> 1399
<211> 376
<212> PRT
<213> Homo sapiens

<400> 1399
Lys Ser Ser Thr Gly Val Ile Pro Asp Glu Ala Lys Ala Leu Ser Leu

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1               5                   10                  15

Leu Ala Pro Ala Asn Ala Val Ala Gly Leu Leu Pro Gly Gly Gly Leu
            20                  25                  30

Leu Pro Thr Pro Asn Pro Leu Thr Gln Ile Gly Ala Val Pro Leu Ala
        35                  40                  45

Ala Leu Gly Ala Pro Thr Leu Asp Pro Ala Leu Ala Ala Leu Gly Leu
    50                  55                  60

Pro Gly Ala Asn Leu Asn Ser Gln Ser Leu Ala Ala Asp Gln Leu Leu
65                  70                  75                      80

Lys Leu Met Ser Thr Val Asp Pro Lys Leu Asn His Val Ala Ala Gly
                85                  90                  95

Leu Val Ser Pro Ser Leu Lys Ser Asp Thr Ser Ser Lys Glu Ile Glu
            100                 105                 110

Glu Ala Met Lys Arg Val Arg Glu Ala Gln Ser Leu Ile Ser Ala Ala
        115                 120                 125

Ile Glu Pro Asp Lys Lys Glu Glu Lys Arg Arg His Ser Arg Ser Arg
    130                 135                 140

Ser Arg Ser Arg Arg Arg Arg Thr Pro Ser Ser Ser Arg His Arg Arg
145                 150                 155                     160

Ser Arg Ser Arg Ser Arg Arg Arg Ser His Ser Lys Ser Arg Ser Arg
                165                 170                 175

Arg Arg Ser Lys Ser Pro Arg Arg Arg Arg Ser His Ser Arg Glu Arg
            180                 185                 190

Gly Arg Arg Ser Arg Ser Thr Ser Lys Thr Arg Asp Lys Lys Lys Glu
        195                 200                 205

Asp Lys Glu Lys Lys Arg Ser Lys Thr Pro Pro Lys Ser Tyr Ser Thr
    210                 215                 220

Ala Arg Arg Ser Arg Ser Ala Ser Arg Glu Arg Arg Arg Arg Arg Ser
225                 230                 235                     240

Arg Ser Gly Thr Arg Ser Pro Lys Lys Pro Arg Ser Pro Lys Arg Lys
                245                 250                 255

Leu Ser Arg Ser Pro Ser Pro Arg Arg His Lys Lys Glu Lys Lys Lys
            260                 265                 270

Asp Lys Asp Lys Glu Arg Ser Arg Asp Glu Arg Glu Arg Ser Thr Ser
```

275 280 285

Lys Lys Lys Lys Ser Lys Asp Lys Glu Lys Asp Arg Glu Arg Lys Ser
290 295 300

Glu Ser Asp Lys Asp Val Lys Gln Val Thr Arg Asp Tyr Asp Glu Glu
305 310 315 320

Glu Gln Gly Tyr Asp Ser Glu Lys Glu Lys Lys Glu Glu Lys Lys Pro
325 330 335

Ile Glu Thr Gly Ser Pro Lys Thr Lys Glu Cys Ser Val Glu Lys Gly
340 345 350

Thr Gly Asp Ser Leu Arg Glu Ser Lys Val Asn Gly Asp Asp His His
355 360 365

Glu Glu Asp Met Asp Met Ser Asp
370 375

<210> 1400
<211> 112
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (21)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1400
Thr Ala Gly Leu Thr Ser Arg Gly Trp Gly Ser Leu Pro Pro Ser Leu
1 5 10 15

Glu Thr Phe Leu Xaa Trp Leu Lys Ser Arg Lys Glu Asn Glu Cys Thr
20 25 30

Ser Arg Leu Ala Gln Ser Leu Ser Pro Ser Ser Ser Leu Phe Pro Ala
35 40 45

Gly Pro Ser Gly Leu Tyr Gly Pro Asp Gly Gly Leu Arg Lys Met Arg
50 55 60

Gly Leu Trp Phe Ser Gly Ile Pro Ala Gly Ala Thr Pro Ser Cys Leu
65 70 75 80

Gln Met Val His Val Pro Ile Pro Pro Ser Arg Pro Leu Leu Cys Leu
85 90 95

Leu Cys His Arg Asp Ser Gln Gln Arg Phe Phe Phe Val Leu Ala Val
100 105 110

<210> 1401
<211> 69
<212> PRT
<213> Homo sapiens

<400> 1401
Arg Arg Gln Val Gly Ala Ala Ala Val Ala Met Thr Arg Gly Asn Gln
1 5 10 15

Arg Glu Leu Ala Arg Gln Lys Asn Met Lys Lys Gln Ser Asp Ser Val
20 25 30

Lys Gly Lys Arg Arg Asp Asp Gly Leu Ser Ala Ala Ala Arg Lys Gln
35 40 45

Arg Asp Ser Glu Ile Met Gln Gln Lys Gln Lys Lys Ala Asn Glu Lys
50 55 60

Lys Glu Glu Pro Lys
65

<210> 1402
<211> 177
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (162)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (166)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1402
Arg Pro Pro Arg Arg Xaa Pro Met Asp Gly Pro Ala Ile Ile Thr Gln
1 5 10 15

Val Thr Asn Pro Lys Glu Asp Glu Gly Arg Leu Pro Gly Ala Gly Glu
20 25 30

Lys Ala Ser Gln Cys Asn Val Ser Leu Lys Lys Gln Arg Ser Arg Ser
35 40 45

Ile Leu Ser Ser Phe Phe Cys Cys Phe Arg Asp Tyr Asn Val Glu Ala
50 55 60

Pro Pro Pro Ser Ser Pro Ser Val Leu Pro Pro Leu Val Glu Glu Asn
65 70 75 80

Gly Gly Leu Gln Lys Pro Pro Ala Lys Tyr Leu Leu Pro Glu Val Thr
85 90 95

Val Leu Asp Tyr Gly Lys Lys Cys Val Val Ile Asp Leu Asp Glu Thr
100 105 110

Leu Val His Ser Ser Phe Lys Pro Ile Ser Asn Ala Asp Phe Ile Val
115 120 125

Pro Val Glu Ile Asp Gly Thr Ile His Gln Val Tyr Val Leu Lys Arg
130 135 140

Pro His Val Asp Glu Phe Leu Gln Arg Met Gly Gln Leu Leu Asn Val
145 150 155 160

Cys Xaa Leu Leu Pro Xaa Gly Gln Val Cys Arg Pro Val Ala Asp Leu
165 170 175

Leu

<210> 1403
<211> 82
<212> PRT
<213> Homo sapiens

<400> 1403
Lys His Ile Leu Ser Thr Phe Glu Thr Ser Val Leu Glu Gly Arg Leu
1 5 10 15

His Lys Leu Ser Ser Pro Arg Leu Arg Arg Leu Gln Ser Gly Lys Leu
20 25 30

Thr Cys Arg Asn Gly Val Pro Phe Met Leu Tyr Leu Asp Lys Gly Asn
35 40 45

Gln Lys Trp Asn Gln Cys Arg Gln Asn Leu Gly Phe Ala Ala Ser Ile
50 55 60

Asn Gln Ser Met Thr Asn Arg Gly Ser Leu Lys Cys Lys Gly Thr Asn
65 70 75 80

Phe Thr

<210> 1404
<211> 251
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (37)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (41)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1404
Thr Thr Lys Pro Ala Thr Thr Pro Ser Ser Thr Thr Arg Thr Cys Arg
1 5 10 15

Arg Ser Pro Ser Thr Leu Pro Ser Ala Thr Trp Thr Pro Leu Ala Ser
20 25 30

Arg Thr Ala His Xaa Leu Pro Arg Xaa Tyr Met Tyr Pro Ser Met Asp
35 40 45

Gln Leu Ala Glu Met Leu Pro Gly Val Leu Gln Gln Phe Gly Leu Lys
50 55 60

Ser Ile Ile Gly Met Gly Thr Gly Ala Gly Ala Tyr Ile Leu Thr Arg
65 70 75 80

Phe Ala Leu Asn Asn Pro Glu Met Val Glu Gly Leu Val Leu Ile Asn
85 90 95

Val Asn Pro Cys Ala Glu Gly Trp Met Asp Trp Ala Ala Ser Lys Ile
100 105 110

Ser Gly Trp Thr Gln Ala Leu Pro Asp Met Val Val Ser His Leu Phe
115 120 125

Gly Lys Glu Glu Met Gln Ser Asn Val Glu Val Val His Thr Tyr Arg
130 135 140

Gln His Ile Val Asn Asp Met Asn Pro Gly Asn Leu His Leu Phe Ile
145 150 155 160

Asn Ala Tyr Asn Ser Arg Arg Asp Leu Glu Ile Glu Arg Pro Met Pro
165 170 175

Gly Thr His Thr Val Thr Leu Gln Cys Pro Ala Leu Leu Val Val Gly
180 185 190

Asp Ser Ser Pro Ala Val Asp Ala Val Val Glu Cys Asn Ser Lys Leu
195 200 205

Asp Pro Thr Lys Thr Thr Leu Leu Lys Met Ala Asp Cys Gly Gly Leu
210 215 220

Pro Gln Ile Ser Gln Pro Ala Lys Leu Ala Glu Ala Phe Lys Tyr Phe
225 230 235 240

Val Gln Gly Met Gly Tyr Met Pro Arg Leu Ala
245 250

<210> 1405
<211> 127
<212> PRT
<213> Homo sapiens

<400> 1405
Phe Glu Gly Phe Tyr Ser Gly Arg Lys Asn Arg Thr Lys Val Tyr Val
1 5 10 15

Pro Ser Ser Val Val Leu Ile Asp Leu Phe Phe Leu Phe Glu Thr Lys
20 25 30

Val Val Ser Val Phe Trp Phe Ser Gly Asn Met Tyr Tyr Ile Val Leu
35 40 45

Lys Glu Cys Cys Pro Thr Asn Tyr Ser Ser Lys Gln Arg Ile Val Thr
50 55 60

Ile Asn Lys Val Ser Val Thr Leu Leu Pro Leu Ser His Asn Ile His
65 70 75 80

Cys Arg Ala Leu Cys Arg Ser Lys Asn Arg Ala Ala Gln Asn Leu Cys

                85   90   95

Gly Ser Phe Leu Ser Phe Cys Asn Leu Arg His Met Phe Gln Arg Thr
            100   105   110

Gly Ile Phe Val Trp Ser Ser Asp Leu Gly Asp His Ser His Asn
        115   120   125

<210> 1406
<211> 230
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (90)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (112)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (118)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (169)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (190)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (192)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (194)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (217)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (218)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1406
Ala Glu Arg Pro Leu Gln Val Pro Arg Ser Ala Gly Glu Ala Ala Pro
1 5 10 15

His Ser Arg Arg Pro Pro Gly Leu Leu Pro His Ala Pro Arg Ala Ala
20 25 30

Ser Ala Gln Leu Glu Glu Arg Arg Arg Asp Pro His Pro Gly Met Thr
35 40 45

Leu Gln Glu Gly Asp Cys Arg Gly Ser Gln Thr Val Ser Leu Thr Met
50 55 60

Gly Thr Ala Asp Ser Asp Glu Met Ala Pro Glu Ala Pro Gln His Thr
65 70 75 80

His Ile Asp Val His Ile His Gln Glu Xaa Ala Leu Ala Lys Leu Leu
85 90 95

Leu Thr Cys Cys Ser Ala Leu Arg Pro Arg Ala Thr Gln Ala Arg Xaa
100 105 110

Ser Ser Arg Leu Leu Xaa Ala Ser Trp Val Met Gln Ile Val Leu Gly
115 120 125

Ile Leu Ser Ala Val Leu Gly Gly Phe Phe Tyr Ile Arg Asp Tyr Thr
130 135 140

Leu Leu Val Thr Ser Gly Ala Ala Ser Gly Gln Gly Leu Trp Leu Cys
145 150 155 160

Cys Trp Ser Cys Cys Leu His Leu Xaa Glu Thr Gly Trp Tyr Ile Leu
165 170 175

Gly Pro Ala Glu Asp Ser Ala Asn Ala Gly Lys Leu Ser Xaa Gln Xaa
180 185 190

Ser Xaa Ala Ser Asn Phe Gly Asn Glu Glu Phe Arg Tyr Gly Leu Leu
195 200 205

Leu Ile Thr Thr Ser Gly Trp Pro Xaa Xaa Gln Val Arg Val Asp Trp
210 215 220

Asn Thr Ser Ser Pro Gln
225 230

<210> 1407
<211> 79
<212> PRT
<213> Homo sapiens

<400> 1407
Arg Gly His Phe Leu Leu Pro Asp Leu Asp Ile Pro Ser Asn Pro Ser
1 5 10 15

Ser Tyr Ser Met Leu Lys Glu Lys Tyr Ser Gln Met His Tyr Val Asn
20 25 30

Gly Glu Lys Lys His Ser Ile Val Glu Thr Pro Ile Leu Ala Asn Val
35 40 45

Phe Trp Ser Val Phe His Phe Thr Val Tyr Ile Pro Ala Leu Lys Thr
50 55 60

Gln Gly Gln Val Leu Thr Lys Glu Val Cys Ser His Ser Lys Tyr
65 70 75

<210> 1408
<211> 289
<212> PRT
<213> Homo sapiens

<400> 1408
Val Arg Pro Pro Ser His Val Thr Ala Asp Ser Gly Arg Ser Pro Leu
1 5 10 15

Ser Leu Thr Tyr Leu Pro Leu Gln Glu Pro Gly Asp Met Ala Ala Ala
20 25 30

Val Pro Arg Ala Ala Phe Leu Ser Pro Leu Leu Pro Leu Leu Leu Gly
35 40 45

Phe Leu Leu Leu Ser Ala Pro His Gly Gly Ser Gly Leu His Thr Lys
50 55 60

Gly Ala Leu Pro Leu Asp Thr Val Thr Phe Tyr Lys Val Ile Pro Lys
65 70 75 80

Ser Lys Phe Val Leu Val Lys Phe Asp Thr Gln Tyr Pro Tyr Gly Glu

85 90 95

Lys Gln Asp Glu Phe Lys Arg Leu Ala Glu Asn Ser Ala Ser Ser Asp
100 105 110

Asp Leu Leu Val Ala Glu Val Gly Ile Ser Asp Tyr Gly Asp Lys Leu
115 120 125

Asn Met Glu Leu Ser Glu Lys Tyr Lys Leu Asp Lys Glu Ser Tyr Pro
130 135 140

Val Phe Tyr Leu Phe Arg Asp Gly Asp Phe Glu Asn Pro Val Pro Tyr
145 150 155 160

Thr Gly Ala Val Lys Val Gly Ala Ile Gln Arg Trp Leu Lys Gly Gln
165 170 175

Gly Val Tyr Leu Gly Met Pro Gly Cys Leu Pro Val Tyr Asp Ala Leu
180 185 190

Ala Gly Glu Phe Ile Arg Ala Ser Gly Val Glu Ala Arg Gln Ala Leu
195 200 205

Leu Lys Gln Gly Gln Asp Asn Leu Ser Ser Val Lys Glu Thr Gln Lys
210 215 220

Lys Trp Ala Glu Gln Tyr Leu Lys Ile Met Gly Lys Ile Leu Asp Gln
225 230 235 240

Gly Glu Asp Phe Pro Ala Ser Glu Met Thr Arg Ile Ala Arg Leu Ile
245 250 255

Glu Lys Asn Lys Met Ser Asp Gly Lys Lys Glu Glu Leu Gln Lys Ser
260 265 270

Leu Asn Ile Leu Thr Ala Phe Gln Lys Lys Gly Ala Glu Lys Glu Glu
275 280 285

Leu

<210> 1409
<211> 488
<212> PRT
<213> Homo sapiens

<400> 1409
Pro Ala Ser Ala Gly Thr Val Ser Glu Gly Pro Pro Gly Thr Asp Gly
1 5 10 15

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Ser Ala Gly Arg Gly Gly Thr Ala Phe Ala Met Ala Ala Thr Val Asn
            20                  25                  30

Leu Glu Leu Asp Pro Ile Phe Leu Lys Ala Leu Gly Phe Leu His Ser
        35                  40                  45

Lys Ser Lys Asp Ser Ala Glu Lys Leu Lys Ala Leu Leu Asp Glu Ser
    50                  55                  60

Leu Ala Arg Gly Ile Asp Ser Ser Tyr Arg Pro Ser Gln Lys Asp Val
65                  70                  75                  80

Glu Pro Pro Lys Ile Ser Ser Thr Lys Asn Ile Ser Ile Lys Gln Glu
                85                  90                  95

Pro Lys Ile Ser Ser Ser Leu Pro Ser Gly Asn Asn Asn Gly Lys Val
            100                 105                 110

Leu Thr Thr Glu Lys Val Lys Lys Glu Ala Glu Lys Arg Pro Ala Asp
        115                 120                 125

Lys Met Lys Ser Asp Ile Thr Glu Gly Val Asp Ile Pro Lys Lys Pro
    130                 135                 140

Arg Leu Glu Lys Pro Glu Thr Gln Ser Ser Pro Ile Thr Val Gln Ser
145                 150                 155                 160

Ser Lys Asp Leu Pro Met Ala Asp Leu Ser Ser Phe Glu Glu Thr Ser
                165                 170                 175

Ala Asp Asp Phe Ala Met Glu Met Gly Leu Ala Cys Val Val Cys Arg
            180                 185                 190

Gln Met Met Val Ala Ser Gly Asn Gln Leu Val Glu Cys Gln Glu Cys
        195                 200                 205

His Asn Leu Tyr His Arg Asp Cys His Lys Pro Gln Val Thr Asp Lys
    210                 215                 220

Glu Ala Asn Asp Pro Arg Leu Val Trp Tyr Cys Ala Arg Cys Thr Arg
225                 230                 235                 240

Gln Met Lys Arg Met Ala Gln Lys Thr Gln Lys Pro Pro Gln Lys Pro
                245                 250                 255

Ala Pro Ala Val Val Ser Val Thr Pro Ala Val Lys Asp Pro Leu Val
            260                 265                 270

Lys Lys Pro Glu Thr Lys Leu Lys Gln Glu Thr Thr Phe Leu Ala Phe
        275                 280                 285
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Lys Arg Thr Glu Val Lys Thr Ser Thr Val Ile Ser Gly Asn Ser Ser
    290   295   300

Ser Ala Ser Val Ser Ser Ser Val Thr Ser Gly Leu Thr Gly Trp Ala
305   310   315   320

Ala Phe Ala Ala Lys Thr Ser Ser Ala Gly Pro Ser Thr Ala Lys Leu
                325   330   335

Ser Ser Thr Thr Gln Asn Asn Thr Gly Lys Pro Ala Thr Ser Ser Ala
            340   345   350

Asn Gln Lys Pro Val Gly Leu Thr Gly Leu Ala Thr Ser Ser Lys Gly
        355   360   365

Gly Ile Gly Ser Lys Ile Gly Ser Asn Asn Ser Thr Thr Pro Thr Val
    370   375   380

Pro Leu Lys Pro Pro Pro Pro Leu Thr Leu Gly Lys Thr Gly Leu Ser
385   390   395   400

Arg Ser Val Ser Cys Asp Asn Val Ser Lys Val Gly Leu Pro Ser Pro
                405   410   415

Ser Ser Leu Val Pro Gly Ser Ser Ser Gln Leu Ser Gly Asn Gly Asn
            420   425   430

Ser Gly Thr Ser Gly Pro Ser Gly Ser Thr Thr Ser Lys Thr Thr Ser
        435   440   445

Glu Ser Ser Ser Ser Pro Ser Ala Ser Leu Lys Gly Pro Thr Ser Gln
    450   455   460

Glu Ser Gln Leu Asn Ala Met Lys Arg Leu Gln Met Val Lys Lys Lys
465   470   475   480

Ala Ala Gln Lys Lys Leu Lys Lys
                485

<210> 1410
<211> 64
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (53)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1410
His Tyr Gly Leu Lys Leu Ala Val Lys Met Pro Asn Thr Val Val Pro
1 5 10 15

Trp Asn Pro Val Tyr Ser Cys Ala Lys Gln Asn Cys Lys Ile Val Lys
20 25 30

Met Ser Tyr Gln Val Ile Arg Arg Leu Gln Arg His His Leu Phe Phe
35 40 45

Ile Ser Phe Phe Xaa Leu Thr His Val Val Val Ile Phe Asn Thr Phe
50 55 60

<210> 1411
<211> 129
<212> PRT
<213> Homo sapiens

<400> 1411
Ala Ala Cys Leu Ala Leu Arg Ile Ala Ala Ala Met Ala Ser Gln Ser
1 5 10 15

Gln Gly Ile Gln Gln Leu Leu Gln Ala Glu Lys Arg Ala Ala Glu Lys
20 25 30

Val Ser Glu Ala Arg Lys Arg Lys Asn Arg Arg Leu Lys Gln Ala Lys
35 40 45

Glu Glu Ala Gln Ala Glu Ile Glu Gln Tyr Arg Leu Gln Arg Glu Lys
50 55 60

Glu Phe Lys Ala Lys Glu Ala Ala Ala Leu Gly Ser Arg Gly Ser Cys
65 70 75 80

Ser Thr Glu Val Glu Lys Glu Thr Gln Glu Lys Met Thr Ile Leu Gln
85 90 95

Thr Tyr Phe Arg Gln Asn Arg Asp Glu Val Leu Asp Asn Leu Leu Ala
100 105 110

Phe Val Cys Asp Ile Arg Pro Glu Ile His Glu Asn Tyr Arg Ile Asn
115 120 125

Gly

<210> 1412
<211> 177
<212> PRT
<213> Homo sapiens

<400> 1412
Val Thr Val Pro Ser Ser Ser Ala Ala Gly Thr Leu Phe Gln Gly Leu
1   5   10   15

Cys Gly Ala Pro Asp Ala Pro His Pro Leu Ser Lys Ile Pro Gly Gly
            20   25   30

Arg Gly Gly Gly Arg Asp Pro Ser Leu Ser Ala Leu Ile Tyr Lys Asp
        35   40   45

Glu Lys Leu Thr Val Thr Gln Asp Leu Pro Val Asn Asp Gly Lys Pro
    50   55   60

His Ile Val His Phe Gln Tyr Glu Val Thr Glu Val Lys Val Ser Ser
65   70   75   80

Trp Asp Ala Val Leu Ser Ser Gln Ser Leu Phe Val Glu Ile Pro Asp
                85   90   95

Gly Leu Leu Ala Asp Gly Ser Lys Glu Gly Leu Leu Ala Leu Leu Glu
            100   105   110

Phe Ala Glu Glu Lys Met Lys Val Asn Tyr Val Phe Ile Cys Phe Arg
        115   120   125

Lys Gly Arg Glu Asp Arg Ala Pro Leu Leu Lys Thr Phe Ser Phe Leu
    130   135   140

Gly Phe Glu Ile Val Arg Pro Gly His Pro Cys Val Pro Ser Arg Pro
145   150   155   160

Asp Val Met Phe Met Val Tyr Pro Leu Asp Gln Asn Leu Ser Asp Glu
                165   170   175

Asp

<210> 1413
<211> 112
<212> PRT
<213> Homo sapiens

<400> 1413
Ser Gly Leu Arg Leu Ala Met Ser Thr Asn Asn Met Ser Asp Pro Arg
1 5 10 15

Arg Pro Asn Lys Val Leu Arg Tyr Lys Pro Pro Pro Ser Glu Cys Asn
20 25 30

Pro Ala Leu Asp Asp Pro Thr Pro Asp Tyr Met Asn Leu Leu Gly Met
35 40 45

Ile Phe Ser Met Cys Gly Leu Met Leu Lys Leu Lys Trp Cys Ala Trp
50 55 60

Val Ala Val Tyr Cys Ser Phe Ile Ser Phe Ala Asn Ser Arg Ser Ser
65 70 75 80

Glu Asp Thr Lys Gln Met Met Ser Ser Phe Met Leu Ser Ile Ser Ala
85 90 95

Val Val Met Ser Tyr Leu Gln Asn Pro Gln Pro Met Thr Pro Pro Trp
100 105 110

<210> 1414
<211> 186
<212> PRT
<213> Homo sapiens

<400> 1414
Cys Leu Gly Gly Arg Pro Arg Cys Val Leu Arg Leu Thr Ala Asn Leu
1 5 10 15

Glu Gly Arg Arg Asp Ser Ala Thr His Ala Pro Pro His Pro Arg Leu
20 25 30

Arg Val Lys Arg Ala Val Gly Pro Glu Ser Pro Pro Leu Trp Gln Trp
35 40 45

Pro Pro Leu Tyr Ser Ile Leu Pro Ser Gly Arg Ser Ala Val Asn Lys
50 55 60

Arg Trp Ala Pro Gln Ser Thr Cys Pro Pro Thr Ala Leu Ala Val Leu
65 70 75 80

Gly Ser Ser Leu Gln Phe Thr Gly Asn Lys Pro Glu Ser Ala Arg Thr
85 90 95

Arg Gly Cys Ser Pro Gly Ser Ala Arg Pro Pro Leu Ser Pro Ala Thr
100 105 110

Gly Trp Arg Cys Arg Ala Arg Ala Ala Ala Ser Arg Arg Phe Pro Gly
115 120 125

Ala Pro Gly Pro Glu Glu Arg Ser Pro Gln Ser Lys Gly Gly Asn Thr
130 135 140

Cys Leu Arg Cys Lys Glu Ile Leu Phe Gln Ser Ile Pro Val Val Gln
145 150 155 160

Thr Asp Thr Val Pro Asn Glu Arg Ser Asp Val Phe Ser Ser Pro Phe
165 170 175

Leu Ile Cys Phe Leu Thr Gly Leu Arg Phe
180 185

<210> 1415
<211> 108
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (46)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (68)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1415
Thr Lys Thr Thr Leu Phe Leu Glu Arg Pro Leu Phe Lys Lys Glu Ser
1 5 10 15

Ile Thr Pro Thr Val Glu Leu Asn Ala Leu Cys Met Lys Leu Gly Lys
20 25 30

Lys Pro Met Tyr Lys Pro Val Asp Pro Tyr Ser Arg Met Xaa Ser Thr
35 40 45

Tyr Asn Tyr Asn Met Arg Gly Gly Ala Tyr Pro Pro Arg Tyr Phe Tyr
50 55 60

Pro Phe Pro Xaa Pro Pro Leu Leu Tyr Gln Val Glu Leu Ser Val Gly
65 70 75 80

```
Gly Gln Gln Phe Asn Gly Lys Gly Lys Thr Arg Gln Ala Ala Lys His
                85                  90                  95

Asp Ala Ala Ala Lys Ala Val Glu Asp Pro Ala Glu
            100                 105
```

<210> 1416
<211> 621
<212> PRT
<213> Homo sapiens

<400> 1416

```
Ala Gly His Arg Ala Gly Val Cys Ser Leu Ser Ala Thr Arg Leu Leu
  1               5                  10                  15

Leu Pro Lys Asp Arg Gly Val Gly Arg Arg Gln Thr Met Trp Thr Leu
             20                  25                  30

Val Ser Trp Val Ala Leu Thr Ala Gly Leu Val Ala Gly Thr Arg Cys
         35                  40                  45

Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu Asp Pro Gly Gly
     50                  55                  60

Ala Ser Tyr Ser Cys Cys Arg Pro Leu Leu Asp Lys Trp Pro Thr Thr
 65                  70                  75                  80

Leu Ser Arg His Leu Gly Gly Pro Cys Gln Val Asp Ala His Cys Ser
                 85                  90                  95

Ala Gly His Ser Cys Ile Phe Thr Val Ser Gly Thr Ser Ser Cys Cys
            100                 105                 110

Pro Phe Pro Glu Ala Val Ala Cys Gly Asp Gly His His Cys Cys Pro
        115                 120                 125

Arg Gly Phe His Cys Ser Ala Asp Gly Arg Ser Cys Phe Gln Arg Ser
    130                 135                 140

Gly Asn Asn Ser Val Gly Ala Ile Gln Cys Pro Asp Ser Gln Phe Glu
145                 150                 155                 160

Cys Pro Asp Phe Ser Thr Cys Cys Val Met Val Asp Gly Ser Trp Gly
                165                 170                 175

Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp Arg Val His Cys
            180                 185                 190
```

```
Cys Pro His Gly Ala Phe Cys Asp Leu Val His Thr Arg Cys Ile Thr
        195                 200                 205

Pro Thr Gly Thr His Pro Leu Ala Lys Lys Leu Pro Ala Gln Arg Thr
    210                 215                 220

Asn Arg Ala Val Ala Leu Ser Ser Ser Val Met Cys Pro Asp Ala Arg
225                 230                 235                 240

Ser Arg Cys Pro Asp Gly Ser Thr Cys Cys Glu Leu Pro Ser Gly Lys
                245                 250                 255

Tyr Gly Cys Cys Pro Met Pro Asn Ala Thr Cys Cys Ser Asp His Leu
            260                 265                 270

His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile Gln Ser Lys Cys
        275                 280                 285

Leu Ser Lys Glu Asn Ala Thr Thr Asp Leu Leu Thr Lys Leu Pro Ala
    290                 295                 300

His Thr Val Gly Asp Val Lys Cys Asp Met Glu Val Ser Cys Pro Asp
305                 310                 315                 320

Gly Tyr Thr Cys Cys Arg Leu Gln Ser Gly Ala Trp Gly Cys Cys Pro
                325                 330                 335

Phe Thr Gln Ala Val Cys Cys Glu Asp His Ile His Cys Cys Pro Ala
            340                 345                 350

Gly Phe Thr Cys Asp Thr Gln Lys Gly Thr Cys Glu Gln Gly Pro His
        355                 360                 365

Gln Val Pro Trp Met Glu Lys Ala Pro Ala His Leu Ser Leu Pro Asp
    370                 375                 380

Pro Gln Ala Leu Lys Arg Asp Val Pro Cys Asp Asn Val Ser Ser Cys
385                 390                 395                 400

Pro Ser Ser Asp Thr Cys Cys Gln Leu Thr Ser Gly Glu Trp Gly Cys
                405                 410                 415

Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp His Gln His Cys Cys
            420                 425                 430

Pro Gln Gly Tyr Thr Cys Val Ala Glu Gly Gln Cys Gln Arg Gly Ser
        435                 440                 445

Glu Ile Val Ala Gly Leu Glu Lys Met Pro Ala Arg Arg Ala Ser Leu
    450                 455                 460
```

Ser His Pro Arg Asp Ile Gly Cys Asp Gln His Thr Ser Cys Pro Val
465 470 475 480

Gly Gln Thr Cys Cys Pro Ser Leu Gly Gly Ser Trp Ala Cys Cys Gln
485 490 495

Leu Pro His Ala Val Cys Cys Glu Asp Arg Gln His Cys Cys Pro Ala
500 505 510

Gly Tyr Thr Cys Asn Val Lys Ala Arg Ser Cys Glu Lys Glu Val Val
515 520 525

Ser Ala Gln Pro Ala Thr Phe Leu Ala Arg Ser Pro His Val Gly Val
530 535 540

Lys Asp Val Glu Cys Gly Glu Gly His Phe Cys His Asp Asn Gln Thr
545 550 555 560

Cys Cys Arg Asp Asn Arg Gln Gly Trp Ala Cys Cys Pro Tyr Arg Gln
565 570 575

Gly Val Cys Cys Ala Asp Arg Arg His Cys Cys Pro Ala Gly Phe Arg
580 585 590

Cys Ala Ala Arg Gly Thr Lys Cys Leu Arg Arg Glu Ala Pro Arg Trp
595 600 605

Asp Ala Pro Leu Arg Asp Pro Ala Leu Arg Gln Leu Leu
610 615 620

<210> 1417
<211> 340
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (24)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1417
Ser Ala His Ala Ser Glu Arg Ile Ala Xaa Ser Gly Cys Gly Ala Pro
1 5 10 15

```
Ala Ala Gly Ala Gly Pro Arg Xaa Arg Ser Leu Gly Ala Asp Pro Gly
            20                  25                  30

Arg Ala Ala Arg Arg His Glu Gly Gln Gly Gly Glu Gly Gly Arg Arg
        35                  40                  45

Thr Ala Gly Arg Trp Arg Arg Lys Pro Glu Lys Ser Pro Ser Ala Gln
    50                  55                  60

Glu Leu Lys Glu Gln Gly Asn Arg Leu Phe Val Gly Arg Lys Tyr Pro
65                  70                  75                  80

Glu Ala Ala Ala Cys Tyr Gly Arg Ala Ile Thr Arg Asn Pro Leu Val
                85                  90                  95

Ala Val Tyr Tyr Thr Asn Arg Ala Leu Cys Tyr Leu Lys Met Gln Gln
            100                 105                 110

His Glu Gln Ala Leu Ala Asp Cys Arg Arg Ala Leu Glu Leu Asp Gly
        115                 120                 125

Gln Ser Val Lys Ala His Phe Phe Leu Gly Gln Cys Gln Leu Glu Met
    130                 135                 140

Glu Ser Tyr Asp Glu Ala Ile Ala Asn Leu Gln Arg Ala Tyr Ser Leu
145                 150                 155                 160

Ala Lys Glu Gln Arg Leu Asn Phe Gly Asp Asp Ile Pro Ser Ala Leu
                165                 170                 175

Arg Ile Ala Lys Lys Lys Arg Trp Asn Ser Ile Glu Glu Arg Arg Ile
            180                 185                 190

His Gln Glu Ser Glu Leu His Ser Tyr Leu Ser Arg Leu Ile Ala Ala
        195                 200                 205

Glu Arg Glu Arg Glu Leu Glu Glu Cys Gln Arg Asn His Glu Gly Asp
    210                 215                 220

Glu Asp Asp Ser His Val Arg Ala Gln Gln Ala Cys Ile Glu Ala Lys
225                 230                 235                 240

His Asp Lys Tyr Met Ala Asp Met Asp Glu Leu Phe Ser Gln Val Asp
                245                 250                 255

Glu Lys Arg Lys Lys Arg Asp Ile Pro Asp Tyr Leu Cys Gly Lys Ile
            260                 265                 270

Ser Phe Glu Leu Met Arg Glu Pro Cys Ile Thr Pro Ser Gly Ile Thr
        275                 280                 285
```

Tyr Asp Arg Lys Asp Ile Glu Glu His Leu Gln Arg Val Gly His Phe
290 295 300

Asp Pro Val Thr Arg Ser Pro Leu Thr Gln Glu Gln Leu Ile Pro Asn
305 310 315 320

Leu Ala Met Lys Glu Val Ile Asp Ala Phe Ile Ser Glu Asn Gly Trp
325 330 335

Val Glu Asp Tyr
340

<210> 1418
<211> 235
<212> PRT
<213> Homo sapiens

<400> 1418
Ser Pro Arg Pro Leu Arg Phe Cys Gly Gly Ala Arg Ala Arg Arg Pro
1 5 10 15

Leu Ser Ala Val Ala Arg Pro Ala Arg Ser Ser Asp Pro Leu Arg Ser
20 25 30

Ala Pro Leu Gly Pro Ala Pro Pro Val Asn Met Ile Arg Cys Gly Leu
35 40 45

Ala Cys Glu Arg Cys Arg Trp Ile Leu Pro Leu Leu Leu Leu Ser Ala
50 55 60

Ile Ala Phe Asp Ile Ile Ala Leu Ala Gly Arg Gly Trp Leu Gln Ser
65 70 75 80

Ser Asp His Gly Gln Thr Ser Ser Leu Trp Trp Lys Cys Ser Gln Glu
85 90 95

Gly Gly Gly Ser Gly Ser Tyr Glu Glu Gly Cys Gln Ser Leu Met Glu
100 105 110

Tyr Ala Trp Gly Arg Ala Ala Ala Ala Met Leu Phe Cys Gly Phe Ile
115 120 125

Ile Leu Val Ile Cys Phe Ile Leu Ser Phe Phe Ala Leu Cys Gly Pro
130 135 140

Gln Met Leu Val Phe Leu Arg Val Ile Gly Gly Leu Leu Ala Leu Ala
145 150 155 160

Ala Val Phe Gln Ile Ile Ser Leu Val Ile Tyr Pro Val Lys Tyr Thr

165 170 175

Gln Thr Phe Thr Leu His Ala Asn Arg Ala Val Thr Tyr Ile Tyr Asn
180 185 190

Trp Ala Tyr Gly Phe Gly Trp Ala Ala Thr Ile Ile Leu Ile Gly Cys
195 200 205

Ala Phe Phe Phe Cys Cys Leu Pro Asn Tyr Glu Asp Asp Leu Leu Gly
210 215 220

Asn Ala Lys Pro Arg Tyr Phe Tyr Thr Ser Ala
225 230 235

<210> 1419
<211> 86
<212> PRT
<213> Homo sapiens

<400> 1419
Arg Arg Gln Ala Leu Gln Glu Arg Cys Pro Phe Asn Pro Leu Ser Ala
1 5 10 15

Leu Asp Arg Arg Cys Cys Val Lys Leu Leu Met Asp Ile Tyr Met Arg
20 25 30

Ser Ser Phe Leu Tyr Ala Ile Pro Ala Val Phe Phe Phe Leu Thr Gly
35 40 45

Pro Cys Leu Arg Ile Asn Lys Ser Val Met Ser Glu Thr Lys Val Tyr
50 55 60

Ser Ser Val Cys Arg Cys Val Ala Pro Pro Phe Ser Pro Ala Ala Pro
65 70 75 80

His Ile Gln Ser Arg Ser
85

<210> 1420
<211> 351
<212> PRT
<213> Homo sapiens

<400> 1420
Thr Trp Cys Thr Thr Thr Met Leu Ala Ala Arg Leu Val Cys Leu Arg
1 5 10 15

```
Thr Leu Pro Ser Arg Val Phe His Pro Ala Phe Thr Lys Ala Ser Pro
            20                  25                  30

Val Val Lys Asn Ser Ile Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser
        35                  40                  45

Arg Glu Tyr Ala Thr Lys Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr
    50                  55                  60

Gly Gln Glu Leu Lys Glu Ala Ala Leu Glu Pro Ser Met Glu Lys Ile
65                  70                  75                  80

Phe Lys Ile Asp Gln Met Gly Arg Trp Phe Val Ala Gly Gly Ala Ala
                85                  90                  95

Val Gly Leu Gly Ala Leu Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu
            100                 105                 110

Ile Gly Ala Ile Glu Lys Ala Val Ile Trp Pro Gln Tyr Val Lys Asp
        115                 120                 125

Arg Ile His Ser Thr Tyr Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr
    130                 135                 140

Ala Leu Ser Ala Ile Ala Ile Ser Arg Thr Pro Val Leu Met Asn Phe
145                 150                 155                 160

Met Met Arg Gly Ser Trp Val Thr Ile Gly Val Thr Phe Ala Ala Met
                165                 170                 175

Val Gly Ala Gly Met Leu Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro
            180                 185                 190

Gly Pro Lys His Leu Ala Trp Leu Leu His Ser Gly Val Met Gly Ala
        195                 200                 205

Val Val Ala Pro Leu Thr Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala
    210                 215                 220

Ala Trp Tyr Thr Ala Gly Ile Val Gly Gly Leu Ser Thr Val Ala Met
225                 230                 235                 240

Cys Ala Pro Ser Glu Lys Phe Leu Asn Met Gly Ala Pro Leu Gly Val
                245                 250                 255

Gly Leu Gly Leu Val Phe Val Ser Ser Leu Gly Ser Met Phe Leu Pro
            260                 265                 270

Pro Thr Thr Val Ala Gly Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly
        275                 280                 285
```

```
Gly Leu Val Leu Phe Ser Met Phe Leu Leu Tyr Asp Thr Gln Lys Val
    290                 295                 300

Ile Lys Arg Ala Glu Val Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp
305                 310                 315                 320

Pro Ile Asn Ser Met Leu Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe
                325                 330                 335

Met Arg Val Ala Thr Met Leu Ala Thr Gly Gly Asn Arg Lys Lys
            340                 345                 350



<210> 1421
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1421
Cys Gly Xaa Leu Leu Met Ala Gln Gly Leu Ser Ala Ser Ala Leu Glu
  1               5                  10                  15

Gly Leu Lys Thr Glu Glu Gly Ser Val Arg Gly Ala Leu Pro Ala Val
            20                  25                  30

Ser Ser Pro Pro Ala Pro Val Ser Pro Ser Ser Pro Thr Thr His Asn
        35                  40                  45

Gly Glu Leu Glu Pro Ser Phe Ser Pro Leu Leu Gly Glu Gly Lys Thr
    50                  55                  60

Pro Glu Thr Leu Leu Pro Gln Lys Cys Trp Gly Gln Gly Gly Pro Gly
 65                  70                  75                  80

Arg



<210> 1422
<211> 484
<212> PRT
<213> Homo sapiens

<400> 1422
```

```
Ala Cys Arg Ser Thr Leu Val Asp Pro Lys Asn Ser Ala Gln Glu Arg
 1               5                  10                  15

Arg Ala Leu Gly Pro Leu Pro Pro Cys Ser Phe Ala Leu Gln Leu Gly
            20                  25                  30

Met Ala Gly Tyr Leu Arg Val Val Arg Ser Leu Cys Arg Ala Ser Gly
        35                  40                  45

Ser Arg Pro Ala Trp Ala Pro Ala Ala Leu Thr Ala Pro Thr Ser Gln
    50                  55                  60

Glu Gln Pro Arg Arg His Tyr Ala Asp Lys Arg Ile Lys Val Ala Lys
65                  70                  75                  80

Pro Val Val Glu Met Asp Gly Asp Glu Met Thr Arg Ile Ile Trp Gln
                85                  90                  95

Phe Ile Lys Glu Lys Leu Ile Leu Pro His Val Asp Ile Gln Leu Lys
            100                 105                 110

Tyr Phe Asp Leu Gly Leu Pro Asn Arg Asp Gln Thr Asp Asp Gln Val
        115                 120                 125

Thr Ile Asp Ser Ala Leu Ala Thr Gln Lys Tyr Ser Val Ala Val Lys
    130                 135                 140

Cys Ala Thr Ile Thr Pro Asp Glu Ala Arg Val Glu Glu Phe Lys Leu
145                 150                 155                 160

Lys Lys Met Trp Lys Ser Pro Asn Gly Thr Ile Arg Asn Ile Leu Gly
                165                 170                 175

Gly Thr Val Phe Arg Glu Pro Ile Ile Cys Lys Asn Ile Pro Arg Leu
            180                 185                 190

Val Pro Gly Trp Thr Lys Pro Ile Thr Ile Gly Arg His Ala His Gly
        195                 200                 205

Asp Gln Tyr Lys Ala Thr Asp Phe Val Ala Asp Arg Ala Gly Thr Phe
    210                 215                 220

Lys Met Val Phe Thr Pro Lys Asp Gly Ser Gly Val Lys Glu Trp Glu
225                 230                 235                 240

Val Tyr Asn Phe Pro Ala Gly Gly Val Gly Met Gly Met Tyr Asn Thr
                245                 250                 255

Asp Glu Ser Ile Ser Gly Phe Ala His Ser Cys Phe Gln Tyr Ala Ile
            260                 265                 270
```

```
Gln Lys Lys Trp Pro Leu Tyr Met Ser Thr Lys Asn Thr Ile Leu Lys
        275                 280                 285

Ala Tyr Asp Gly Arg Phe Lys Asp Ile Phe Gln Glu Ile Phe Asp Lys
    290                 295                 300

His Tyr Lys Thr Asp Phe Asp Lys Asn Lys Ile Trp Tyr Glu His Arg
305                 310                 315                 320

Leu Ile Asp Asp Met Val Ala Gln Val Leu Lys Ser Ser Gly Gly Phe
                325                 330                 335

Val Trp Ala Cys Lys Asn Tyr Asp Gly Asp Val Gln Ser Asp Ile Leu
            340                 345                 350

Ala Gln Gly Phe Gly Ser Leu Gly Leu Met Thr Ser Val Leu Val Cys
        355                 360                 365

Pro Asp Gly Lys Thr Ile Glu Ala Glu Ala Ala His Gly Thr Val Thr
    370                 375                 380

Arg His Tyr Arg Glu His Gln Lys Gly Arg Pro Thr Ser Thr Asn Pro
385                 390                 395                 400

Ile Ala Ser Ile Phe Ala Trp Thr Arg Gly Leu Glu His Arg Gly Lys
                405                 410                 415

Leu Asp Gly Asn Gln Asp Leu Ile Arg Phe Ala Gln Met Leu Glu Lys
            420                 425                 430

Val Cys Val Glu Thr Val Glu Ser Gly Ala Met Thr Lys Asp Leu Ala
        435                 440                 445

Gly Cys Ile His Gly Leu Ser Asn Val Lys Leu Asn Glu His Phe Leu
    450                 455                 460

Asn Thr Thr Asp Phe Leu Asp Thr Ile Lys Ser Asn Leu Asp Arg Ala
465                 470                 475                 480

Leu Gly Arg Gln


<210> 1423
<211> 240
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
```

<222> (153)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1423
Val Arg Ile Pro Gly Ser Thr His Ala Ser Gly Gly Gly Asp Gly Asp
1 5 10 15

Met Glu Ser Gly Ala Tyr Gly Ala Ala Lys Ala Gly Gly Ser Phe Asp
20 25 30

Leu Arg Arg Phe Leu Thr Gln Pro Gln Val Val Ala Arg Ala Val Cys
35 40 45

Leu Val Phe Ala Leu Ile Val Phe Ser Cys Ile Tyr Gly Glu Gly Tyr
50 55 60

Ser Asn Ala His Glu Ser Lys Gln Met Tyr Cys Val Phe Asn Arg Asn
65 70 75 80

Glu Asp Ala Cys Arg Tyr Gly Ser Ala Ile Gly Val Leu Ala Phe Leu
85 90 95

Ala Ser Ala Phe Phe Leu Val Val Asp Ala Tyr Phe Pro Gln Ile Ser
100 105 110

Asn Ala Thr Asp Arg Lys Tyr Leu Val Ile Gly Asp Leu Leu Phe Ser
115 120 125

Ala Leu Trp Thr Phe Leu Trp Phe Val Gly Phe Cys Phe Leu Thr Asn
130 135 140

Gln Trp Ala Val Thr Asn Pro Lys Xaa Val Leu Val Gly Ala Asp Ser
145 150 155 160

Val Arg Ala Ala Ile Thr Phe Ser Phe Phe Ser Ile Phe Ser Trp Gly
165 170 175

Val Leu Ala Ser Leu Ala Tyr Gln Arg Tyr Lys Ala Gly Val Asp Asp
180 185 190

Phe Ile Gln Asn Tyr Val Asp Pro Thr Pro Asp Pro Asn Thr Ala Tyr
195 200 205

Ala Ser Tyr Pro Gly Ala Ser Val Asp Asn Tyr Gln Gln Pro Pro Phe
210 215 220

Thr Gln Asn Ala Glu Thr Thr Glu Gly Tyr Gln Pro Pro Pro Val Tyr
225 230 235 240

<210> 1424
<211> 244
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (59)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (62)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (221)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1424
```
Arg Val Arg Arg Gln Ser Ser Gly Asn Leu Thr Met Ala Trp Thr Pro
  1               5                  10                  15

Leu Leu Leu Pro Leu Leu Thr Phe Cys Thr Val Ser Glu Ala Ser Tyr
             20                  25                  30

Glu Leu Thr Gln Pro Pro Ser Val Ser Val Ser Pro Gly Gln Thr Ala
         35                  40                  45

Arg Ile Thr Cys Ser Gly Asp Ala Leu Pro Xaa Lys Tyr Xaa Tyr Trp
     50                  55                  60

Tyr Gln Gln Lys Ser Gly Gln Ala Pro Val Leu Val Ile Tyr Glu Asp
 65                  70                  75                  80

Thr Arg Arg Pro Ser Ala Ile Pro Glu Arg Phe Ser Ala Ser Ser Ser
                 85                  90                  95

Gly Thr Met Ala Thr Leu Thr Ile Ser Gly Ala Gln Val Glu Asp Glu
            100                 105                 110

Ala Asp Tyr Tyr Cys Tyr Ser Thr Asp Ser Ser Ser Tyr Tyr Arg Val
        115                 120                 125

Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly Gln Pro Lys Ala Ala
    130                 135                 140
```

Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu Glu Leu Gln Ala Asn
145 150 155 160

Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe Tyr Pro Gly Ala Val
165 170 175

Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val Lys Ala Gly Val Glu
180 185 190

Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys Tyr Ala Ala Ser Ser
195 200 205

Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser His Xaa Ser Tyr Ser
210 215 220

Cys Gln Val Thr His Glu Gly Ser Thr Val Glu Lys Thr Val Ala Pro
225 230 235 240

Thr Glu Cys Ser

<210> 1425
<211> 173
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (115)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (137)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (159)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1425

```
Xaa Val Arg Val Gln Thr Arg Gly Ser Ala Asp Pro Ala Gln Leu Arg
  1               5                  10                  15

Arg His Pro Gly Tyr Lys Arg Thr Ala Ser Ala Thr Leu Ser Asp Pro
             20                  25                  30

Ala Ala Ala Ala Met Gln Pro Ser Ser Leu Leu Pro Leu Ala Leu Cys
         35                  40                  45

Leu Leu Ala Ala Pro Ala Ser Ala Leu Val Arg Ile Pro Leu His Lys
     50                  55                  60

Phe Thr Ser Ile Arg Arg Thr Met Ser Glu Val Gly Gly Ser Val Glu
 65                  70                  75                  80

Asp Leu Ile Ala Lys Gly Pro Val Ser Lys Tyr Ser Gln Ala Val Pro
                 85                  90                  95

Ala Val Thr Glu Gly Pro Ile Pro Glu Val Leu Lys Asn Tyr Met Asp
            100                 105                 110

Ala Gln Xaa Tyr Gly Glu Ile Gly Ile Gly Thr Pro Pro Gln Cys Phe
        115                 120                 125

Thr Val Val Phe Asp Thr Gly Xaa Xaa Asn Leu Trp Val Pro Ser Ile
    130                 135                 140

His Cys Lys Leu Leu Asp Ile Ala Cys Trp Ile His His Lys Xaa Asn
145                 150                 155                 160

Ser Asp Lys Ser Ser Asn Tyr Val Lys Asn Gly Asn Ser
                165                 170
```

<210> 1426
<211> 351
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1426

```
Ile Arg His Glu Ile Leu Trp Leu Leu Cys Ser His Arg Pro Ala Pro
  1               5                  10                  15
```

Gly Arg Pro Pro Thr His Asn Ala His Asn Trp Arg Leu Gly Gln Ala
20 25 30

Pro Ala Xaa Trp Tyr Asn Asp Thr Tyr Pro Leu Ser Pro Pro Gln Arg
35 40 45

Thr Pro Ala Gly Ile Arg Tyr Arg Ile Ala Val Ile Ala Asp Leu Asp
50 55 60

Thr Glu Ser Arg Ala Gln Glu Glu Asn Thr Trp Phe Ser Tyr Leu Lys
65 70 75 80

Lys Gly Tyr Leu Thr Leu Ser Asp Ser Gly Asp Lys Val Ala Val Glu
85 90 95

Trp Asp Lys Asp His Gly Val Leu Glu Ser His Leu Ala Glu Lys Gly
100 105 110

Arg Gly Met Glu Leu Ser Asp Leu Ile Val Phe Asn Gly Lys Leu Tyr
115 120 125

Ser Val Asp Asp Arg Thr Gly Val Val Tyr Gln Ile Glu Gly Ser Lys
130 135 140

Ala Val Pro Trp Val Ile Leu Ser Asp Gly Asp Gly Thr Val Glu Lys
145 150 155 160

Gly Phe Lys Ala Glu Trp Leu Ala Val Lys Asp Glu Arg Leu Tyr Val
165 170 175

Gly Gly Leu Gly Lys Glu Trp Thr Thr Thr Thr Gly Asp Val Val Asn
180 185 190

Glu Asn Pro Glu Trp Val Lys Val Val Gly Tyr Lys Gly Ser Val Asp
195 200 205

His Glu Asn Trp Val Ser Asn Tyr Asn Ala Leu Arg Ala Ala Ala Gly
210 215 220

Ile Gln Pro Pro Gly Tyr Leu Ile His Glu Ser Ala Cys Trp Ser Asp
225 230 235 240

Thr Leu Gln Arg Trp Phe Phe Leu Pro Arg Arg Ala Ser Gln Glu Arg
245 250 255

Tyr Ser Glu Lys Asp Asp Glu Arg Lys Gly Ala Asn Leu Leu Leu Ser
260 265 270

Ala Ser Pro Asp Phe Gly Asp Ile Ala Val Ser His Val Gly Ala Val
275 280 285

Val Pro Thr His Gly Phe Ser Ser Phe Lys Phe Ile Pro Asn Thr Asp
290 295 300

Asp Gln Ile Ile Val Ala Leu Lys Ser Glu Glu Asp Ser Gly Arg Val
305 310 315 320

Ala Ser Tyr Ile Met Ala Phe Thr Leu Asp Gly Arg Phe Leu Leu Pro
325 330 335

Glu Thr Lys Ile Gly Ser Val Lys Tyr Glu Gly Ile Glu Phe Ile
340 345 350

<210> 1427
<211> 510
<212> PRT
<213> Homo sapiens

<400> 1427
Glu Arg Ser Trp Phe Ala Gln Val Arg Arg Leu Gly Pro His Gly Ala
1 5 10 15

Val Ala Arg Leu Arg Val Arg Gly Leu Pro Gly Ala Gly Arg Gly Leu
20 25 30

Arg Leu Pro Ala Gly Ala Arg Ala Ala Arg Leu Gly Ala Ala Leu Ser
35 40 45

Leu Glu Leu Ala Val Ser Gly Ala Arg Ala Cys Ala Pro Gly Thr Arg
50 55 60

Leu Pro Arg Gly Pro Val Gly Gly Ser Trp Asp Ala Leu Ile Val Arg
65 70 75 80

Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn Ala Cys Val
85 90 95

Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu Gly Leu Ser
100 105 110

Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg Asn Asp Leu
115 120 125

Glu Glu Ala Phe Ile His Phe Met Gly Lys Gly Ala Ala Ala Glu Arg
130 135 140

Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln Val Ala Ser
145 150 155 160

```
Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala Ala Leu Ile
                165                 170                 175

Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu Leu Cys Gly
            180                 185                 190

Pro Val Gly Pro Lys Leu His Glu Leu Leu Asp Asp Asn Val Phe Val
        195                 200                 205

Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu Ile Leu Glu
    210                 215                 220

Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro His Ala Asn
225                 230                 235                 240

Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met Asn Met Leu
                245                 250                 255

Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp Leu Val Val
            260                 265                 270

Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu Leu Gln Arg
        275                 280                 285

Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile Pro Thr Gly
    290                 295                 300

Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg Glu Leu Met
305                 310                 315                 320

Ser Ser Ile Val His Gln Gln Val Phe Pro Ala Val Thr Ser Leu Gly
                325                 330                 335

Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala Ser Gly Pro
            340                 345                 350

His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val Gly Met Val
        355                 360                 365

Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg Ser Lys Ser
    370                 375                 380

Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu Val Tyr His
385                 390                 395                 400

Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu Ala Ala Val
                405                 410                 415

Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala Thr Glu Thr
            420                 425                 430
```

Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu Phe Met Thr
        435   440   445

Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro Asn Lys Pro
    450   455   460

Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe Thr Pro Val
465   470   475   480

Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly Asp Ala Ile
                485   490   495

Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His Tyr
            500   505   510

<210> 1428
<211> 316
<212> PRT
<213> Homo sapiens

<400> 1428
Pro Pro Leu Pro Pro Arg Ser Phe Pro Asn Leu Phe Ser Arg Pro Glu
  1   5   10   15

Pro Leu Pro Glu Pro Gly Arg Arg Gly Cys Asn Arg Ser Arg Glu Pro
            20   25   30

Ala Ala Arg Ala Pro Ser Pro Pro Pro Pro Phe Glu Gly Ala Pro Gly
        35   40   45

Arg Ala Met Val Lys Val Thr Phe Asn Ser Ala Leu Ala Gln Lys Glu
    50   55   60

Ala Lys Lys Asp Glu Pro Lys Ser Gly Glu Glu Ala Leu Ile Ile Pro
65   70   75   80

Pro Asp Ala Val Ala Val Asp Cys Lys Asp Pro Asp Asp Val Val Pro
                85   90   95

Val Gly Gln Arg Arg Ala Trp Cys Trp Cys Met Cys Phe Gly Leu Ala
            100   105   110

Phe Met Leu Ala Gly Val Ile Leu Gly Gly Ala Tyr Leu Tyr Lys Tyr
        115   120   125

Phe Ala Leu Gln Pro Asp Asp Val Tyr Tyr Cys Gly Ile Lys Tyr Ile
    130   135   140

Lys Asp Asp Val Ile Leu Asn Glu Pro Ser Ala Asp Ala Pro Ala Ala

145 150 155 160

Leu Tyr Gln Thr Ile Glu Glu Asn Ile Lys Ile Phe Glu Glu Glu Glu
165 170 175

Val Glu Phe Ile Ser Val Pro Val Pro Glu Phe Ala Asp Ser Asp Pro
180 185 190

Ala Asn Ile Val His Asp Phe Asn Lys Lys Leu Thr Ala Tyr Leu Asp
195 200 205

Leu Asn Leu Asp Lys Cys Tyr Val Ile Pro Leu Asn Thr Ser Ile Val
210 215 220

Met Pro Pro Arg Asn Leu Leu Glu Leu Leu Ile Asn Ile Lys Ala Gly
225 230 235 240

Thr Tyr Leu Pro Gln Ser Tyr Leu Ile His Glu His Met Val Ile Thr
245 250 255

Asp Arg Ile Glu Asn Ile Asp His Leu Gly Phe Phe Ile Tyr Arg Leu
260 265 270

Cys His Asp Lys Glu Thr Tyr Lys Leu Gln Arg Arg Glu Thr Ile Lys
275 280 285

Gly Ile Gln Lys Arg Glu Ala Ser Asn Cys Phe Ala Ile Arg His Phe
290 295 300

Glu Asn Lys Phe Ala Val Glu Thr Leu Ile Cys Ser
305 310 315

<210> 1429
<211> 398
<212> PRT
<213> Homo sapiens

<400> 1429
His Thr Arg Val Asp Phe Asn Val Pro Met Lys Asn Asn Gln Ile Thr
1 5 10 15

Asn Asn Gln Arg Ile Lys Ala Ala Val Pro Ser Ile Lys Phe Cys Leu
20 25 30

Asp Asn Gly Ala Lys Ser Val Val Leu Met Ser His Leu Gly Arg Pro
35 40 45

Asp Gly Val Pro Met Pro Asp Lys Tyr Ser Leu Glu Pro Val Ala Val
50 55 60

```
Glu Leu Lys Ser Leu Leu Gly Lys Asp Val Leu Phe Leu Lys Asp Cys
 65                  70                  75                  80

Val Gly Pro Glu Val Glu Lys Ala Cys Ala Asn Pro Ala Ala Gly Ser
                 85                  90                  95

Val Ile Leu Leu Glu Asn Leu Arg Phe His Val Glu Glu Glu Gly Lys
            100                 105                 110

Gly Lys Asp Ala Ser Gly Asn Lys Val Lys Ala Glu Pro Ala Lys Ile
        115                 120                 125

Glu Ala Phe Arg Ala Ser Leu Ser Lys Leu Gly Asp Val Tyr Val Asn
    130                 135                 140

Asp Ala Phe Gly Thr Ala His Arg Ala His Ser Ser Met Val Gly Val
145                 150                 155                 160

Asn Leu Pro Gln Lys Ala Gly Gly Phe Leu Met Lys Lys Glu Leu Asn
                165                 170                 175

Tyr Phe Ala Lys Ala Leu Glu Ser Pro Glu Arg Pro Phe Leu Ala Ile
            180                 185                 190

Leu Gly Gly Ala Lys Val Ala Asp Lys Ile Gln Leu Ile Asn Asn Met
        195                 200                 205

Leu Asp Lys Val Asn Glu Met Ile Ile Gly Gly Gly Met Ala Phe Thr
    210                 215                 220

Phe Leu Lys Val Leu Asn Asn Met Glu Ile Gly Thr Ser Leu Phe Asp
225                 230                 235                 240

Glu Glu Gly Ala Lys Ile Val Lys Asp Leu Met Ser Lys Ala Glu Lys
                245                 250                 255

Asn Gly Val Lys Ile Thr Leu Pro Val Asp Phe Val Thr Ala Asp Lys
            260                 265                 270

Phe Asp Glu Asn Ala Lys Thr Gly Gln Ala Thr Val Ala Ser Gly Ile
        275                 280                 285

Pro Ala Gly Trp Met Gly Leu Asp Cys Gly Pro Glu Ser Ser Lys Lys
    290                 295                 300

Tyr Ala Glu Ala Val Thr Arg Ala Lys Gln Ile Val Trp Asn Gly Pro
305                 310                 315                 320

Val Gly Val Phe Glu Trp Glu Ala Phe Ala Arg Gly Thr Lys Ala Leu
                325                 330                 335
```

Met Asp Glu Val Val Lys Ala Thr Ser Arg Gly Cys Ile Thr Ile Ile
340 345 350

Gly Gly Gly Asp Thr Ala Thr Cys Cys Ala Lys Trp Asn Thr Glu Asp
355 360 365

Lys Val Ser His Val Ser Thr Gly Gly Gly Ala Ser Leu Glu Leu Leu
370 375 380

Glu Gly Lys Val Leu Pro Gly Val Asp Ala Leu Ser Asn Ile
385 390 395

<210> 1430
<211> 249
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (245)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1430
Pro Ala Met Gly Ala Ala Val Phe Phe Gly Cys Thr Phe Val Ala Phe
1 5 10 15

Gly Pro Ala Phe Ala Leu Phe Leu Ile Thr Val Ala Gly Asp Pro Leu
20 25 30

Arg Val Ile Ile Leu Val Ala Gly Ala Phe Phe Trp Leu Val Ser Leu
35 40 45

Leu Leu Ala Ser Val Val Trp Phe Ile Leu Val His Val Thr Asp Arg
50 55 60

Ser Asp Ala Arg Leu Gln Tyr Gly Leu Leu Ile Phe Gly Ala Ala Val
65 70 75 80

Ser Val Leu Leu Gln Glu Val Phe Arg Phe Ala Tyr Tyr Lys Leu Leu
85 90 95

Lys Lys Ala Asp Glu Gly Leu Ala Ser Leu Ser Glu Asp Gly Arg Ser
100 105 110

Pro Ile Ser Ile Arg Gln Met Ala Tyr Val Ser Gly Leu Ser Phe Gly
115 120 125

Ile Ile Ser Gly Val Phe Ser Val Ile Asn Ile Leu Ala Asp Ala Leu

```
    130                 135                 140

Gly Pro Gly Val Val Gly Ile His Gly Asp Ser Pro Tyr Tyr Phe Leu
145                 150                 155                 160

Thr Ser Ala Phe Leu Thr Ala Ala Ile Ile Leu Leu His Thr Phe Trp
                165                 170                 175

Gly Val Val Phe Phe Asp Ala Cys Glu Arg Arg Arg Tyr Trp Ala Leu
            180                 185                 190

Gly Leu Val Val Gly Ser His Leu Leu Thr Ser Gly Leu Thr Phe Leu
        195                 200                 205

Asn Pro Trp Tyr Glu Ala Ser Leu Leu Pro Ile Tyr Ala Val Thr Val
    210                 215                 220

Ser Met Gly Leu Trp Ala Phe Ile Thr Ala Gly Gly Ser Leu Arg Ser
225                 230                 235                 240

Ile Gln Arg Ser Xaa Leu Cys Lys Asp
                245


<210> 1431
<211> 271
<212> PRT
<213> Homo sapiens

<400> 1431
Arg Pro Thr Arg Pro Val Met Ala Pro Arg Ser Leu Leu Leu Leu Leu
  1               5                  10                  15

Ser Gly Ala Leu Ala Leu Thr Asp Thr Trp Ala Gly Ser His Ser Leu
             20                  25                  30

Arg Tyr Phe Ser Thr Ala Val Ser Arg Pro Gly Arg Gly Glu Pro Arg
         35                  40                  45

Tyr Ile Ala Val Glu Tyr Val Asp Asp Thr Gln Phe Leu Arg Phe Asp
     50                  55                  60

Ser Asp Ala Ala Ile Pro Arg Met Glu Pro Arg Glu Pro Trp Val Glu
 65                  70                  75                  80

Gln Glu Gly Pro Gln Tyr Trp Glu Trp Thr Thr Gly Tyr Ala Lys Ala
                 85                  90                  95

Asn Ala Gln Thr Asp Arg Val Ala Leu Arg Asn Leu Leu Arg Arg Tyr
            100                 105                 110
```

Asn Gln Ser Glu Ala Gly Ser His Thr Leu Gln Gly Met Asn Gly Cys
115 120 125

Asp Met Gly Pro Asp Gly Arg Leu Leu Arg Gly Tyr His Gln His Ala
130 135 140

Tyr Asp Gly Lys Asp Tyr Ile Ser Leu Asn Glu Asp Leu Arg Ser Trp
145 150 155 160

Thr Ala Ala Asp Thr Val Ala Gln Ile Thr Gln Arg Phe Tyr Glu Ala
165 170 175

Glu Glu Tyr Ala Glu Glu Phe Arg Thr Tyr Leu Glu Gly Glu Cys Leu
180 185 190

Glu Leu Leu Arg Arg Tyr Leu Glu Asn Gly Lys Glu Thr Leu Gln Arg
195 200 205

Ala Asp Pro Pro Lys Ala His Val Ala His His Pro Ile Ser Asp His
210 215 220

Glu Ala Thr Leu Arg Cys Trp Ala Leu Gly Phe Tyr Pro Ala Glu Ile
225 230 235 240

Thr Leu Thr Trp Gln Arg Asp Gly Glu Glu Gln Thr Gln Asp Thr Glu
245 250 255

Leu Val Glu Thr Arg Pro Ala Gly Asp Gly Thr Phe Arg Ser Gly
260 265 270

<210> 1432
<211> 455
<212> PRT
<213> Homo sapiens

<400> 1432
Ala His Ala Ser Gly Ala Pro Glu Gln Arg Pro Arg Pro Pro Arg Leu
1 5 10 15

Leu Arg Arg Asp Leu Glu Arg Lys Thr Pro Ala Arg Arg Pro Ala Leu
20 25 30

Ala Ser Leu Pro Thr Gly His Thr Ala Pro Pro Pro Arg Pro Arg Cys
35 40 45

Ala Arg Pro Val Arg Cys Thr Pro Ala Cys Trp Arg Leu Arg Arg Arg
50 55 60

```
Ala Arg Pro Gly Leu Leu Leu Arg Ala Thr Met Ser Ser Arg Ile Ala
65                  70                  75                  80

Arg Ala Leu Ala Leu Val Val Thr Leu Leu His Leu Thr Arg Leu Ala
                85                  90                  95

Leu Ser Thr Cys Pro Ala Ala Cys His Cys Pro Leu Glu Ala Pro Lys
            100                 105                 110

Cys Ala Pro Gly Val Gly Leu Val Arg Asp Gly Cys Gly Cys Cys Lys
        115                 120                 125

Val Cys Ala Lys Gln Leu Asn Glu Asp Cys Ser Lys Thr Gln Pro Cys
    130                 135                 140

Asp His Thr Lys Gly Leu Glu Cys Asn Phe Gly Ala Ser Ser Thr Ala
145                 150                 155                 160

Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu Gly Arg Pro Cys Glu Tyr
                165                 170                 175

Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser Phe Gln Pro Asn Cys Lys
            180                 185                 190

His Gln Cys Thr Cys Ile Asp Gly Ala Val Gly Cys Ile Pro Leu Cys
        195                 200                 205

Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly Cys Pro Asn Pro Arg Leu
    210                 215                 220

Val Lys Val Thr Gly Gln Cys Cys Glu Glu Trp Val Cys Asp Glu Asp
225                 230                 235                 240

Ser Ile Lys Asp Pro Met Glu Asp Gln Asp Gly Leu Leu Gly Lys Glu
                245                 250                 255

Leu Gly Phe Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn Glu Leu
            260                 265                 270

Ile Ala Val Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val Phe Gly
        275                 280                 285

Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu Gln Gly Gln Lys Cys Ile
    290                 295                 300

Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Thr Cys Gly Thr Gly
305                 310                 315                 320

Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys
                325                 330                 335
```

Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln Pro Val Tyr Ser
340 345 350

Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys Lys Ser Pro Glu
355 360 365

Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu Ser Val Lys Lys Tyr Arg
370 375 380

Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Gln
385 390 395 400

Leu Thr Arg Thr Val Lys Met Arg Phe Arg Cys Glu Asp Gly Glu Thr
405 410 415

Phe Ser Lys Asn Val Met Met Ile Gln Ser Cys Lys Cys Asn Tyr Asn
420 425 430

Cys Pro His Ala Asn Glu Ala Ala Phe Pro Phe Tyr Arg Leu Phe Asn
435 440 445

Asp Ile His Lys Phe Arg Asp
450 455

<210> 1433
<211> 87
<212> PRT
<213> Homo sapiens

<400> 1433
Thr Glu Gly Glu Thr Trp Arg Ser Asp Ser Glu Val Arg Leu Gln Leu
1 5 10 15

Ala His His Leu Arg Pro Gly Pro Asp Glu Pro Pro Val Ala Ser Ala
20 25 30

Gly Ala Ala Ala Ala Ser Arg Gly Ala Cys Gly Pro Ser His Ser Arg
35 40 45

His Cys Leu Pro Ala Gly Leu Glu Pro Ser Glu Arg Pro Asn Pro Arg
50 55 60

Pro Gly Arg Asp Leu Arg Gly Met Thr Ala Glu Pro Pro Lys Gly Gly
65 70 75 80

Glu Phe Glu Gly Arg Gly Pro
85

<210> 1434
<211> 110
<212> PRT
<213> Homo sapiens

<400> 1434
Val Trp Arg Ala Gly Ala Gly Met Ala Ser Leu Arg Ser Gln His Gly
1 5 10 15

Pro Gly Ala Pro Glu Ser Leu Arg Lys Val Leu Met Pro Ser Ser Met
20 25 30

Gly Leu Leu Leu Ile Leu Tyr Ala Arg Leu Pro Pro Ser Leu Val Gly
35 40 45

Gln Ala Gly Arg Trp Ile Gly Trp Ala Gly Arg Ala Gly Gly Gln Ala
50 55 60

Val Arg Gln Pro Ser Pro Thr Val Leu Ile Asp Gly Val Glu Cys Ser
65 70 75 80

Asp Val Lys Phe Phe Gln Leu Ala Ala Gln Trp Ser Ser His Val Lys
85 90 95

His Phe Pro Ile Cys Ile Phe Gly His Ser Lys Ala Thr Phe
100 105 110

<210> 1435
<211> 103
<212> PRT
<213> Homo sapiens

<400> 1435
Gly Ser Gln Asp Ala Arg Arg Gly Ser Gly Leu Gly Val Ser Ser Phe
1 5 10 15

Leu Arg Gly Ser Gly Gly Ser Gly Pro Leu Trp Val Gln His Gly Lys
20 25 30

Arg Gly Arg Tyr Phe Ser Ser Trp Ala Phe Ile Lys Glu Lys Thr Met
35 40 45

Leu Ala Gly Arg Gly Gly Ser Arg Leu Gln Ser Gln His Phe Gly Arg
50 55 60

Pro Arg Arg Val Asp His Leu Arg Ser Gly Val Gln Asp Gln Pro Gly
65 70 75 80

Gln His Gly Glu Thr Pro Ser Leu Leu Lys Asn Thr Lys Ile Ser Gln
85 90 95

Val Trp Trp Leu Thr Leu Met
100

<210> 1436
<211> 413
<212> PRT
<213> Homo sapiens

<400> 1436
Asn Glu Cys Thr Gly Pro Glu Phe Arg Val Asp Pro Arg Val Ala Ser
1 5 10 15

Ala Pro Arg Ala Gln Ser Leu Ala Phe Ala Asp Pro Pro Pro Val His
20 25 30

Thr Arg Arg Gln Leu Thr Met Asp Asp Asp Ile Ala Ala Leu Val Val
35 40 45

Asp Asn Gly Ser Gly Met Cys Lys Ala Gly Phe Ala Gly Asp Asp Ala
50 55 60

Pro Arg Ala Val Phe Pro Ser Ile Val Gly Arg Pro Arg His Gln Gly
65 70 75 80

Val Met Val Gly Met Gly Gln Lys Asp Ser Tyr Val Gly Asp Glu Ala
85 90 95

Gln Ser Lys Arg Gly Ile Leu Thr Leu Lys Tyr Pro Ile Glu His Gly
100 105 110

Ile Val Thr Asn Trp Asp Asp Met Glu Lys Ile Trp His His Thr Phe
115 120 125

Tyr Asn Glu Leu Arg Val Ala Pro Glu Glu His Pro Val Leu Leu Thr
130 135 140

Glu Ala Pro Leu Asn Pro Lys Ala Asn Arg Glu Lys Met Thr Gln Ile
145 150 155 160

Met Phe Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile Gln Ala
165 170 175

Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Ile Val Met Asp
180 185 190

Ser Gly Asp Gly Val Thr His Thr Val Pro Ile Tyr Glu Gly Tyr Ala

```
        195                 200                 205

Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr
    210                 215                 220

Asp Tyr Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr
225                 230                 235                 240

Thr Ala Glu Arg Glu Ile Val Arg Asp Ile Lys Glu Lys Leu Cys Tyr
                245                 250                 255

Val Ala Leu Asp Phe Glu Gln Glu Met Ala Thr Ala Ala Ser Ser Ser
            260                 265                 270

Ser Leu Glu Lys Ser Tyr Glu Leu Pro Asp Gly Gln Val Ile Thr Ile
        275                 280                 285

Gly Asn Glu Arg Phe Arg Cys Pro Glu Ala Leu Phe Gln Pro Ser Phe
    290                 295                 300

Leu Gly Met Glu Ser Cys Gly Ile His Glu Thr Thr Phe Asn Ser Ile
305                 310                 315                 320

Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Ala Asn Thr Val
                325                 330                 335

Leu Ser Gly Gly Thr Thr Met Tyr Pro Gly Ile Ala Asp Arg Met Gln
            340                 345                 350

Lys Glu Ile Thr Ala Leu Ala Pro Ser Thr Met Lys Ile Lys Ile Ile
        355                 360                 365

Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu
    370                 375                 380

Ala Ser Leu Ser Thr Phe Gln Gln Met Trp Ile Ser Lys Gln Glu Tyr
385                 390                 395                 400

Asp Glu Ser Gly Pro Ser Ile Val His Arg Lys Cys Phe
                405                 410
```

<210> 1437
<211> 97
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (28)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1437
Val Val Pro Ser Thr Lys Asp Phe Leu Val Gly Val Lys Gly Ser Gly
1 5 10 15

Gly His Arg Gly Gly Gly Glu Met Ala Phe Ser Xaa Ser Gln Ala Pro
20 25 30

Tyr Leu Ser Pro Ala Val Pro Phe Ser Gly Thr Ile Gln Gly Gly Leu
35 40 45

Gln Asp Gly Leu Gln Ile Thr Val Asn Gly Thr Val Leu Ser Ser Ser
50 55 60

Gly Thr Ser Gly Asn Asp Ile Ala Phe His Phe Asn Pro Arg Phe Glu
65 70 75 80

Asp Gly Gly Tyr Val Val Cys Thr Ala Gly Arg Thr Glu Ala Gly Gly
85 90 95

Pro

<210> 1438
<211> 153
<212> PRT
<213> Homo sapiens

<400> 1438
Leu Ala Pro Leu Arg Cys Gln Pro Gly Thr Arg Thr Gln Pro Arg Ser
1 5 10 15

His Pro Ala Ala Asn Asp Pro Ser Ala Ala Met Ser Ala Ala Gly Ala
20 25 30

Arg Gly Leu Arg Ala Thr Tyr His Arg Leu Leu Asp Lys Val Glu Leu
35 40 45

Met Leu Pro Glu Lys Leu Arg Pro Leu Tyr Asn His Pro Ala Gly Pro
50 55 60

Arg Thr Val Phe Phe Trp Ala Pro Ile Met Lys Trp Gly Leu Val Cys
65 70 75 80

Ala Gly Leu Ala Asp Met Ala Arg Pro Ala Glu Lys Leu Ser Thr Ala
85 90 95

Gln Ser Ala Val Leu Met Ala Thr Gly Phe Ile Trp Ser Arg Tyr Ser

100 105 110

Leu Val Ile Ile Pro Lys Asn Trp Ser Leu Phe Ala Val Asn Phe Phe
115 120 125

Val Gly Ala Ala Gly Ala Ser Gln Leu Phe Arg Ile Trp Arg Tyr Asn
130 135 140

Gln Glu Leu Lys Ala Lys Ala His Lys
145 150

<210> 1439
<211> 343
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (244)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (305)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (325)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (328)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (340)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1439
Trp Ile Gln Arg Ile Arg Ala Arg Gly Lys Thr Asn Leu Arg Arg Thr
1 5 10 15

Thr Tyr Leu Val Leu Asp Glu Ala Asp Arg Met Leu Asp Met Gly Phe
20 25 30

Glu Pro Gln Ile Arg Lys Ile Val Asp Gln Ile Arg Pro Asp Arg Gln

```
        35                  40                  45

Thr Leu Met Trp Ser Ala Thr Trp Pro Lys Glu Val Arg Gln Leu Ala
     50                  55                  60

Glu Asp Phe Leu Lys Asp Tyr Ile His Ile Asn Ile Gly Ala Leu Glu
 65                  70                  75                  80

Leu Ser Ala Asn His Asn Ile Leu Gln Ile Val Asp Val Cys His Asp
                 85                  90                  95

Val Glu Lys Asp Glu Lys Leu Ile Arg Leu Met Glu Glu Ile Met Ser
            100                 105                 110

Glu Lys Glu Asn Lys Thr Ile Val Phe Val Glu Thr Lys Arg Arg Cys
        115                 120                 125

Asp Glu Leu Thr Arg Lys Met Arg Arg Asp Gly Trp Pro Ala Met Gly
    130                 135                 140

Ile His Gly Asp Lys Ser Gln Gln Glu Arg Asp Trp Val Leu Asn Glu
145                 150                 155                 160

Phe Lys His Gly Lys Ala Pro Ile Leu Ile Ala Thr Asp Val Ala Ser
                165                 170                 175

Arg Gly Leu Asp Val Glu Asp Val Lys Phe Val Ile Asn Tyr Asp Tyr
            180                 185                 190

Pro Asn Ser Ser Glu Asp Tyr Ile His Arg Ile Gly Arg Thr Ala Arg
        195                 200                 205

Ser Thr Lys Thr Gly Thr Ala Tyr Thr Phe Phe Thr Pro Asn Asn Ile
    210                 215                 220

Lys Gln Val Ser Asp Leu Ile Ser Val Leu Arg Glu Ala Asn Gln Ala
225                 230                 235                 240

Ile Asn Pro Xaa Leu Leu Gln Leu Val Glu Asp Arg Gly Ser Gly Arg
                245                 250                 255

Ser Arg Gly Arg Gly Gly Met Lys Asp Asp Arg Arg Asp Arg Tyr Ser
            260                 265                 270

Ala Gly Lys Arg Gly Gly Phe Asn Thr Phe Arg Asp Arg Glu Asn Tyr
        275                 280                 285

Asp Arg Gly Tyr Ser Ser Leu Leu Lys Arg Asp Phe Gly Ala Lys Thr
    290                 295                 300

Xaa Asn Gly Gly Tyr Ser Ala Cys Lys Phe Thr Asn Gly Ser Phe Gly
```

305 310 315 320

Ser Asn Phe Gly Xaa Cys Trp Xaa Ser Gly Pro Val Leu Gly Leu Gly
325 330 335

Ile Pro Thr Xaa Ala Leu Pro
340

<210> 1440
<211> 122
<212> PRT
<213> Homo sapiens

<400> 1440
Ile Cys Val Ser Ala Arg Arg Ala Leu Ser Gly Leu Glu His Gly Leu
1 5 10 15

Gly Trp Glu Arg Val Trp Glu Lys Met Gly Asn Lys Glu Pro Gly Ser
20 25 30

His Gly His Arg Ser Asp Ala Asp Pro Ser Arg Phe Ser Pro Val Leu
35 40 45

Pro Pro Ala Val Gln Leu Gly Val Trp Arg Glu Glu Gly Arg Gly Gly
50 55 60

Ser Cys Pro Phe Ser Trp Gly Arg Gly Pro Val Ser Ser Thr Trp Leu
65 70 75 80

Phe Pro Lys Gly Ser Lys Arg Glu Gly Leu Gly Glu Lys Thr Met Glu
85 90 95

Arg Gly Pro Ala Lys Glu Asn Arg Glu Glu Val Ser Gly Leu Ile Ser
100 105 110

Leu Leu Ser Arg Cys Ser Gly Ser Leu Ile
115 120

<210> 1441
<211> 74
<212> PRT
<213> Homo sapiens

<400> 1441
Gly His Arg His Thr Pro Pro His Leu Ala Asn Phe Tyr Tyr Phe Phe
1 5 10 15

Cys Arg Asp Glu Val Ser Leu Cys Pro Gly Trp Ser Gln Thr Pro Val
20 25 30

Leu Lys Gln Ser Ser His Leu Gly Ser Leu Ser Ala Gly Ile Ile Gly
35 40 45

Met Ser His Arg Ala Arg Pro His Val Cys Met Leu Lys Val Leu Arg
50 55 60

Ile Pro Met Glu Asn Lys Phe Asp Phe Ala
65 70

<210> 1442
<211> 103
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1442
Ala Xaa Xaa His Gln Pro Ser Leu Lys Gly Thr Lys Ala Gly Ala Pro
1 5 10 15

Pro Arg Cys Gly Arg Ser Arg Thr Ser Gly Ser Pro Gly Leu Gln Glu
20 25 30

Phe Gly Thr Arg Glu Ala Glu Ala Gly Val Gln Trp Cys Asp Leu Gly
35 40 45

Ser Leu Gln Pro Leu Pro Pro Arg Phe Gln Gln Phe Ser Cys Leu Ser
50 55 60

Leu Pro Ser Gly Trp Asp Asp Arg Arg Leu Pro Ser Cys Leu Thr Ser
65 70 75 80

Phe Cys Ile Phe Ser Arg Asp Gly Val Ser Pro Cys Trp Pro Gly Trp
85 90 95

Ser Gln Thr Pro Asp Leu Arg
100

<210> 1443
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (48)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (53)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (57)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (58)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (63)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (66)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (70)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (83)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (99)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (100)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (102)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1443
Leu His Ala Ala Ala Cys Ala Ala Ala Met Ser Leu Val Ile Pro Glu
1 5 10 15

Lys Phe Gln His Ile Leu Arg Val Leu Asn Thr Asn Ile Asp Gly Arg
20 25 30

Arg Lys Ile Ala Phe Ala Ile Thr Ala Ile Lys Gly Val Gly Arg Xaa
35 40 45

Tyr Ala His Val Xaa Leu Arg Lys Xaa Xaa Ile Asp Leu Thr Xaa Arg
50 55 60

Ala Xaa Glu Leu Thr Xaa Asp Xaa Val Glu Arg Val Ile Thr Ile Met
65 70 75 80

Gln Asn Xaa Arg Gln Tyr Lys Ile Pro Asp Trp Phe Leu Asn Arg Gln
85 90 95

Asn Asp Xaa Xaa Asp Xaa Ser Thr Ser Ser
100 105

<210> 1444
<211> 14
<212> PRT
<213> Homo sapiens

<400> 1444
Pro Val Trp Pro Lys Trp Ser Gly Trp Pro Leu Ala Leu Pro
1 5 10

<210> 1445
<211> 126
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (104)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (119)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (123)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (124)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1445
Phe Leu Arg Leu Val Leu Gly Leu Leu Ile Gly Arg Cys Leu Gln Glu
1 5 10 15

Met Leu Lys Leu Gly Thr Leu Pro Pro Thr Ser Lys Pro Gln Leu Leu
20 25 30

Cys Gln Met Val Ser Leu Lys Ile Ser Ala Cys Leu Thr Thr Lys Gly
35 40 45

Lys Tyr Val Val Phe Phe Phe Tyr Pro Leu Asp Phe Thr Phe Val Cys
50 55 60

Pro Thr Glu Ile Ile Ala Phe Ser Asp Arg Ala Glu Glu Phe Lys Lys
65 70 75 80

Leu Asn Cys Gln Val Ile Gly Ala Ser Val Asp Ser His Phe Cys His
85 90 95

Leu Ala Trp Val Asn Thr Pro Xaa Lys Gln Gly Gly Leu Gly Pro Met
100 105 110

Asn Ile Pro Leu Val Ser Xaa Pro Thr His Xaa Xaa Ser Gly
115 120 125

<210> 1446
<211> 97
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (92)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1446
Cys Asp Lys Glu Lys Asn Leu Leu His Val Thr Asp Thr Gly Val Gly
1 5 10 15

Met Thr Arg Glu Glu Leu Val Lys Asn Leu Gly Thr Ile Ala Lys Ser
20 25 30

Gly Thr Ser Glu Phe Leu Asn Lys Met Thr Glu Ala Gln Glu Asp Gly
35 40 45

Gln Ser Thr Ser Asp Leu Ile Gly Gln Phe Gly Val Gly Phe Tyr Ser
50 55 60

Ala Phe Leu Val Ala Asp Lys Val Ile Val Thr Ser Lys His Asn Asn
65 70 75 80

Asp Thr Gln His Ile Trp Glu Ser Asp Ser Asn Xaa Phe Ser Val Asn
85 90 95

Cys

<210> 1447
<211> 47
<212> PRT
<213> Homo sapiens

<400> 1447
His Ser Arg His Arg Gly Val Phe Leu Thr Pro Leu Leu Ala Met Ser
1 5 10 15

Ser His Lys Thr Phe Arg Ile Lys Arg Phe Leu Ala Lys Lys Gln Lys
20 25 30

Gln Asn Arg Pro Ile Pro Gln Trp Ile Arg Met Lys Thr Gly Lys
35 40 45

<210> 1448
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (85)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (104)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1448
Val Phe Arg Val Glu Ala Trp Arg Thr Ser Gly Glu Thr Pro Ala Ile
1 5 10 15

Ser Pro Ser Lys Arg Ala Arg Pro Ala Glu Val Gly Gly Met Gln Leu
20 25 30

Arg Phe Ala Arg Leu Ser Glu His Ala Thr Ala Pro Thr Arg Gly Ser
35 40 45

Ala Arg Ala Ala Gly Tyr Asp Leu Tyr Ser Ala Tyr Asp Tyr Thr Ile
50 55 60

Pro Pro Met Glu Lys Ala Val Val Lys Thr Asp Ile Gln Ile Ala Leu
65 70 75 80

Pro Ser Gly Cys Xaa Gly Arg Val Ala Pro Arg Ser Gly Leu Ala Ala
85 90 95

Lys His Phe Ile Asp Val Gly Xaa Val Ser
100 105

<210> 1449
<211> 60
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (41)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (44)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1449
Thr Met Ala Val Gly Lys Asn Lys Arg Leu Thr Lys Gly Gly Lys Lys
1 5 10 15

Gly Ala Lys Lys Lys Val Val Asp Pro Phe Phe Lys Lys Asp Trp Tyr
20 25 30

Asp Val Lys Ala Pro Ala Met Phe Xaa Ile Arg Xaa Ile Gly Lys Thr
35 40 45

Leu Val Thr Arg Thr Gln Gly Thr Lys Ile Ala Ser
50 55 60

<210> 1450
<211> 45
<212> PRT
<213> Homo sapiens

<400> 1450
Asn Phe Gly Ser Leu Leu Gly Ala Cys Leu Ile Leu Gln Ile Thr Thr
1 5 10 15

Gly Leu Phe Leu Ala Met His Tyr Ser Pro Asp Ala Ser Thr Ala Phe
20 25 30

Ser Ser Ile Ala His Ile Thr Arg Asp Val Asn Tyr Gly
35 40 45

<210> 1451
<211> 34
<212> PRT
<213> Homo sapiens

<400> 1451
Lys Leu Leu Asp Asp Asn Gly Asn Ile Ala Glu Glu Leu Ser Ile Leu
1 5 10 15

Lys Trp Asn Thr Asp Ser Val Glu Glu Phe Leu Ser Glu Lys Leu Glu
20 25 30

Arg Ile

<210> 1452
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1452
Pro Arg Val Arg Leu Xaa Asp Glu Thr Asn Ile Cys Asn Gly Lys Pro
1 5 10 15

Val Asp Gly Leu Thr Thr Leu Arg Asn Gly Thr Leu Val Ala Phe Arg
20 25 30

Gly His Tyr Phe Trp Met Leu Ser Pro Phe Ser Pro Pro Ser Pro Ala
35 40 45

Arg Arg Ile Thr Glu Val Leu Gly Asn Pro Phe Pro His
50 55 60

<210> 1453
<211> 44
<212> PRT
<213> Homo sapiens

<400> 1453
Arg Glu Gln Lys Leu Glu Leu His Arg Gly Ala Ala Ala Leu Glu Leu
1 5 10 15

Val Asp Pro Pro Gly Cys Arg Asn Ser Ala Arg Gly Cys Ser Glu Pro
20 25 30

Arg Ser His His Cys Thr Pro Val Trp Ala Thr Glu
35 40

<210> 1454
<211> 118
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (76)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (84)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (98)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (99)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (106)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (111)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1454
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Thr Arg Val Ala Pro Ser Val Leu Arg Leu Ala Met Thr Ser Tyr Ser
  1               5                  10                  15

Tyr Arg Gln Ser Ser Ala Thr Ser Ser Phe Gly Gly Leu Gly Gly Gly
             20                  25                  30

Ser Val Arg Ile Gly Pro Gly Val Ala Phe Arg Ala Pro Ser Ile His
         35                  40                  45

Gly Gly Ser Gly Gly Arg Gly Val Ser Val Ser Ser Ala Arg Phe Val
     50                  55                  60

Ser Ser Ser Ser Ser Gly Gly Tyr Gly Gly Gly Xaa Gly Gly Val Leu
 65                  70                  75                  80

Thr Ala Ser Xaa Gly Leu Leu Ala Gly Asn Glu Lys Leu Thr Met Gln
                 85                  90                  95

Asn Xaa Xaa Thr Ala Trp Leu Leu Leu Xaa Lys Phe Ala Pro Xaa Gly
            100                 105                 110

Ala Lys Gly Thr Lys Ser
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115

<210> 1455
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (34)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (43)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1455
Ala Xaa Glu Asn Ser Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu
1 5 10 15

Ala Ala Asp Asp Phe Arg Thr Lys Phe Glu Thr Glu Gln Ala Leu Arg
20 25 30

Met Xaa Val Glu Ala Asp Ile Asn Gly Leu Xaa Arg Cys Trp Met Ser
35 40 45

<210> 1456
<211> 143
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (131)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (137)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1456
Gly Asp Tyr Ser His Tyr Tyr Thr Thr Ile Gln Asp Leu Arg Asp Lys
1 5 10 15

Ile Leu Gly Ala Thr Ile Glu Asn Ser Arg Ile Val Leu Gln Ile Asp
20 25 30

Asn Ala Arg Leu Ala Ala Asp Asp Phe Arg Thr Lys Phe Glu Thr Glu
35 40 45

Gln Ala Leu Arg Met Ser Val Glu Ala Asp Ile Asn Gly Leu Arg Arg
50 55 60

Val Leu Asp Glu Leu Thr Leu Ala Arg Thr Asp Leu Glu Met Gln Ile
65 70 75 80

Glu Gly Leu Lys Glu Glu Leu Ala Tyr Leu Lys Lys Asn His Glu Glu
85 90 95

Glu Ile Ser Thr Leu Arg Gly Gln Val Gly Gly Gln Val Ser Val Glu
100 105 110

Val Asp Ser Ala Pro Gly Thr Asp Leu Ala Lys Ile Leu Ser Asp Met
115 120 125

Arg Ser Xaa Tyr Glu Val Met Ala Xaa Gln Asn Arg Lys Asp Ala
130 135 140

<210> 1457
<211> 116
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (21)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1457
Gly Cys Val Gly Val Arg Pro Ser Leu His Pro Ala Thr Ser Thr Ala
1 5 10 15

Ser Gly Ser Ala Xaa Pro Thr Leu Ala Arg Ala Met Ala Ser Val Ser
20 25 30

Glu Leu Ala Cys Ile Tyr Ser Ala Leu Ile Leu His Asp Asp Glu Val

35 40 45

Thr Val Thr Glu Asp Lys Ile Asn Ala Leu Ile Lys Ala Ala Gly Val
50 55 60

Asn Val Glu Pro Phe Trp Pro Gly Leu Phe Ala Lys Ala Leu Ala Asn
65 70 75 80

Val Asn Ile Gly Ser Leu Ile Cys Asn Val Gly Ala Gly Gly Pro Ala
85 90 95

Pro Ala Ala Gly Ala Ala Thr Ser Arg Arg Ser Cys Pro Leu His Cys
100 105 110

Cys Cys Ser Ser
115

<210> 1458
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (47)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1458
Leu Val Pro Asn Ser Ala Arg Ala Ala Ala Ser Ala Ala Asp Ala Ala
1 5 10 15

Ala Met Arg Tyr Val Ala Ser Tyr Leu Leu Ala Ala Leu Gly Gly Asn
20 25 30

Ser Ser Pro Ser Ala Lys Gly Ile Lys Lys Ile Leu Asp Asn Xaa Gly
35 40 45

Ile Glu Ala Asp Asp Asp Arg Leu Asn Lys Val Ile Ser Glu Leu Asn
50 55 60

Gly Lys Asn Ile Glu Asp Val Ile Ala Gln Gly Ile Gly Lys Leu Ala
65 70 75 80

Ser Val Pro Ala Gly Gly Ala Val Ala Val Ser Ala Ala Pro Gly Ser
85 90 95

Ala Ala Pro Ala Ala Gly Ser Ala Pro Ala Ala Ala Glu Glu Lys Lys
100 105 110

Asp Glu Lys
        115

<210> 1459
<211> 132
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (115)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (123)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (126)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (129)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1459
Ala Ser Asp Ala Leu His Ser Leu Ser Ala Pro Val Leu Arg Leu Ser
  1   5   10   15

Ser Arg Ser Ala Ala Arg Pro Ala Thr Met Thr Glu Gln Ala Ile Ser
             20   25   30

Phe Ala Lys Asp Phe Leu Ala Gly Gly Ile Ala Ala Ala Ile Ser Lys
         35   40   45

Thr Ala Val Ala Pro Ile Glu Arg Val Lys Leu Leu Leu Gln Val Gln
     50   55   60

His Ala Ser Lys Gln Ile Ala Ala Asp Lys Gln Tyr Lys Gly Ile Val
 65   70   75   80

Asp Cys Ile Val Arg Ile Pro Lys Glu Gln Gly Val Leu Ser Phe Trp
                 85   90   95

Arg Gly Asn Leu Ala Asn Val Ile Arg Tyr Phe Pro Thr Gln Ala Leu
            100   105   110

Asn Phe Xaa Phe Lys Asp Lys Tyr Lys Gln Xaa Phe Leu Xaa Gly Val
115 120 125

Xaa Lys His Thr
130

<210> 1460
<211> 124
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (80)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (85)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (107)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (112)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (117)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (119)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (120)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (121)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1460
Xaa Ser Xaa Lys Thr Gly Phe Xaa Asp Trp Ile Ser Val Ala Tyr Tyr
1 5 10 15

Gly Cys Phe Arg Glu Gly Ala Thr Ile Ile Gln Val Gly Lys Leu Ile
20 25 30

Lys Glu Ala Ala Gly Lys Ser Asn Leu Lys Arg Val Thr Leu Glu Leu
35 40 45

Gly Gly Lys Ser Pro Cys Ile Val Leu Ala Asp Ala Asp Leu Asp Asn
50 55 60

Ala Val Glu Phe Ala His His Gly Val Phe Tyr His Gln Gly Gln Xaa
65 70 75 80

Cys Ile Ala Ala Xaa Arg Ile Phe Val Glu Glu Ser Ile Tyr Asp Glu
85 90 95

Phe Val Arg Arg Ser Val Glu Arg Val Lys Xaa Ile Ser Leu Gly Xaa
100 105 110

Pro Leu Thr Pro Xaa Val Xaa Xaa Xaa Pro Ser Asp
115 120

<210> 1461
<211> 179
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (102)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (125)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (142)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (145)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (157)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (163)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (173)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (174)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (176)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1461
Trp Ile Pro Arg Ala Ala Gly Ile Arg His Glu Val Val Pro Leu Ala
1 5 10 15

Gly Thr Asn Gly Glu Thr Thr Thr Gln Gly Leu Asp Gly Leu Ser Glu
20 25 30

Arg Cys Ala Gln Tyr Lys Lys Asp Gly Ala Asp Phe Ala Lys Trp Arg
        35   40   45

Cys Val Leu Lys Ile Gly Glu His Thr Pro Ser Ala Leu Ala Ile Met
    50   55   60

Glu Asn Ala Asn Val Leu Ala Arg Tyr Ala Ser Ile Cys Gln Gln Asn
65   70   75   80

Gly Ile Val Pro Ile Val Glu Pro Glu Ile Leu Pro Asp Gly Asp His
                85   90   95

Asp Leu Lys Arg Leu Xaa Val Cys Asp Arg Lys Gly Ala Trp Leu Ala
            100   105   110

Ala Thr Arg Leu Leu Ser Asp His His Ile Tyr Leu Xaa Gly Thr Leu
        115   120   125

Leu Lys Pro Asn Met Val Pro Gln Ala Met Leu Ala Leu Xaa Ser Phe
    130   135   140

Xaa Met Lys Glu Ile Ala His Gly Glu Pro Val Ser Xaa Ala Val Pro
145   150   155   160

Ala Gln Xaa Pro Pro Arg Leu Ser Leu Gly Ile Asn Xaa Xaa Cys Xaa
                165   170   175

Gly Arg Pro

<210> 1462
<211> 31
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1462
Ala Asn Ser Leu Ala Cys Gln Gly Lys Tyr Thr Pro Xaa Gly Gln Ala
1   5   10   15

Gly Ala Ala Ala Ser Glu Ser Leu Phe Val Ser Asn His Ala Tyr
            20   25   30

<210> 1463
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (65)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (69)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1463
```
Asp Asp Cys Glu Phe Lys Ala Glu Gly Asn Ser Lys Phe Thr Tyr Thr
  1               5                  10                  15

Val Leu Glu Asp Gly Cys Thr Lys His Thr Gly Glu Trp Ser Lys Thr
             20                  25                  30

Val Phe Glu Tyr Arg Thr Arg Lys Ala Val Arg Leu Pro Ile Val Asp
         35                  40                  45

Ile Ala Pro Tyr Asp Ile Gly Gly Pro Asp Gln Glu Phe Gly Val Asp
     50                  55                  60

Xaa Gly Pro Val Xaa Phe Leu
 65                  70
```

<210> 1464
<211> 77
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (10)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1464
Xaa Gly Thr Arg His Xaa Leu Arg Thr Xaa Asn Gln Ser Ser Asp Glu
1   5   10   15

Leu Gln Leu Ser Met Gly Asn Ala Met Phe Val Lys Glu Gln Leu Ser
            20   25   30

Leu Leu Asp Arg Phe Thr Glu Asp Ala Lys Arg Leu Tyr Gly Ser Glu
        35   40   45

Ala Phe Ala Thr Asp Phe Gln Asp Ser Ala Ala Ala Lys Lys Leu Ile
    50   55   60

Asn Asp Tyr Val Lys Asn Gly Thr Arg Gly Thr Ile Thr
65   70   75

<210> 1465
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (83)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (98)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (104)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1465
Leu Lys Gly Arg Pro Gly Phe Pro Gly Ser Lys Gly Glu Ala Gly Phe
1   5   10   15

Phe Gly Ile Pro Gly Leu Lys Gly Leu Ala Gly Glu Pro Gly Phe Lys
            20   25   30

Gly Ser Arg Gly Asp Pro Gly Pro Pro Gly Pro Pro Pro Val Ile Leu
35 40 45

Pro Gly Met Lys Asp Ile Lys Gly Glu Lys Gly Asp Glu Gly Pro Met
50 55 60

Gly Leu Lys Gly Tyr Leu Gly Ala Lys Gly Ile Gln Gly Met Pro Gly
65 70 75 80

Ile Pro Xaa Leu Ser Gly Ile Pro Gly Leu Pro Gly Arg Pro Gly His
85 90 95

Ile Xaa Gly Ile Lys Gly Xaa Xaa Gly
100 105

<210> 1466
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1466
Arg Pro Gly Leu Cys Ala Lys Thr Val Phe Lys Ala Leu Gln Ala Pro
1 5 10 15

Ala Leu Xaa Glu Glu His Gly Glu Gly Trp Arg Leu His Pro Trp Gly
20 25 30

Val Trp Glu Thr
35

<210> 1467
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (76)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (79)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (80)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (82)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1467
Arg Val Pro Ala Met Ala Ala Lys Gly Gly Thr Val Lys Ala Ala Ser
1 5 10 15

Ala Phe Asn Ala Thr Glu Asp Ala Gln Thr Leu Arg Lys Ala Met Lys
20 25 30

Gly Leu Gly Thr Asp Glu Asp Ala Ile Ile Ser Val Leu Ala Tyr Arg
35 40 45

Asn Thr Ala Gln Arg Gln Glu Ile Arg Thr Ala Leu Gln Glu His His
50 55 60

Ser Ala Gly Asp Leu Val Leu Arg Asn Gly Pro Xaa Phe Val Xaa Xaa
65 70 75 80

Trp Xaa

<210> 1468
<211> 83
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (24)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>

<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (61)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (66)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (79)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (82)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (83)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1468
Gly Trp His Leu Gly Pro Pro Gly Ser Trp Cys Trp Trp Ser Xaa Cys
1 5 10 15

Ile Thr Gly Pro Asn Thr Ser Xaa Cys Cys Trp Thr His Phe Glu Lys
20 25 30

Pro Arg Xaa Ile Asp Asn Val Leu Val Ile Phe Ser His Asp Phe Trp
35 40 45

Ser Thr Glu Ile Asn Gln Leu Ile Ala Gly Val Asn Xaa Cys Pro Val
50 55 60

Leu Xaa Val Phe Phe Pro Phe Ser Ile Gln Leu Phe Pro Asn Xaa Phe
65 70 75 80

Pro Xaa Xaa

<210> 1469

<211> 26
<212> PRT
<213> Homo sapiens

<400> 1469
Glu Lys Asp Glu Tyr Ala Cys Arg Val Asn His Val Thr Leu Ser Gln
1 5 10 15

Pro Lys Ile Val Lys Trp Asp Arg Asp Met
20 25

<210> 1470
<211> 168
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (139)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (141)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (143)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (146)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (148)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (152)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (153)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (158)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1470
```
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Gly Arg Ser
1               5                   10                  15

Xaa Gly Ser Lys Leu Thr Tyr Ala Cys Met Arg Arg His Ser Ser Ser
            20                  25                  30

Ile Val Ser Pro Lys Phe Asn Ser Leu Ala Val Val Leu Gln Arg Arg
        35                  40                  45

Asp Trp Glu Asn Pro Gly Val Thr Gln Leu Asn Arg Leu Ala Ala His
    50                  55                  60

Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu Glu Ala Arg Thr Asp Arg
65                  70                  75                  80

Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly Lys Trp Asp Ala Pro Cys
                85                  90                  95

Ser Gly Ala Leu Ser Ala Ala Gly Val Val Val Thr Arg Ser Val Thr
            100                 105                 110

Ala Thr Leu Ala Ser Ala Leu Arg Pro Val Leu Ser Phe Leu Pro Phe
        115                 120                 125

Leu Ser Arg His Val Arg Arg Xaa Ser Pro Xaa Ser Xaa Lys Xaa Gly
    130                 135                 140

Ala Xaa Phe Xaa Val Pro Ile Xaa Xaa Leu Arg Asp Leu Xaa Pro Lys
145                 150                 155                 160

Asn Leu Ile Arg Val Met Val Thr
                165
```

<210> 1471
<211> 131
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (88)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (111)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (116)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (119)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1471
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Cys His Leu Asn Ser Ile His Trp Pro Ser Phe Tyr Asn Val Val Thr
  1               5                  10                  15

Gly Lys Thr Leu Ala Xaa Pro Asn Leu Ile Ala Leu Gln His Ile Pro
             20                  25                  30

Leu Ser Pro Ala Gly Ser Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro
         35                  40                  45

Ser Gln Gln Leu Arg Ser Leu Asn Gly Glu Trp Asp Ala Pro Cys Ser
     50                  55                  60

Gly Ala Leu Ser Ala Ala Gly Val Val Val Thr Arg Ser Val Thr Ala
 65                  70                  75                  80

Thr Leu Ala Ser Ala Leu Ala Xaa Ala Pro Phe Ala Phe Phe Pro Ser
                 85                  90                  95
```

```
Phe Leu Ala Thr Phe Ala Gly Phe Pro Arg Gln Ala Leu Asn Xaa Gly
            100                 105                 110

Leu Pro Leu Xaa Phe Arg Xaa Ser Ala Val Arg His Leu Asp Pro Lys
        115                 120                 125

Lys Leu Asp
    130
```

<210> 1472
<211> 179
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (24)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (25)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (40)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (51)
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<400> 1472
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Lys Lys Lys Lys Xaa Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
  1               5                  10                  15

Lys Lys Lys Lys Gly Gly Arg Xaa Xaa Gly Ser Lys Leu Thr Tyr Ala
             20                  25                  30

Cys Met Xaa Arg His Ser Ser Xaa Ile Gly Ser Pro Lys Phe Asn Ser
         35                  40                  45

Leu Ala Xaa Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr
     50                  55                  60

Gln Leu Asn Arg Leu Ala Xaa His Pro Xaa Phe Ala Ser Trp Arg Asn
 65                  70                  75                  80

Ser Xaa Lys Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu
                 85                  90                  95

Asn Gly Lys Trp Asp Xaa Pro Cys Xaa Gly Ala Leu Xaa Xaa Ala Gly
            100                 105                 110
```

Val Xaa Val Thr Xaa Xaa Xaa Thr Ala Thr Leu Ala Xaa Ala Leu Ala
115 120 125

Pro Ala Pro Phe Ala Phe Phe Pro Ser Phe Xaa Ala Thr Phe Ala Gly
130 135 140

Phe Pro Arg Gln Ala Xaa Asn Arg Gly Leu Pro Leu Gly Phe Arg Leu
145 150 155 160

Xaa Ala Leu Arg Asp Leu Xaa Pro Gln Lys Asn Leu Ile Arg Gly Asp
165 170 175

Gly Ser Xaa

<210> 1473
<211> 58
<212> PRT
<213> Homo sapiens

<400> 1473
Ile Ala Ser Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1 5 10 15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
35 40 45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala
50 55

<210> 1474
<211> 70
<212> PRT
<213> Homo sapiens

<400> 1474
Ile Ala Ser Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1 5 10 15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
35 40 45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
50 55 60

Glu Ala Arg Thr Asp Arg
65 70

<210> 1475
<211> 62
<212> PRT
<213> Homo sapiens

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1475
Leu Pro Xaa Ala Xaa Tyr Thr Xaa Xaa Gly Thr Thr Pro His Tyr Arg

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 1               5                   10                  15

Glu Ser Trp Tyr Ala Cys Arg Tyr Arg Ser Gly Ile Pro Gly Ser Thr
            20                  25                  30

His Ala Ser Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Arg Xaa
        35                  40                  45

Asp Asp Leu Glu Asp Pro Lys Leu Thr Tyr Xaa Xaa Met Gln
    50                  55                  60
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<210> 1476
<211> 80
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (73)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1476
Ile Arg Xaa Xaa Xaa Leu Arg Xaa Asp Thr Thr His Tyr Arg Glu Ser
1 5 10 15

Trp Tyr Ala Cys Arg Tyr Arg Ser Gly Ile Pro Gly Xaa Thr His Ala
20 25 30

Ser Val Glu Ile Cys Pro Pro Xaa Ser Arg Pro Xaa Ser Ser Gln Ser
35 40 45

Asn Gly Glu Gly Tyr Ser Xaa Cys Arg Arg Pro Gln Ala Leu Glu Ala
50 55 60

Ala Thr Tyr Leu Asn Pro Val Pro Xaa Arg Ile Leu Leu Lys Pro Phe
65 70 75 80

<210> 1477
<211> 52
<212> PRT
<213> Homo sapiens

<400> 1477
Arg Gln Val Pro His Glu Arg Ala Val Arg Asp Gly Arg Gly Gly Gly
1 5 10 15

Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met Arg Arg His Ser
20 25 30

Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala Val Val Leu Gln
35 40 45

Arg Arg Asp Trp
50

<210> 1478
<211> 154
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (140)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1478
Ile Ala Ser Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1   5   10   15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
            20   25   30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
        35   40   45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
    50   55   60

Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
65   70   75   80

Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val
                85   90   95

Val Thr Arg Ser Val Thr Ala Thr Leu Ala Ser Ala Leu Ala Pro Ala
            100   105   110

Pro Phe Ala Phe Phe Pro Ser Phe Leu Ala Thr Phe Ala Gly Phe Pro
        115   120   125

Arg Gln Ala Leu Asn Arg Gly Leu Pro Leu Gly Xaa Arg Phe Lys Cys
    130   135   140

Phe Thr Asp Leu Asp Pro Lys Lys Leu Asp
145   150

<210> 1479
<211> 130
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
<222> (122)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1479
Ile Ala Gly Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1 5 10 15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
35 40 45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
50 55 60

Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
65 70 75 80

Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val
85 90 95

Val Thr Arg Ser Val Thr Ala Thr Leu Ala Lys Arg Pro Lys Arg Pro
100 105 110

Phe Leu Ser Leu Ser Ser Phe Leu Phe Xaa Pro Arg Ser Ala Gly Phe
115 120 125

Ser Pro
130

<210> 1480
<211> 131
<212> PRT
<213> Homo sapiens

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<221> SITE
<222> (103)
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<222> (129)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1480
Ile Ala Ser Gly Arg Ser Arg Gly Ser Lys Leu Thr Tyr Ala Cys Met
1 5 10 15

Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe Asn Ser Leu Ala
20 25 30

Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly Val Thr Gln Leu
35 40 45

Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp Arg Asn Ser Glu
50 55 60

Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg Ser Leu Asn Gly
65 70 75 80

Glu Trp Asp Ala Pro Cys Ser Gly Ala Leu Ser Ala Ala Gly Val Val
85 90 95

Val Thr Arg Ser Val Thr Xaa Thr Leu Ala Ser Ala Leu Ala Pro Xaa
100 105 110

Pro Phe Ala Phe Phe Leu Leu Ser Arg His Gly Arg Pro Ala Xaa Pro
115 120 125

Xaa Lys Leu
130

<210> 1481
<211> 112
<212> PRT
<213> Homo sapiens

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<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE
<222> (88)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1481
Xaa Ser Ser Arg Ser Arg Ala Ala Arg Ser Arg Gly Ser Lys Leu Thr
1 5 10 15

Tyr Ala Cys Met Arg Arg His Ser Ser Ser Ile Val Ser Pro Lys Phe
20 25 30

Asn Ser Leu Ala Val Val Leu Gln Arg Arg Asp Trp Glu Asn Pro Gly
35 40 45

Val Thr Gln Leu Asn Arg Leu Ala Ala His Pro Pro Phe Ala Ser Trp
50 55 60

His Asn Ser Glu Glu Ala Arg Thr Asp Arg Pro Ser Gln Gln Leu Arg
65 70 75 80

Ser Leu Asn Gly Glu Trp Asp Xaa Pro Cys Ser Gly Ala Leu Ser Ala
85 90 95

Ala Gly Val Val Val Thr Arg Ser Val Thr Ala Thr Leu Ala Ala Pro
100 105 110

<210> 1482
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (50)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1482
Glu Asn Val Lys Ala Lys Ile Gln Asp Lys Glu Gly Ile Pro Pro Glu

1 5 10 15

Xaa Ser Arg Glu Leu Asn Leu Cys Leu Xaa Lys Gln Leu Gly Arg Met
20 25 30

Gly Arg Tyr Phe Val Leu Asn Leu Gln Tyr Phe Lys Arg Gly Ser Tyr
35 40 45

Phe Xaa Ile Leu Cys
50

<210> 1483
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (59)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1483
Ala Asn Met Gln Ile Phe Val Lys Thr Leu Thr Gly Lys Thr Ile Thr
1 5 10 15

Leu Glu Val Glu Pro Ser Asp Thr Ile Glu Asn Val Lys Ala Lys Ile
20 25 30

Gln Asp Lys Glu Gly Ile Pro Pro Asp Gln Gln Arg Leu Ile Phe Ala
35 40 45

Gly Lys Gln Leu Glu Gly Trp Xaa Gln Leu Xaa Gln Thr
50 55 60

<210> 1484
<211> 27
<212> PRT
<213> Homo sapiens

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<222> (6)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (23)
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<400> 1484
Gly Glu Gly Pro Thr Xaa Pro Leu Pro Ser Glu Thr Xaa Gly Asp Val
1 5 10 15

Ala Pro Leu Xaa Cys Xaa Xaa Gly Leu Asn Met
20 25

<210> 1485
<211> 45
<212> PRT
<213> Homo sapiens

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<222> (24)
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<221> SITE
<222> (34)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1485
Phe Leu Ala Ala Gly Asn Pro Leu Arg Trp Pro Xaa Ile Leu Thr Ser
1   5   10   15

Arg Trp Lys Ser Asp Ile Tyr Xaa Arg Lys Ser Asp Gly Xaa Tyr Ile
            20   25   30

Ile Xaa Leu Lys Arg Thr Trp Glu Lys Leu Leu Leu Gly
        35   40   45

<210> 1486
<211> 140
<212> PRT
<213> Homo sapiens

<400> 1486
Pro Arg Val Arg Arg Ala Glu Trp Leu Cys Gly Arg Val Ser Glu Thr
1   5   10   15

Gly Ser Ala Cys Ser Met Ala Asp Gln Leu Thr Glu Glu Gln Ile Ala
            20   25   30

Glu Phe Lys Glu Ala Phe Ser Leu Phe Asp Lys Asp Gly Asp Gly Thr
        35   40   45

Ile Thr Thr Lys Glu Leu Gly Thr Val Met Arg Ser Leu Gly Gln Asn
    50   55   60

Pro Thr Glu Ala Glu Leu Gln Asp Met Ile Asn Glu Val Asp Ala Asp
65   70   75   80

Gly Asn Gly Thr Ile Asp Phe Pro Glu Phe Leu Thr Met Met Ala Arg
                85   90   95

Lys Met Lys Asp Thr Asp Ser Glu Glu Glu Ile Arg Glu Ala Phe Arg
            100   105   110

Val Phe Asp Lys Asp Gly Asn Gly Tyr Ile Ser Ala Ala Glu Leu Arg
        115   120   125

His Val Met Thr Asn Leu Gly Arg Glu Val Asn Arg
    130   135   140

<210> 1487
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1487
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Xaa Leu Gly Arg Asn Trp Ala Xaa Phe Thr Gly Lys Xaa Val Gly Xaa
  1               5                  10                  15

Ala Ser Xaa Asn Val Tyr Val His Ile Pro His Leu Arg Asn Ser His
             20                  25                  30

Glu Lys Xaa Ser
         35
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<210> 1488
<211> 34
<212> PRT

<213> Homo sapiens

<400> 1488
Ser Gly Pro Leu Trp Ile Leu Gly Asp Val Phe Ile Gly Arg Tyr Tyr
1 5 10 15

Thr Val Phe Asp Arg Asp Asn Asn Arg Val Gly Phe Ala Glu Ala Ala
20 25 30

Arg Leu

<210> 1489
<211> 160
<212> PRT
<213> Homo sapiens

<220>
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<222> (4)
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<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (160)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1489
Pro Thr Asn Xaa Xaa Lys Ser Xaa Glu Leu His Arg Gly Gly Gly Arg
1 5 10 15

Ser Arg Thr Ser Gly Ser Pro Gly Leu Gln Glu Phe Gly Thr Ser Thr
20 25 30

Gln Arg Pro Val Asp Ile Val Phe Leu Leu Asp Gly Ser Glu Arg Leu
35 40 45

Gly Glu Gln Asn Phe His Lys Ala Arg Arg Phe Val Glu Gln Val Ala
50 55 60

Arg Arg Leu Thr Leu Ala Arg Arg Asp Asp Asp Pro Leu Asn Ala Arg
65 70 75 80

Val Ala Leu Leu Gln Phe Gly Gly Pro Gly Glu Gln Gln Val Ala Phe
85 90 95

Pro Leu Ser His Asn Leu Thr Ala Ile His Glu Ala Leu Glu Thr Thr
100 105 110

Gln Tyr Leu Asn Ser Phe Ser His Val Gly Ala Gly Val Val His Ala
115 120 125

Ile Asn Ala Ile Val Arg Ser Pro Arg Gly Gly Ala Arg Arg His Ala
130 135 140

Glu Leu Pro Ser Trp Ser Ser Arg Thr Ala Ser Arg Ala Thr Thr Xaa
145 150 155 160

<210> 1490
<211> 105
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
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<400> 1490
Ala Gln Met Gly Met Leu Lys Gly Pro Leu Leu Asn Lys Phe Leu Thr
1 5 10 15

Thr Ala Lys Asp Lys Asn Arg Trp Glu Asp Xaa Gly Lys Gln Leu Tyr
20 25 30

Asn Val Glu Ala Thr Ser Tyr Xaa Leu Xaa Ala Leu Leu Gln Leu Lys
35 40 45

Xaa Phe Asp Phe Val Pro Pro Val Val Xaa Xaa Leu Asn Xaa Gln Arg
50 55 60

Xaa Tyr Gly Gly Gly Tyr Gly Ser Thr Gln Ala Thr Phe Met Val Phe
65 70 75 80

Gln Xaa Leu Ala Gln Xaa Gln Lys Asp Gly Pro Asp His Gln Ala Leu
85 90 95

Asn Leu Xaa Val Xaa Leu Gln Met Leu
100 105

<210> 1491
<211> 125
<212> PRT
<213> Homo sapiens

<400> 1491
Arg Asn Thr Leu Ile Ile Tyr Leu Asp Lys Val Ser His Ser Glu Asp
1 5 10 15

Asp Cys Leu Ala Phe Lys Val His Gln Tyr Phe Asn Val Glu Leu Ile
20 25 30

Gln Pro Gly Ala Val Lys Val Tyr Ala Tyr Tyr Asn Leu Glu Glu Ser
35 40 45

Cys Thr Arg Phe Tyr His Pro Glu Lys Glu Asp Gly Lys Leu Asn Lys
50 55 60

Leu Cys Arg Asp Glu Leu Cys Arg Cys Ala Glu Glu Asn Cys Phe Ile
65 70 75 80

Gln Lys Ser Asp Asp Lys Val Thr Leu Glu Glu Arg Leu Asp Lys Ala
85 90 95

Cys Glu Pro Gly Val Asp Tyr Val Tyr Lys Thr Arg Leu Ala Arg Phe
100 105 110

Lys Leu Ser Asn Asp Phe Asp Arg Val His His Gly His
115 120 125

<210> 1492
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (62)

<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1492
Arg Pro Thr Arg Pro Ala Leu Ser Ile Ile Ala Leu Glu Ile Gln Ala
1 5 10 15

Gln Lys Cys Val Glu Leu Thr Glu Gly Ile Glu Cys Leu Gln Thr His
20 25 30

Ser Lys Ile Asn Gly Arg Asp Leu Thr Phe Trp Gln Glu Leu Val Ser
35 40 45

Lys Cys Leu Thr Glu Tyr Ser Ser Lys Gln Ser Gly Ser Xaa Pro Asn
50 55 60

Val Pro Glu Val
65

<210> 1493
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (14)
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<220>
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<222> (17)
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<222> (29)
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<222> (52)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (55)
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<221> SITE
<222> (62)
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<220>
<221> SITE
<222> (63)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1493
Glu Glu Ile Gln Lys His Asn His Ser Lys Ser Thr Trp Xaa Asp Pro
1 5 10 15

Xaa Thr Thr Arg Cys Thr Asn Leu Thr Lys Phe Leu Xaa Glu Ala Ser
20 25 30

Leu Val Gly Glu Glu Val Leu Arg Gly Thr Ser Leu Glu Val Thr Leu
35 40 45

Leu Glu Glu Xaa Leu Arg Xaa Val Arg Gly Thr Phe Thr Xaa Xaa Pro
50 55 60

Lys Gly Lys Leu Phe Pro Lys Thr Phe Xaa
65 70

<210> 1494
<211> 54
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (46)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1494
Asp Ala Thr Ser Pro Ile Ile Glu Glu Leu Ile Thr Phe His Asp His
1 5 10 15

Ala Leu Ile Ile Ile Phe Leu Ile Cys Phe Leu Val Leu Tyr Ala Leu
20 25 30

Phe Leu Thr Leu Thr Thr Lys Leu Thr Asn Thr Asn Ile Xaa Asp Ala
35 40 45

Xaa Glu Ile Glu Thr Val
50

<210> 1495
<211> 38
<212> PRT
<213> Homo sapiens

<400> 1495
Phe Phe Gly His Pro Glu Val Tyr Ile Leu Ile Leu Pro Gly Phe Gly
1 5 10 15

Ile Ile Ser His Ile Val Thr Tyr Tyr Ser Gly Lys Lys Glu Pro Phe
20 25 30

Gly Tyr Ile Gly Met Val
35

<210> 1496
<211> 46
<212> PRT
<213> Homo sapiens

<400> 1496
Ala Phe Tyr His Ser Ser Leu Ala Pro Thr Pro Gln Leu Gly Gly His
1 5 10 15

Trp Pro Pro Thr Gly Ile Thr Pro Leu Asn Pro Leu Glu Val Pro Leu
20 25 30

Leu Asn Thr Ser Val Leu Leu Ala Ser Gly Val Ser Ile Thr
35 40 45

<210> 1497
<211> 60
<212> PRT
<213> Homo sapiens

<400> 1497

Ala Gln Val Gly Leu Gln Asp Ala Thr Ser Pro Ile Ile Glu Glu Leu
1 5 10 15

Ile Thr Phe His Asp His Ala Leu Ile Ile Ile Phe Leu Ile Cys Phe
20 25 30

Leu Val Leu Tyr Ala Leu Phe Leu Thr Leu Thr Thr Lys Leu Thr Asn
35 40 45

Thr Asn Ile Ser Asp Ala Gln Glu Ile Glu Thr Val
50 55 60

<210> 1498
<211> 45
<212> PRT
<213> Homo sapiens

<400> 1498
Thr Tyr Glu Tyr Thr Asp Tyr Gly Gly Leu Ile Phe Asn Ser Tyr Ile
1 5 10 15

Leu Pro Pro Leu Phe Leu Glu Pro Gly Asp Leu Arg Leu Leu Asp Gly
20 25 30

Asp Asn Arg Val Val Leu Pro Ile Glu Ala Pro Phe Val
35 40 45

<210> 1499
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<212> PRT
<213> Homo sapiens

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<400> 1499
His Arg Leu Asp Phe Leu Gln Leu Met Ile Asp Ser Gln Asn Ser Lys
1 5 10 15

Glu Thr Glu Ser His Lys Ala Leu Ser Asp Leu Glu Leu Ala Ala Gln
20 25 30

Ser Ile Ile Phe Ile Phe Ala Gly Tyr Glu Thr Thr Ser Ser Val Leu
35 40 45

Ser Phe Thr Leu Tyr Glu Leu Ala Thr His Pro Asp Val Gln Xaa Lys
50 55 60

Leu Gln Lys Gly Asp
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<210> 1500
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<400> 1500
Arg Leu Thr Ser Thr Ala Cys Ala Glu Ser Trp Asp Glu Leu Thr Leu
1 5 10 15

Ala Arg Xaa Asp Leu Glu Xaa Gln Ile Glu Gly Leu Asn Glu Xaa Ala
20 25 30

Ser Leu Thr
35

<210> 1501
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Phe Xaa Ala Pro Ser Arg Ile Ser Ala Trp Xaa Gly Pro Pro Ala Ser
1 5 10 15

Thr Pro Ala Ser Thr Met Ser Ile Lys Val Thr Gln Lys Ser Tyr Lys
20 25 30

Xaa Ser Thr Ser Ser Pro Arg Ala Phe Ser Ser Arg Ser Tyr Thr Asn
35 40 45

Xaa Pro Gly Ser Arg Ile Asn Xaa Ser Xaa Phe Ser Arg Ile Gly Ser
50 55 60

Ser Asn Xaa Xaa Ser Gly Leu Gly Gly Gly Tyr Xaa Gly Ala Ser Xaa
65 70 75 80

Met Xaa Gly Ile Thr Ala Val Thr Val Asn Gln Ser Leu Leu Xaa Pro
85 90 95

Leu Xaa Leu Glu Val Asp Pro Asn Ile Gln Ala Val Arg Thr Gln Glu
100 105 110

Lys Glu Gln Ile Xaa Thr Leu Asn Asn Lys Phe Ala Ser Ser
115 120 125

<210> 1502
<211> 84
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<213> Homo sapiens

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Gln Arg Asn Ser Xaa Gly Ser Arg Thr Xaa Xaa Ser Arg Xaa Xaa Cys
1   5   10   15

Lys Xaa Val Ala Met Phe Ser Trp Asp Pro Xaa Leu Val Xaa Gly Gly
            20   25   30

Gly Ala Ser Lys Met Ala Val Ala His Ala Leu Xaa Glu Lys Ser Xaa
        35   40   45

Ala Met Asp Trp Cys Gly Asn Asn Gly His Thr Gly Leu Leu Xaa Arg
    50   55   60

Ala Leu Xaa Val His Ser Ser Xaa Pro Trp Ile Xaa Lys Leu Trp Gly
65   70   75   80

Xaa Ser His His

<210> 1503
<211> 70
<212> PRT
<213> Homo sapiens

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<222> (70)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1503
Val Gly Val Leu Gly Leu Asp Leu Trp Gln Val Lys Ser Gly Thr Ile
1 5 10 15

Phe Asp Asn Phe Leu Ile Thr Asn Asp Glu Ala Tyr Ala Glu Glu Phe
20 25 30

Gly Asn Glu Thr Trp Gly Val Thr Lys Ala Ala Glu Lys Gln Met Lys
35 40 45

Asp Lys Gln Asp Glu Glu Gln Arg Leu Lys Glu Glu Glu Glu Asp Lys
50 55 60

Lys Arg Lys Glu Xaa Xaa
65 70

<210> 1504
<211> 42
<212> PRT
<213> Homo sapiens

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<400> 1504
Asn Thr Leu Xaa Tyr Xaa Met Lys Ala Thr Xaa Ile Leu Leu Leu Xaa
1 5 10 15

Ala Gln Leu Ser Trp Ala Gly Pro Phe His Gln Thr Gly Leu Leu Asp
20 25 30

Ser Met Leu Glu His Glu Ala Tyr Xaa Ile
35 40

<210> 1505
<211> 72
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1505
Xaa His Xaa Asp Cys Ser Xaa Pro Ile Val Ala Ala Gly Val Gly Glu
1 5 10 15

Phe Glu Ala Gly Ile Ser Lys Asn Gly Gln Thr Arg Glu His Ala Leu
20 25 30

Leu Ala Tyr Thr Leu Gly Val Lys Gln Leu Ile Val Gly Xaa Asn Lys
35 40 45

Met Asp Ser Thr Glu Pro Pro Tyr Ser Gln Lys Arg Tyr Glu Glu Ile
50 55 60

Xaa Lys Glu Val Ser Thr Tyr Xaa
65 70

<210> 1506
<211> 23
<212> PRT
<213> Homo sapiens

<400> 1506
Ala Glu Thr Arg Lys Arg Lys Gly Leu Lys Glu Gly Ile Pro Ala Leu
1 5 10 15

Asp Asn Phe Leu Asp Lys Leu
20

<210> 1507
<211> 87
<212> PRT
<213> Homo sapiens

<220>
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<222> (79)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1507
Lys Leu Pro Leu Lys Ala Lys Met Gly Lys Glu Lys Thr His Ile Asn
1 5 10 15

Ile Val Val Ile Gly His Val Asp Ser Gly Lys Ser Thr Thr Thr Gly
20 25 30

His Leu Ile Tyr Lys Cys Gly Gly Ile Asp Lys Arg Thr Ile Glu Lys
35 40 45

Phe Glu Lys Glu Ala Ala Glu Met Gly Lys Gly Ser Phe Lys Tyr Ala
50 55 60

Trp Val Leu Asp Lys Leu Lys Ala Glu Arg Glu Arg Gly Ile Xaa Ile
65 70 75 80

Gly Tyr Leu Leu Val Glu Ile
85

<210> 1508
<211> 110
<212> PRT
<213> Homo sapiens

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<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1508
Pro Asp Pro Xaa Ile Phe Ala Pro Pro Ile Ser Ala Pro Pro Pro Ser
1 5 10 15

Ser Gly Thr Arg Asp Arg Ser Gln Arg Ser Leu Asp His Tyr Glu Pro
20 25 30

Pro Val Gln Pro Arg Gly Pro Cys Pro Arg Ser Phe Glu Leu Leu Val
35 40 45

Arg Ala Val Gly Ala Ala Ala Ala Ala Asp Ala Ala Arg Ala His Arg
50 55 60

Gln Arg Trp Ser Cys Arg Cys Cys Val Xaa Arg Ala Ala Leu Pro Phe
65 70 75 80

Val Tyr Arg Pro Arg Lys Glu Ser Ile Pro Lys Met Ile Ser Asn Xaa
85 90 95

Gln Val Xaa Ala Ile Gly Pro Thr Val Leu Gln Xaa Gly Lys
100 105 110

<210> 1509
<211> 60
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1509
Ser Phe Val Glu Leu Pro Leu Ala Ser Ile Val Ser Leu His Ala Ser
1 5 10 15

Ser Xaa Gly Gly Arg Leu Gln Thr Ser Pro Xaa Pro Ile Gln Xaa Thr
20 25 30

Pro Pro Lys Asp Thr Cys Ser Pro Xaa Leu Xaa Met Ser Leu Xaa Pro
35 40 45

Xaa Lys Leu Cys Arg Arg Arg His Gly Pro Trp Tyr
50 55 60

<210> 1510
<211> 116
<212> PRT
<213> Homo sapiens

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<222> (108)
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<222> (115)
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<400> 1510
Gly Thr Ser Ser Ser Gln Arg Phe Tyr Lys Glu Asn Leu Gly Gln Gly
1 5 10 15

Trp Met Thr Gln Lys His Glu Arg Met Lys Val Tyr Val Pro Thr Gly
20 25 30

Phe Ser Ala Phe Pro Phe Glu Leu Leu His Thr Pro Glu Lys Trp Val
35 40 45

Arg Phe Lys Tyr Pro Lys Leu Ile Ser Tyr Ser Tyr Met Val Arg Gly

50 55 60

Gly His Phe Ala Ala Phe Glu Glu Pro Glu Leu Leu Ala Gln Asp Ile
65 70 75 80

Arg Lys Phe Leu Ser Val Leu Glu Arg His Xaa Xaa Thr Pro Leu Pro
85 90 95

Pro Leu Ala Thr Ser Pro His Asn Ala Leu Gln Xaa Phe Leu Gly Glu
100 105 110

Asp Asn Xaa Phe
115

<210> 1511
<211> 156
<212> PRT
<213> Homo sapiens

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<222> (11)
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<400> 1511
Arg Glu Gln Lys Leu Glu Leu His Arg Gly Xaa Gly Arg Ser Arg Thr
1 5 10 15

Ser Gly Ser Pro Gly Leu Gln Glu Phe Gly Thr Arg Asp Arg Gly Gly
20 25 30

Phe Pro Pro Arg Gly Pro Arg Gly Ser Arg Gly Asn Pro Ser Gly Gly
35 40 45

Gly Asn Val Gln His Arg Ala Gly Asp Trp Gln Cys Pro Asn Pro Ser
50 55 60

Ile Gly Asp Phe Cys Cys Asp Val Ile Val Cys Arg Gly Cys Gly Asn
65 70 75 80

```
Gln Asn Phe Ala Trp Arg Thr Glu Cys Asn Gln Cys Gly Asp Arg Gly
                85                  90                  95

Arg Gly Gly Pro Gly Gly Met Xaa Gly Gly Arg Gly Gly Leu Met Asp
            100                 105                 110

Arg Gly Gly Pro Gly Gly Met Phe Arg Gly Gly Arg Gly Gly Asp Arg
        115                 120                 125

Gly Gly Phe Arg Gly Gly Arg Gly Met Asp Arg Gly Gly Phe Xaa Gly
    130                 135                 140

Gly Arg Arg Gly Gly Pro Gly Gly Pro Leu Asp Leu
145                 150                 155
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<210> 1512
<211> 102
<212> PRT
<213> Homo sapiens

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<400> 1512

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Pro Met Arg Arg Pro Arg Gly Glu Pro Ala Pro Gly Pro Arg Asp Arg
  1               5                  10                  15

Leu Arg Glu Arg Pro Ala Gln Gly Pro Gly Ser His Val Arg Val Ala
             20                  25                  30

Pro Leu Ala Thr Val Asn Ile Leu Xaa Ser Leu Cys Gln Leu Arg Cys
         35                  40                  45

Leu Pro Phe Xaa Ala Leu His Phe Val Xaa Ser Pro Gly Phe Ile Xaa
     50                  55                  60

Tyr Ile Ser Gly Thr Pro His Ala Leu Ile Val Arg Arg Tyr Leu Ser
 65                  70                  75                  80

Leu Leu Asp Thr Ala Val Glu Leu Xaa Leu Pro Arg Tyr Arg Gly Pro
                 85                  90                  95

Arg Leu Pro Arg Xaa Gln
            100
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<210> 1513
<211> 139
<212> PRT
<213> Homo sapiens

<220>
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<222> (131)
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<400> 1513

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Glu Thr Glu Arg Gly Phe Glu Glu Leu Pro Leu Cys Ser Cys Arg Met
  1               5                  10                  15

Glu Ala Pro Lys Ile Asp Ser Ile Ser Glu Arg Ala Gly His Lys Cys
             20                  25                  30

Met Ala Thr Glu Ser Val Asp Gly Glu Leu Ser Gly Cys Asn Ala Ala
         35                  40                  45

Ile Leu Lys Arg Glu Thr Met Arg Pro Ser Ser Arg Val Ala Leu Met
     50                  55                  60

Val Leu Cys Glu Thr His Arg Ala Arg Met Val Lys His His Cys Cys
 65                  70                  75                  80
```

```
Pro Gly Cys Gly Tyr Phe Cys Thr Ala Gly Thr Phe Leu Glu Cys His
                85                  90                  95

Pro Asp Phe Arg Val Ala His Arg Phe His Lys Ala Cys Val Ser Gln
            100                 105                 110

Leu Asn Gly Met Val Phe Cys Pro His Cys Gly Glu Asp Thr Ser Glu
        115                 120                 125

Ala Gln Xaa Val Thr Ile Pro Gly Val Thr Gly
    130                 135
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<210> 1514
<211> 72
<212> PRT
<213> Homo sapiens

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<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1514
Ile Arg His Glu Ser Ile Ser Gly Ala Ser Xaa Lys Asp Ile Val His
1 5 10 15

Ser Gly Xaa Ala Tyr Thr Xaa Glu Xaa Ser Ala Arg Gln Xaa Met Arg
20 25 30

Thr Ala Met Lys Xaa Asn Leu Gly Xaa Asp Leu Arg Thr Ala Ser Tyr
35 40 45

Xaa Asn Ala Ile Xaa Xaa Val Phe Lys Val Tyr Xaa Glu Ala Gly Val
50 55 60

Thr Phe Thr Xaa Met Xaa His Gly
65 70

<210> 1515
<211> 88
<212> PRT
<213> Homo sapiens

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<222> (85)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1515
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Leu Tyr Pro Pro Ala Cys Ser Ala Thr Arg Thr Pro Ser Thr Met Thr
  1               5                  10                  15

Thr Ser Ala Ser Ser His Leu Asn Lys Gly Ile Lys Gln Val Tyr Met
             20                  25                  30

Ser Leu Pro Gln Gly Glu Lys Val Gln Ala Met Tyr Ile Trp Ile Asp
         35                  40                  45

Gly Thr Gly Glu Gly Leu Arg Cys Lys Thr Arg Thr Leu Asp Ser Glu
     50                  55                  60

Pro Lys Cys Val Glu Glu Leu Pro Glu Trp Asn Phe Asp Gly Ser Ser
 65                  70                  75                  80

Thr Xaa Gln Ser Xaa Gly Ser Ser
                 85
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<210> 1516
<211> 105
<212> PRT
<213> Homo sapiens

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<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1516
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Gly Arg Glu Ser Gln Asp Thr Xaa Phe Xaa Xaa Leu Val Glu Arg Val
  1               5                  10                  15

Ile Gln Gln Leu Glu Gly Ala Phe Ala Leu Xaa Phe Lys Ser Val His
             20                  25                  30

Phe Pro Gly Gln Ala Xaa Gly Thr Arg Arg Gly Ser Pro Leu Leu Ile
         35                  40                  45

Gly Val Arg Ser Glu His Lys Leu Ser Thr Asp His Ile Pro Ile Leu
     50                  55                  60

Tyr Arg Thr Gly Lys Asp Lys Lys Gly Ser Cys Asn Leu Ser Arg Val
 65                  70                  75                  80
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Asp Ser Thr Thr Cys Leu Xaa Pro Xaa Glu Glu Lys Ala Xaa Glu Tyr
85 90 95

Tyr Phe Ala Ser Asp Ala Xaa Ala Ala
100 105

<210> 1517
<211> 121
<212> PRT
<213> Homo sapiens

<220>
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<222> (2)
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<220>
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<400> 1517
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Gly Xaa Glu Lys Arg Glu Arg Glu Arg Glu Arg Leu Val Ile Arg Gln
  1               5                  10                  15

Xaa Pro Xaa Val Gln Xaa Leu Gln Ala Tyr Lys Pro Arg Glu Asn Asp
             20                  25                  30

Xaa Leu Ala Leu Glu Lys Ala Asp Val Val Met Val Thr His Gln Ser
         35                  40                  45

Ser Ala Arg Leu Ala Gly Gly Arg Glu Ala Leu Arg Arg Gly Ala Arg
     50                  55                  60

Leu Val Ser Cys Asp Ser Xaa Xaa Ser Ser Phe Pro Thr Gln Arg Ser
 65                  70                  75                  80

Val Thr Gln Asn Leu Lys Gly Ser Phe Ile Glu Cys Lys Thr Cys Gln
                 85                  90                  95

Thr Thr Ala Xaa Gly Asn Ser Lys Pro Xaa Phe Ser Xaa Xaa Glu Gly
            100                 105                 110

Val Phe Val Ser Trp Lys Asn Lys Leu
        115                 120
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<210> 1518
<211> 146
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
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<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (132)
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<222> (135)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1518
Arg Gly Pro Ala Gln Arg Gly Glu Gly Ala Arg Glu Ala Asn Lys Lys
1 5 10 15

Ile Glu Lys Gln Leu Gln Lys Asp Lys Gln Val Tyr Arg Ala Thr His
20 25 30

Arg Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr Ile Val
35 40 45

Lys Gln Met Arg Ile Leu His Val Asn Gly Phe Asn Gly Asp Ser Glu
50 55 60

Lys Ala Thr Lys Val Gln Xaa Ile Lys Asn Asn Leu Lys Glu Ala Ile
65 70 75 80

Glu Thr Ile Val Ala Ala Met Ser Asn Leu Val Pro Pro Val Glu Leu
85 90 95

Ala Asn Pro Glu Asn Gln Phe Arg Val Asp Tyr Ile Leu Ser Val Met
100 105 110

Asn Val Pro Asp Phe Xaa Phe Pro Pro Glu Phe Tyr Glu His Ala Lys
115 120 125

Ala Leu Trp Xaa Asp Glu Xaa Val Arg Xaa Cys Tyr Glu Arg Ser Asn
130 135 140

Glu Tyr
145

<210> 1519
<211> 137
<212> PRT
<213> Homo sapiens

<220>
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<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1519
Asp Ser Gln Arg Gln Ala Thr Lys Asp Ala Gly Val Ile Ala Gly Leu
1 5 10 15

Asn Val Leu Arg Ile Ile Asn Glu Pro Thr Ala Ala Ala Ile Ala Tyr
20 25 30

Gly Leu Asp Arg Thr Gly Lys Gly Glu Arg Asn Val Leu Ile Phe Asp
35 40 45

Leu Gly Gly Gly Thr Phe Asp Val Ser Ile Leu Thr Ile Asp Asp Gly
50 55 60

Ile Phe Glu Val Lys Ala Thr Xaa Gly Asp Thr His Leu Gly Gly Glu
65 70 75 80

Asp Phe Asp Asn Arg Leu Val Asn His Phe Val Glu Glu Phe Lys Arg
85 90 95

Lys His Lys Lys Asp Ile Ser Gln Asn Lys Arg Ala Val Arg Arg Leu
100 105 110

Arg Thr Ala Ala Arg Gly Pro Arg Gly Pro Cys Arg Pro Ala Pro Arg
115 120 125

Pro Ala Trp Arg Ser Thr Ser Leu Phe
130 135

<210> 1520
<211> 100
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (99)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1520
Cys Arg Lys Ser Ser Trp Lys Arg Trp Trp Pro Gln Ser Lys Leu Xaa
1 5 10 15

Thr Arg Xaa Ile Val Thr Ile Gly Ile Lys Ala Met Ala Thr Met Asp
20 25 30

Ile Thr Ala Lys Val Thr Val Val Met Glu Asp Met Xaa Tyr Thr Gly
35 40 45

Tyr Asn Asn Tyr Tyr Gly Tyr Gly Asp Tyr Ser Asn Gln Gln Ser Gly
50 55 60

Tyr Gly Lys Val Ser Arg Arg Gly Gly His Gln Asn Ser Tyr Lys Pro
65 70 75 80

Tyr Leu Asn Tyr Ser Ile Cys Asn Leu Ser Pro Thr Gly Gly Glu Ala
85 90 95

Tyr Phe Xaa Ile
100

<210> 1521
<211> 129
<212> PRT
<213> Homo sapiens

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<222> (72)
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<222> (123)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1521
Asp Ala Trp Ala Leu Ala Pro Gly Pro Val Leu Phe Ser Asn Met Val
1 5 10 15

Cys Leu Lys Phe Pro Gly Ser Ser Cys Met Ala Ala Leu Thr Val Thr
20 25 30

Leu Met Val Leu Asn Ser Pro Leu Ala Leu Ala Gly Asp Thr Arg Pro
35 40 45

Arg Phe Leu Glu Gln Val Lys His Glu Cys His Phe Phe Asn Gly Thr
50 55 60

Glu Arg Val Arg Phe Leu Asp Xaa Tyr Phe Tyr His Gln Glu Glu Tyr
65 70 75 80

Val Arg Phe Asp Ser Asp Val Gly Glu Tyr Arg Ala Val Thr Xaa Leu
85 90 95

Gly Arg Pro Asn Ser Glu Tyr Trp Asn Ser Gln Lys Asp Xaa Xaa Asp
100 105 110

Arg Ser Gly Pro Arg Trp Thr Pro Thr Ala Xaa Thr Leu Arg Gly Trp
115 120 125

Val

<210> 1522
<211> 113
<212> PRT
<213> Homo sapiens

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<400> 1522
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Xaa Xaa Thr Asp Ser Xaa Arg Pro Asp Ser Arg Val Asp Pro Arg Val
  1               5                  10                  15

Arg Glu Val Thr Asp Tyr Ala Ile Ala Arg Arg Ile Val Asp Leu His
             20                  25                  30

Ser Arg Ile Glu Glu Ser Ile Xaa Asn Ile Tyr Xaa Leu Asp Asp Ile
         35                  40                  45

Arg Arg Tyr Leu Xaa Tyr Ala Arg Lys Xaa Lys Pro Lys Asn Ser Lys
     50                  55                  60

Xaa Ser Xaa Asp Phe Ile Val Glu Gln Xaa Lys His Leu Arg Pro Xaa
 65                  70                  75                  80

Asp Gly Phe Trp Ser Ser Pro Val Phe Xaa Glu Gly Xaa Ser Cys Gly
                 85                  90                  95

Xaa Ile Glu Gly Leu Gly Ser Val Ser Leu Gly Ser Gln Xaa Leu Arg
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100 105 110

Val

<210> 1523
<211> 32
<212> PRT
<213> Homo sapiens

<220>
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<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (31)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1523
Pro Cys Lys Gly Ser Ile Ile Thr Trp Ser Leu Ile Arg Asp Leu Xaa
1 5 10 15

Glu Trp Leu His Glu Gly Gln Leu Ala Leu Thr Phe Asn Gln Xaa Asn
20 25 30

<210> 1524
<211> 28
<212> PRT
<213> Homo sapiens

<400> 1524
Pro Cys Lys Gly Ser Ile Ile Thr Cys Ser Leu Asn Arg Asp Leu Tyr
1 5 10 15

Glu Trp Leu His Glu Gly Ser Ala Val Ser Tyr Phe
20 25

<210> 1525
<211> 92
<212> PRT

<213> Homo sapiens

<220>
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<222> (1)
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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (92)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1525
Xaa Glu Gln Lys Leu Xaa Leu His Arg Gly Gly Gly Arg Ser Arg Thr
1 5 10 15

Ser Gly Ser Pro Xaa Leu Xaa Glu Phe Gly Thr Ser Gly Thr Arg Pro
20 25 30

Cys Gly Val Tyr Thr Pro Arg Cys Gly Ser Gly Leu Leu Cys Tyr Pro
35 40 45

Pro Arg Gly Val Glu Lys Pro Leu His Thr Leu Met His Gly Gln Gly
50 55 60

Val Cys Met Glu Leu Ala Xaa Ile Glu Ala Xaa Xaa Glu Ser Leu Xaa
65 70 75 80

Pro Ser Asp Lys Asp Glu Gly Asp His Pro Asn Xaa
85 90

<210> 1526
<211> 154
<212> PRT
<213> Homo sapiens

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<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (118)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1526
Xaa Glu Pro Ser Pro Gly Ile Phe Arg Trp Phe His Leu Val Asn Arg
1 5 10 15

Thr Glu Gln Arg Glu Leu Thr Met Glu Phe Gly Leu Ser Trp Leu Phe
20 25 30

Leu Val Ala Ile Leu Lys Gly Val Gln Cys Glu Val Gln Leu Val Glu
35 40 45

Ser Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys
50 55 60

Thr Val Ser Gly Phe Thr Phe Arg Asn Tyr Ala Met Ser Trp Val Arg
65 70 75 80

Gln Gly Pro Gly Lys Gly Leu Glu Trp Val Ser Ala Ile Asp Gly Ser
85 90 95

Gly Tyr Asn Thr Tyr Tyr Glu Arg Ser Leu Gln Gly Arg Phe Ser Val
            100   105   110

Ser Arg Asp Asn Ser Xaa Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu
        115   120   125

Gly Ala Glu Asp Thr Ala Ile Tyr Tyr Cys Ala Lys Thr Glu Arg Met
    130   135   140

Gly Thr Gly Trp Tyr Gly Arg Asn Asp Tyr
145   150

<210> 1527
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (95)
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<220>
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<220>
<221> SITE
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1527
Gly Lys Leu Val Arg Leu Gln Val Pro Val Arg Asn Ser Arg Val Asp
  1   5   10   15

Pro Arg Val Arg Thr Val Thr Pro Gly Glu Thr Ala Ser Ile Ser Cys
             20   25   30

Arg Ser Ser Gln Thr Leu Leu His Val Asn Gly His Asn Tyr Leu Asp
         35   40   45

Trp Tyr Met Gln Lys Pro Gly Gln Pro Pro Gln Leu Val Val Tyr Arg
     50   55   60

```
Gly Ser Asn Arg Ala Ser Gly Val Pro Asp Arg Phe Ser Gly Gly Gly
 65                  70                  75                  80

Ser Gly Thr Asp Phe Thr Leu Arg Ile Thr Thr Val Glu Ala Xaa Asp
                85                  90                  95

Val Gly Val Tyr Tyr Cys Met Gln Ala Leu Gln Ser Pro Tyr Thr Phe
            100                 105                 110

Gly Gln Gly Thr Lys Leu Glu Ile Lys Arg Thr Val Gly Cys Thr Ile
        115                 120                 125

Xaa Leu His Leu Xaa Xaa Ile
    130                 135
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<210> 1528
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (117)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (137)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1528
Arg Glu Gln Lys Leu Glu Leu His Arg Gly Gly Gly Arg Ser Arg Thr
  1               5                  10                  15

Ser Gly Ser Pro Gly Leu Gln Glu Phe Gly Thr Ser Gly Trp Ala Leu
            20                  25                  30

Arg Ile Ser Arg Phe Leu Pro Gly Phe His Ser Phe Ala Pro Cys Thr
        35                  40                  45

Val Ala Pro Ser Leu Arg Ala Gln Pro Ala Lys Gln Arg Ala Pro Val
    50                  55                  60

Ala Gly Val Met Gln Arg Ala Arg Pro Thr Leu Trp Ala Ala Ala Leu
 65                  70                  75                  80

Thr Leu Leu Val Leu Leu Arg Gly Pro Pro Val Ala Arg Ala Gly Ala
                85                  90                  95
```

Ser Ser Gly Gly Leu Gly Pro Val Val Arg Cys Glu Pro Cys Asp Ala
100 105 110

Arg Ala Leu Ala Xaa Cys Ala Pro Ser Ala Arg Arg Val Arg Arg Asn
115 120 125

Leu Val Arg Gln Ala Gly Leu Ala Xaa Ala Ala
130 135

<210> 1529
<211> 135
<212> PRT
<213> Homo sapiens

<400> 1529
Trp Ile Pro Arg Ala Ala Gly Ile Arg His Glu Ile Asp Asp Thr Asn
1 5 10 15

Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu Glu
20 25 30

Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu Gln
35 40 45

Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro Lys
50 55 60

Ser Gln Asp Leu Ala Lys Ile Met Ala Asp Ile Arg Ala Gln Tyr Asp
65 70 75 80

Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser Gln
85 90 95

Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val
100 105 110

Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser
115 120 125

Leu Glu Ile Asp Leu Gly Leu
130 135

<210> 1530
<211> 132
<212> PRT
<213> Homo sapiens

<400> 1530
Trp Ile Pro Arg Ala Ala Gly Ile Arg His Glu Gln Val Pro Ala Arg
1   5   10   15

Lys Lys Arg Pro Lys Arg Leu Arg Thr Gly Asn Met Val Arg Ser Gly
            20   25   30

Asn Lys Ala Ala Val Val Leu Cys Met Asp Val Gly Phe Thr Met Ser
        35   40   45

Asn Ser Ile Pro Gly Ile Glu Ser Pro Phe Glu Gln Ala Lys Lys Val
    50   55   60

Ile Thr Met Phe Val Gln Arg Gln Val Phe Ala Glu Asn Lys Asp Glu
65   70   75   80

Ile Ala Leu Val Leu Phe Gly Thr Asp Gly Thr Asp Asn Pro Leu Ser
                85   90   95

Gly Gly Asp Gln Tyr Gln Asn Ile Thr Val His Arg His Leu Met Leu
            100   105   110

Pro Asp Phe Asp Leu Leu Glu Asp Ile Glu Lys Gln Asn Pro Thr Arg
        115   120   125

Phe Ser Thr Gly
    130

<210> 1531
<211> 94
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
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<220>
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<222> (69)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (94)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1531
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Arg Lys Arg Leu Lys Gly Glu Glu Gln Lys Leu Leu Arg Asn Ala Arg
  1               5                  10                  15

Arg Xaa Gln Lys Met Ala Cys Gln Met Thr Xaa Asn His Ser Ser Val
             20                  25                  30

Ser Xaa Leu Lys Gly Ser Ser Leu Gln Asp Arg Arg Ala Ser Arg Phe
         35                  40                  45

Leu Ile Lys Ser Val Gln Lys Ser Ser Gly Val Gln Xaa Asp Pro Ser
     50                  55                  60

Ser Ser Ile Ser Xaa Pro Ser Leu Thr Ala Xaa Trp Ser Xaa Leu Pro
 65                  70                  75                  80

Trp His Leu Arg Gly Pro Lys Ala Ala Lys Thr Leu Lys Xaa
                 85                  90
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<210> 1532
<211> 153
<212> PRT
<213> Homo sapiens

<400> 1532
Gln Thr Thr Met Cys Tyr Gly Lys Cys Ala Arg Cys Ile Gly His Ser
1 5 10 15

Leu Val Gly Leu Ala Leu Leu Cys Ile Ala Ala Asn Ile Leu Leu Tyr
20 25 30

Phe Pro Asn Gly Glu Thr Lys Tyr Ala Ser Glu Asn His Leu Ser Arg
35 40 45

Phe Val Trp Phe Phe Ser Gly Ile Val Gly Gly Gly Leu Leu Met Leu
50 55 60

Leu Pro Ala Phe Val Phe Ile Gly Leu Glu Gln Asp Asp Cys Cys Gly
65 70 75 80

Cys Cys Gly His Glu Asn Cys Gly Lys Arg Cys Ala Met Leu Ser Ser
85 90 95

Val Leu Ala Ala Leu Ile Gly Ile Ala Gly Ser Gly Tyr Cys Val Ile
100 105 110

Val Ala Ala Leu Gly Leu Ala Glu Gly Pro Leu Cys Leu Asp Ser Leu
115 120 125

Gly Gln Trp Asn Tyr Thr Phe Ala Ser Thr Glu Gly Gln Val Pro Ser
130 135 140

Gly Tyr Leu His Met Val Arg Val His
145 150

<210> 1533
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1533
Leu Cys Leu Leu Arg Thr Thr Val Thr Glu Val Ser Arg Ala Phe Ser
1 5 10 15

Leu Leu Cys Lys Met Ala Thr Leu Lys Glu Lys Leu Ile Ala Pro Val
20 25 30

Ala Glu Glu Glu Ala Thr Val Pro Asn Asn Lys Ile Thr Val Val Gly
35 40 45

Val Gly Gln Val Gly Met Ala Cys Ala Ile Ser Ile Leu Gly Lys Ser
50 55 60

Leu Ala Asp Glu Leu Ala Leu Val Asp Val Leu Glu Asp Lys Leu Lys
65 70 75 80

Gly Glu Met Met Asp Leu Gln His Gly Ser Leu Phe Leu Gln Thr Pro
85 90 95

Lys Ile Leu Ala Asp Lys Asp Tyr Ser Val Thr Ala Asn Ser Lys Ile
100 105 110

Val Val Val Thr Ala Gly Val Arg Gln Gln Glu Gly Glu Ser Arg Leu
115 120 125

Asn Leu Val Gln Arg Asn Val Asn Val Phe Lys Phe Ile Ile
130 135 140

<210> 1534
<211> 67
<212> PRT
<213> Homo sapiens

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<221> SITE
<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (54)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (61)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1534
Ala His Cys His Ala Pro Pro Thr Thr Ala Arg Arg Ala Phe Pro Ile
1 5 10 15

Pro Phe Gly Ser Lys Ser Asn Met Ala Thr Leu Lys Asp Gln Leu Ile
20 25 30

Tyr Asn Leu Leu Lys Glu Glu Gln Thr Xaa Gln Asn Lys Ile Thr Xaa
35 40 45

Val Gly Val Gly Ala Xaa Gly Met Ala Cys Ala Ile Xaa Ile Leu Met
50 55 60

Lys Asp Leu
65

<210> 1535
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1535
Xaa Lys Lys Tyr Leu Gly Asp Xaa Ile Glu Gly Thr Pro Ala Gly Thr
1 5 10 15

Gly Pro Glu Phe Pro Gly Leu Leu Thr Cys Leu Leu Gln Leu Ile Met
20 25 30

Val Thr Asn Lys Ala Ile Ala Ser Gln Ile Ser Gln Ile Lys His Phe
35 40 45

Phe His Cys Ile Leu Val Val Val Cys Pro Asn Ser Ser Met Tyr Leu
50 55 60

Ile Met Ser Gly Ser Ile Leu His
65 70

<210> 1536
<211> 80
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (20)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<220>
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<222> (58)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (68)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1536
Gly Lys Ala Trp Gly Ser Glu Cys Glu Lys Cys Pro Leu Pro Gly Thr
1 5 10 15

Glu Ala Phe Xaa Glu Ile Cys Pro Ala Gly His Gly Tyr Thr Tyr Ala
20 25 30

Ser Ser Asp Ile Arg Leu Ser Met Arg Lys Ala Glu Xaa Glu Glu Leu
35 40 45

Ala Xaa Pro Pro Arg Glu Gln Gly Gln Xaa Ser Ser Trp Ala Leu Pro
50 55 60

Gly Pro Thr Xaa Lys Gln Pro Leu Arg Val Arg His Gly His Leu Ala
65 70 75 80

<210> 1537
<211> 137
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (58)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (137)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1537
Arg Lys Gln Cys Gln Asp Ser Lys Asp Ser Asn His Leu Pro Lys Met
1 5 10 15

Ser Leu Ser Ala Phe Thr Leu Phe Leu Ala Leu Ile Gly Gly Thr Ser
20 25 30

Gly Gln Tyr Tyr Asp Tyr Asp Phe Pro Leu Ser Ile Tyr Gly Gln Ser
35 40 45

Ser Pro Asn Cys Ala Pro Glu Cys Asn Xaa Pro Glu Ser Tyr Pro Ser
50 55 60

Ala Met Tyr Cys Asp Glu Leu Lys Leu Xaa Ser Val Pro Met Val Pro
65 70 75 80

Pro Gly Ile Lys Tyr Leu Tyr Leu Arg Asn Asn Gln Ile Asp His Ile
85 90 95

Asp Glu Lys Ala Phe Glu Asn Val Thr Asp Leu Gln Trp Leu Ile Leu
100 105 110

Asp His Asn Leu Leu Glu Asn Ser Lys Xaa Lys Gly Arg Val Phe Ser
115 120 125

Lys Leu Lys Gln Leu Xaa Lys Xaa Xaa
130 135

<210> 1538
<211> 144
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (134)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (137)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1538
Tyr Gln Val Tyr Ser Lys Ile Gln Ala Thr Asn Thr Trp Leu Phe Leu
1 5 10 15

Ser Ser Cys Asn Gly Asn Glu Thr Ser Leu Trp Asp Cys Lys Asn Trp
20 25 30

Gln Trp Gly Gly Leu Thr Cys Asp His Tyr Glu Glu Ala Lys Ile Thr
35 40 45

Cys Ser Ala His Arg Glu Pro Arg Leu Val Gly Gly Asp Ile Pro Cys
50 55 60

Ser Gly Arg Val Glu Val Lys His Gly Asp Thr Trp Gly Ser Ile Cys
65 70 75 80

Asp Ser Asp Phe Ser Leu Glu Ala Ala Ser Val Leu Cys Arg Glu Leu
85 90 95

Gln Cys Gly Thr Val Val Ser Ile Leu Gly Gly Ala His Phe Gly Glu
100 105 110

Gly Met Asp Arg Ser Gly Leu Lys Asn Ser Ser Val Glu Gly His Glu
115 120 125

Ser Pro Ser Phe Ile Xaa Pro Val Xaa Thr Pro Pro Lys Arg Asn Leu
130 135 140

<210> 1539
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1539
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Asn Met Ala Gly Val Glu Glu Val Ala Ala Ser Gly Ser His Leu Asn
 1               5                  10                  15

Gly Asp Leu Asp Pro Asp Asp Arg Glu Glu Gly Ala Ala Ser Thr Ala
             20                  25                  30

Glu Glu Xaa Ala Lys Lys Lys Arg Arg Lys Lys Lys Lys Ser Lys Gly
         35                  40                  45

Pro Ser Ala Gly Lys Glu Ser Phe Met Phe Ser Gln Ser Pro Pro Gly
     50                  55                  60

Thr Ala Glu Leu Phe Gly Ser Gly Pro Leu Arg Gly Pro Gly Pro Gly
 65                  70                  75                  80

Pro Gln Ser Pro Asp
                 85
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<210> 1540
<211> 36
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (9)
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1540
Gly Val Gly Phe Arg Glu Gly Thr Xaa Gly Ala Gln Thr Gln Arg Ile
1 5 10 15

Arg Xaa Arg Val Pro Xaa Asn Trp Lys Met Xaa Phe Glu Pro Ile Ser
20 25 30

Ser Thr Lys Phe
35

<210> 1541
<211> 144
<212> PRT
<213> Homo sapiens

<220>
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<400> 1541
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Arg Thr Xaa Ala Xaa Gly Glu Arg Ala Cys Arg Ser Thr Leu Val Asp
  1               5                  10                  15

Pro Lys Xaa Val Xaa Thr Val Phe Ser Leu Gly Ala Cys Met Glu Gly
             20                  25                  30

Leu Asn Ile Leu Leu Asn Arg Leu Leu Gly Ile Ser Leu Tyr Ala Glu
         35                  40                  45

Gln Pro Ala Lys Gly Glu Val Trp Ser Glu Asp Val Arg Lys Leu Ala
     50                  55                  60

Val Val His Glu Ser Glu Gly Leu Leu Gly Tyr Ile Tyr Cys Asp Phe
 65                  70                  75                  80

Phe Gln Arg Ala Asp Lys Pro His Gln Asp Cys His Phe Thr Ile Arg
                 85                  90                  95

Gly Gly Arg Leu Lys Gly Arg Trp Glu Thr Xaa Gln Leu Pro Val Val
            100                 105                 110

Ser Ser Tyr Ala Gly Ile Phe Pro Val Pro Xaa Arg Glu Phe Ser Asn
        115                 120                 125

Phe Gly Xaa Xaa Leu Gly Met Met Gly Lys Pro Phe Pro Gly Xaa Gly
    130                 135                 140
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<210> 1542
<211> 145
<212> PRT
<213> Homo sapiens

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1542
Ala Glu Arg Thr Pro Cys Arg Arg Pro Ala Glu Met Leu Arg Leu Pro
1 5 10 15

Thr Val Phe Arg Gln Met Arg Pro Val Ser Arg Val Leu Ala Pro His
20 25 30

Leu Thr Arg Ala Tyr Ala Lys Xaa Val Lys Phe Gly Ala Asp Ala Arg
35 40 45

Ala Leu Met Leu Gln Gly Val Asp Leu Leu Ala Asp Ala Val Ala Val
50 55 60

Thr Met Gly Pro Lys Gly Arg Thr Val Ile Ile Glu Gln Ser Trp Gly
65 70 75 80

Ser Pro Lys Val Thr Lys Asp Gly Val Thr Val Ala Lys Ser Ile Asp
85 90 95

Leu Lys Asp Lys Tyr Lys Asn Ile Gly Ala Lys Leu Val Gln Asp Val
100 105 110

Ala Asn Asn Thr Asn Glu Glu Ala Gly Asp Gly Thr Thr Thr Ala Thr
115 120 125

Val Leu Ala Arg Ser Ile Ala Lys Glu Gly Phe Glu Lys Ile Ser Lys
130 135 140

Gly
145

<210> 1543
<211> 135
<212> PRT
<213> Homo sapiens

<400> 1543
Lys Phe Gly Ala Asp Ala Arg Ala Leu Met Leu Gln Gly Val Asp Leu
1 5 10 15

```
Leu Ala Asp Ala Val Ala Val Thr Met Gly Pro Lys Gly Arg Thr Val
            20                  25                  30

Ile Ile Glu Gln Ser Trp Gly Ser Pro Lys Val Thr Lys Asp Gly Val
        35                  40                  45

Thr Val Ala Lys Ser Ile Asp Leu Lys Asp Lys Tyr Lys Asn Ile Gly
    50                  55                  60

Ala Lys Leu Val Gln Asp Val Ala Asn Asn Thr Asn Glu Glu Ala Gly
65                  70                  75                  80

Asp Gly Thr Thr Thr Ala Thr Val Leu Ala Arg Ser Ile Ala Lys Glu
                85                  90                  95

Gly Phe Glu Lys Ile Ser Lys Gly Ala Asn Pro Val Glu Ile Arg Arg
            100                 105                 110

Gly Val Met Leu Ala Val Asp Ala Val Ile Ala Glu Leu Lys Lys Gln
        115                 120                 125

Ser Lys Pro Val Thr Thr Pro
    130                 135
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<210> 1544
<211> 84
<212> PRT
<213> Homo sapiens

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<400> 1544
Cys Glu Phe Lys Arg Val Pro Gln Cys Pro Ser Gly Arg Val Tyr Val
1 5 10 15

Leu Lys Phe Lys Ala Gly Ser Lys Arg Leu Phe Phe Trp Met Gln Glu
20 25 30

Pro Lys Thr Asp Gln Asp Glu Glu His Cys Arg Lys Val Asn Glu Leu
35 40 45

Ser Gly Thr Thr Pro Arg Cys Leu Gly His Trp Gly Pro Ala Glu Gln
50 55 60

Arg Pro Arg Xaa Leu Cys Ala Xaa Arg Leu Arg Trp Xaa Ala Glu Xaa
65 70 75 80

Ala Gly Glu Thr

<210> 1545
<211> 22
<212> PRT
<213> Homo sapiens

<400> 1545
Tyr Leu Arg Leu Ile Tyr Ser Thr Ser Ile Thr Leu Leu Pro Ile Ser
1 5 10 15

Asn Asn Val Lys Ile Lys
20

<210> 1546
<211> 112
<212> PRT
<213> Homo sapiens

<220>
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<400> 1546
Pro Ser Ala Ala Ala Gly Asp Leu Gln Arg Thr Ala Ala Met Gly Ala
1 5 10 15

His Leu Val Arg Arg Tyr Leu Gly Asp Ala Ser Val Xaa Pro Asp Pro
20 25 30

Leu Gln Met Pro Thr Phe Pro Pro Asp Tyr Gly Phe Pro Glu Arg Lys
35 40 45

Xaa Arg Xaa Met Val Ala Thr Xaa Xaa Xaa Met Met Asp Ala His Xaa
50 55 60

Ser Ser Xaa Cys Gly Xaa Thr Ala Pro Thr Asn Ser Ser Gly Cys Ser
65 70 75 80

Ile Xaa Thr Leu Xaa Leu Pro Pro Leu Pro Trp Leu Ala Asn Gln Glu
85 90 95

Arg Asp Lys Xaa Glu Xaa Xaa Gln Thr Pro Xaa Xaa Phe Xaa Xaa Pro
100 105 110

<210> 1547
<211> 142
<212> PRT
<213> Homo sapiens

<400> 1547
Lys Val Ser Ala Val Met Ala Phe Leu Ala Ser Gly Pro Tyr Leu Thr
1 5 10 15

His Gln Gln Lys Val Leu Arg Leu Tyr Lys Arg Ala Leu Arg His Leu
20 25 30

Glu Ser Trp Cys Val Gln Arg Asp Lys Tyr Arg Tyr Phe Ala Cys Leu
35 40 45

Met Arg Ala Arg Phe Glu Glu His Lys Asn Glu Lys Asp Met Ala Lys
50 55 60

Ala Thr Gln Leu Leu Lys Glu Ala Glu Glu Glu Phe Trp Tyr Arg Gln
65 70 75 80

His Pro Gln Pro Tyr Ile Phe Pro Asp Ser Pro Gly Gly Thr Ser Tyr
85 90 95

Glu Arg Tyr Asp Cys Tyr Lys Val Pro Glu Trp Cys Leu Asp Asp Trp
100 105 110

His Pro Ser Glu Lys Ala Met Tyr Pro Asp Tyr Phe Ala Lys Arg Glu
115 120 125

Gln Trp Lys Lys Leu Arg Glu Gly Lys Leu Gly Thr Arg Gly
130 135 140

<210> 1548
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
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<222> (84)
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<222> (92)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (97)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1548
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Leu Tyr Tyr Xaa Leu Gly Phe Leu Xaa Leu Xaa Xaa Arg Leu Pro Leu
  1               5                  10                  15

Asp Ala Ala Lys Arg Xaa His Asp Glu Leu Gly Asn Glu Arg Pro Xaa
             20                  25                  30

Ala Tyr Met Xaa Glu His Asn Gln Leu Asn Gly Trp Xaa Ser Asp Glu
         35                  40                  45

Asn Asp Trp Asn Glu Lys Leu Tyr Pro Val Trp Lys Arg Xaa Asp Met
     50                  55                  60

Xaa Xaa Glu Lys Leu Leu Glu Gly Arg Pro Val Cys Lys Ala Val Leu
 65                  70                  75                  80

Thr Xaa Asp Xaa Pro Thr Leu Gly Gly Leu Lys Xaa Asn Ile Xaa Arg
                 85                  90                  95

Xaa Thr
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<210> 1549
<211> 138
<212> PRT
<213> Homo sapiens

<220>
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<222> (60)
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<220>
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<220>
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<222> (128)
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<220>
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<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1549
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Gly Cys Ser Leu Glu Gln Arg Ser Phe Ile Ser Val Arg Leu Leu Ser
  1               5                  10                  15

Tyr Leu Ser Ala Cys Arg His Pro Met Glu Asp Ser Met Asp Met Asp
             20                  25                  30

Met Ser Pro Leu Arg Pro Gln Asn Tyr Leu Phe Gly Cys Glu Leu Lys
         35                  40                  45

Ala Asp Lys Asp Tyr His Phe Lys Val Asp Asn Xaa Glu Asn Glu His
     50                  55                  60

Gln Leu Ser Leu Arg Thr Val Xaa Xaa Gly Ala Gly Ala Lys Asp Glu
 65                  70                  75                  80
```

```
Leu His Ile Val Glu Ala Glu Ala Met Asn Tyr Glu Gly Ser Pro Ile
                 85                  90                  95

Lys Val Thr Leu Ala Thr Leu Lys Met Ser Val Gln Pro Thr Val Phe
            100                 105                 110

Pro Leu Gly Ala Leu Asn Asn Thr Thr Xaa Xaa Leu Lys Val Glu Xaa
        115                 120                 125

Trp Phe Arg Ala Met Pro Ile Xaa Gly Gln
    130                 135



<210> 1550
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1550
Thr Leu Ala Phe Phe Leu Ile Pro Cys Ile Gly Ser Pro Ala Cys Pro
  1               5                  10                  15

Thr Met Ser Asp Ala Ala Val Asp Thr Ser Ser Glu Ile Thr Thr Lys
             20                  25                  30

Asp Leu Lys Glu Lys Lys Glu Val Val Glu Glu Ala Glu Met Glu Glu
         35                  40                  45

Thr Pro Cys
     50



<210> 1551
<211> 73
<212> PRT
<213> Homo sapiens

<220>
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<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1551
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Lys Ala Xaa Ser Val Xaa Leu Tyr Lys Val Arg Leu Gln Val Pro Val
  1               5                  10                  15

Arg Asn Ser Arg Val Asp Pro Arg Val Arg Xaa Gly Gly Glu Gln Val
             20                  25                  30

Ser Ser Thr Ile Xaa Gly Leu Ser Gly Pro Pro Ser Arg Arg Gly Pro
         35                  40                  45

Phe Pro Leu Ala Trp Val Ile Leu Phe Leu Leu Glu Ala Gln Xaa Gly
     50                  55                  60

Pro Trp Xaa Leu Leu Pro Ser Ala His
 65                  70
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<210> 1552
<211> 131
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<220>
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<222> (129)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1552
Asn Ser Ala Xaa Xaa Glu Leu Leu Thr Gln Pro Gly Asp Trp Thr Leu
1   5   10   15

Phe Val Pro Thr Asn Asp Ala Phe Lys Gly Met Thr Ser Glu Glu Lys
            20   25   30

Glu Ile Leu Ile Arg Asp Lys Asn Ala Leu Gln Asn Ile Ile Leu Tyr
        35   40   45

His Leu His Gln Glu Phe Ser Leu Glu Lys Asp Leu Asn Leu Val Leu
    50   55   60

Leu Thr Phe Leu Lys Thr Thr Gln Gly Ser Lys Ile Phe Leu Glu Gly
65   70   75   80

Ser Glu Met Val Thr Leu Leu Val Asn Gly Phe Gly Asn Pro Lys Xaa
85 90 95

Ser Asp Ile His Gly Pro Pro Xaa Val Val Ile Ser Cys Cys Arg Leu
100 105 110

Asn Xaa Xaa Phe Pro Ala Xaa Thr Pro Phe Gly Xaa Gly Ser Thr Gly
115 120 125

Xaa Asp Thr
130

<210> 1553
<211> 106
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (3)
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<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (94)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1553
Trp Ile Xaa Arg Ala Ala Gly Ile Arg His Glu Val Ala Asp Thr Met
1 5 10 15

Leu Pro Pro Met Ala Leu Pro Ser Val Ser Trp Met Leu Leu Ser Cys
20 25 30

Leu Met Leu Leu Ser Gln Val Gln Gly Glu Glu Pro Gln Arg Glu Leu
35 40 45

Pro Ser Ala Arg Ile Arg Xaa Pro Lys Gly Ser Lys Ala Tyr Gly Ser

50 55 60

His Cys Tyr Ala Leu Phe Leu Ser Pro Lys Ser Trp Thr Asp Ala Asp
65 70 75 80

Leu Ala Cys Gln Lys Arg Pro Ser Gly Asn Leu Val Ser Xaa Leu Ser
85 90 95

Gly Ala Glu Gly Ser Phe Xaa Pro Pro Trp
100 105

<210> 1554
<211> 117
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (109)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1554
Ala Thr Phe Pro Arg Glu Trp Leu Cys Asp Arg His Leu Arg Glu Lys
1 5 10 15

Met Phe Ser Ser Val Ala His Leu Ala Arg Ala Asn Pro Phe Asn Thr
20 25 30

Pro His Leu Gln Leu Val His Asp Gly Leu Gly Asp Leu Arg Ser Ser
35 40 45

Ser Pro Gly Pro Thr Gly Gln Pro Arg Arg Pro Arg Asn Leu Ala Ala
50 55 60

Ala Ala Val Glu Glu Gln Tyr Ser Cys Asp Tyr Gly Ser Gly Arg Phe
65 70 75 80

Phe Ile Leu Cys Gly Leu Gly Gly Ile Ile Ser Cys Gly Thr Thr His
85 90 95

Thr Ala Leu Val Pro Leu Asp Leu Val Lys Cys Arg Xaa Arg Phe Val
100 105 110

Phe Ala Cys Trp Thr
115

<210> 1555

<211> 164
<212> PRT
<213> Homo sapiens

<220>
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<400> 1555
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Glu Lys Lys Val Glu Arg Gln Thr Glu Leu Lys Arg Lys Phe Glu Gln
  1               5                  10                  15

Met Lys Gln Asp Arg Ile Thr Arg Tyr Gln Gly Val Asn Leu Tyr Val
             20                  25                  30

Lys Asn Leu Asp Asp Gly Ile Asp Asp Glu Arg Leu Arg Lys Glu Phe
         35                  40                  45

Ser Pro Phe Gly Thr Ile Thr Ser Ala Lys Val Met Met Glu Gly Gly
     50                  55                  60

Arg Ser Lys Gly Phe Gly Phe Val Cys Phe Ser Ser Pro Glu Xaa Ala
 65                  70                  75                  80

Thr Lys Ala Val Thr Xaa Met Asn Gly Arg Ile Val Ala Thr Lys Pro
                 85                  90                  95

Leu Tyr Val Ala Leu Ala Gln Arg Lys Glu Glu Arg Gln Ala His Leu
            100                 105                 110

Thr Asn Gln Tyr Met Gln Arg Met Ala Ser Val Arg Xaa Val Pro Asn
        115                 120                 125

Pro Val Ile Asn Pro Tyr Gln Pro Ala Pro Pro Ser Gly Tyr Phe Met
    130                 135                 140

Ala Ala Ile Pro Gln Thr Gln Asn Val Leu His Thr Ile Leu Leu Ala
145                 150                 155                 160

Lys Leu Leu Asn
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<210> 1556
<211> 166
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)
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<220>
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<220>
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<222> (14)
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<222> (150)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<400> 1556
Xaa Xaa Leu Thr Leu Thr Xaa Gly Xaa Lys Xaa Xaa Xaa Xaa Thr Ala
1   5   10   15

Val Ala Ala Ala Leu Ala Thr Ser Gly Ser Pro Gly Pro Val Arg Asn
            20   25   30

Ser Ala Arg Ala Gly Thr Ser Glu Phe Leu Asn Lys Val Thr Glu Ala
        35   40   45

Gln Glu Asp Gly Gln Ser Thr Ser Glu Leu Ile Gly Gln Phe Gly Val
    50   55   60

Gly Phe Tyr Ser Ala Phe Leu Val Ala Asp Lys Val Ile Val Thr Ser
65   70   75   80

Lys His Asn Asn Asp Thr Gln His Ile Trp Glu Ser Asp Ser Asn Glu
                85   90   95

Phe Ser Val Ile Ala Asp Pro Arg Gly Asn Thr Leu Gly Arg Gly Thr
            100   105   110

Thr Ile Thr Leu Val Leu Lys Glu Glu Ala Ser Asp Tyr Leu Glu Leu
        115   120   125

Asp Thr Ile Lys Asn Leu Val Lys Lys Tyr Ser Gln Phe Ile Asn Phe
    130   135   140

Pro Ile Tyr Val Trp Xaa Ser Lys Thr Glu Thr Val Xaa Glu Pro Met
145   150   155   160

Glu Glu Glu Gly Ala Ala
                165

<210> 1557
<211> 127
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)
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<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1557
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Xaa Asn Val Val Glu Ala Gln Phe Asp Ser Arg Val Arg Ala Thr Gly
  1               5                  10                  15

His Ser Xaa Xaa Xaa Tyr Asn Lys Trp Glu Thr Ile Glu Ala Trp Thr
             20                  25                  30

Gln Gln Val Ala Thr Xaa Asn Pro Ala Leu Ile Ser Arg Ser Val Ile
         35                  40                  45

Gly Thr Thr Phe Glu Gly Arg Ala Ile Tyr Leu Leu Lys Val Gly Lys
     50                  55                  60

Ala Gly Gln Asn Lys Pro Ala Ile Phe Met Asp Cys Gly Phe Pro Met
 65                  70                  75                  80

Pro Xaa Xaa Trp Ile Ser Pro Cys Ile Xaa Pro Val Gly Phe Xaa Lys
                 85                  90                  95
```

Xaa Ala Val Pro Phe Leu Xaa Thr Phe Xaa Xaa Xaa Leu Thr Asn Phe
100 105 110

Xaa Asn Asn Leu Xaa Phe Tyr Xaa Pro Ala Leu Trp Pro Gln Tyr
115 120 125

<210> 1558
<211> 109
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (80)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (101)
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1558
Lys Ala Gly Ala Ala Ala Gly Gly Pro Gly Val Ser Gly Val Cys Val
1 5 10 15

Cys Lys Ser Arg Tyr Pro Val Cys Gly Ser Asp Gly Thr Thr Tyr Pro
20 25 30

Ser Gly Cys Gln Leu Arg Ala Ala Ser Gln Arg Ala Glu Ser Arg Gly
35 40 45

Glu Lys Ala Ile Thr Gln Val Ser Lys Gly Thr Cys Glu Gln Gly Pro
50 55 60

Ser Ile Val Thr Pro Pro Lys Asp Ile Trp Asn Val Thr Gly Ala Xaa
65 70 75 80

Val Tyr Leu Ser Cys Glu Val Ile Gly Ile Pro Thr Pro Val Leu Ile
85 90 95

Trp Asn Lys Val Xaa Arg Gly His Tyr Gly Xaa Xaa Arg
100 105

<210> 1559
<211> 102
<212> PRT
<213> Homo sapiens

<400> 1559
Gly Leu Arg Gly His Leu Arg Ser Ser Gly Ser Ser Ile Trp Asn Tyr
1 5 10 15

Ile Lys Phe Arg Lys His Val Ser Arg Tyr Asp Ser Arg Thr Thr Ile
20 25 30

Phe Ser Pro Glu Gly Arg Leu Tyr Gln Val Glu Tyr Ala Met Glu Ala
35 40 45

Ile Gly His Ala Gly Thr Cys Leu Gly Ile Leu Ala Asn Asp Gly Val
50 55 60

Leu Leu Ala Ala Glu Arg Arg Asn Ile His Lys Leu Leu Asp Glu Val
65 70 75 80

Phe Phe Ser Glu Lys Ile Tyr Lys Leu Asn Glu Asp Met Ala Cys Ser
85 90 95

Val Ala Gly Ile Thr Phe
100

<210> 1560
<211> 159
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (146)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1560
Ser Thr His Ala Ser Ala Ala His Pro Ser Thr Leu Thr His Pro Gln
1 5 10 15

Arg Arg Ile Asp Thr Leu Asn Ser Asp Gly Tyr Thr Pro Glu Pro Asp
20 25 30

Lys Pro Arg Pro Met Pro Met Asp Thr Ser Val Tyr Glu Ser Pro Tyr
35 40 45

Ser Asp Pro Glu Glu Leu Lys Asp Lys Lys Leu Phe Leu Lys Arg Asp
50 55 60

Asn Leu Leu Ile Ala Asp Ile Glu Leu Gly Cys Gly Asn Phe Gly Ser
65 70 75 80

Val Arg Gln Gly Val Tyr Arg Met Arg Lys Lys Gln Ile Asp Val Ala
85 90 95

Ile Lys Val Leu Lys Gln Gly Thr Glu Lys Ala Asp Thr Glu Glu Met
100 105 110

Met Arg Glu Ala Gln Ile Met His Gln Leu Asp Asn Pro Tyr Ile Val
115 120 125

Arg Leu Ile Gly Val Cys Gln Ala Glu Ala Leu Met Leu Val Met Glu
130 135 140

Met Xaa Gly Ala Gly Ala Ala Gln Val Pro Gly Arg Gln Glu Gly
145 150 155

<210> 1561
<211> 155
<212> PRT
<213> Homo sapiens

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (140)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1561
Arg Ala His Glu Asn Glu Ile Thr Lys Val Arg Lys Val Thr Phe Asn
1 5 10 15

Gly Leu Asn Gln Met Ile Val Ile Glu Leu Gly Thr Asn Pro Leu Lys
20 25 30

Ser Ser Gly Ile Glu Asn Gly Ala Phe Gln Gly Met Lys Lys Leu Ser
35 40 45

Tyr Ile Arg Ile Ala Asp Thr Asn Ile Thr Ser Ile Pro Gln Gly Leu
50 55 60

Pro Pro Ser Leu Thr Glu Leu His Leu Asp Gly Asn Lys Ile Ser Arg
65 70 75 80

Val Asp Ala Ala Ser Leu Lys Gly Leu Asn Asn Leu Ala Lys Leu Gly
85 90 95

Leu Ser Phe Asn Ser Ile Ser Ala Val Asp Asn Gly Ser Leu Ala Asn
100 105 110

Thr Pro His Leu Arg Glu Leu His Leu Asp Asn Asn Lys Leu Thr Arg
115 120 125

Val Pro Gly Gly Leu Gln Ser Ile Lys Tyr Xaa Xaa Gly Gly Tyr Leu
130 135 140

His Asn Asn His Ile Ser Val Val Gly Ser Lys
145 150 155

<210> 1562
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1562
Xaa Asn Gln Asn Ser Asn Gly Leu Val Phe Leu Leu Trp Gly Ser Tyr
1 5 10 15

Ala Gln Lys Lys Gly Ser Ala Ile Asp Arg Lys Arg His His Val Leu
20 25 30

Gln Thr Ala His Pro Ser Pro Leu Ser Val Tyr Arg Gly Phe Phe Gly
35 40 45

Cys Arg His Phe Ser Lys Thr Asn Glu Leu Leu Gln Lys Ser Gly Lys
50 55 60

Lys Pro Ile Asp Trp Lys Glu Leu
65 70

<210> 1563
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (104)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1563
Arg Thr Arg Gly Arg Leu Leu Gly His Leu Lys Glu Thr Trp Gly His
1 5 10 15

Pro Arg Arg Ala Ser Trp Val Val Arg Ser Arg Arg Cys Arg His Cys
20 25 30

Leu Cys Phe Met Arg Lys Met Leu Ala Ala Val Ser Arg Val Leu Ser
35 40 45

Gly Ala Ser Gln Lys Pro Ala Ser Arg Val Leu Val Ala Ser Arg Asn
50 55 60

Phe Ala Asn Asp Ala Thr Phe Glu Ile Xaa Lys Cys Asp Leu His Arg
65 70 75 80

Leu Glu Glu Ala Leu Leu Ser Gln Gln Cys Ser Pro Arg Glu Asp Gly
85 90 95

Leu Lys Tyr Tyr Arg Met Met Xaa Thr Val Pro Glu Trp Asn
100 105 110

<210> 1564
<211> 95
<212> PRT
<213> Homo sapiens

<220>
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<222> (38)
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<222> (94)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1564
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Leu His Ser Xaa Cys Thr Arg Arg Gly Ser Gly Ser Leu Arg Leu Cys
 1               5                  10                  15

Ser Val Ala Arg Val Gly Gln Arg Arg Met Thr Ser Ala Ala Met Ser
            20                  25                  30

Lys Pro His Ser Glu Xaa Gly Thr Ala Phe Ile Gln Thr Gln Xaa Leu
        35                  40                  45

His Ala Xaa Met Ala Asp Thr Phe Leu Glu His Met Xaa Arg Leu Asp
    50                  55                  60
```

Ile Asp Ser Pro Pro Xaa Thr Gly Arg Asn Thr Gly Ile Ile Cys Thr
65 70 75 80

Ile Gly Pro Ala Ser Arg Ser Xaa Gly Asp Gly Xaa Gly Xaa Asp
85 90 95

<210> 1565
<211> 50
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (29)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (37)
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<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1565
Pro Thr Met Ala Ala Ile Arg Lys Lys Leu Val Ile Val Gly Asp Gly
1 5 10 15

Ala Cys Gly Lys Thr Cys Leu Leu Ile Val Phe Ser Xaa Asp Gln Phe
20 25 30

Pro Glu Val Tyr Xaa Pro Thr Val Leu Xaa Glu Leu Tyr Cys Ala His
35 40 45

Xaa Gly
50

<210> 1566
<211> 161

<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (155)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1566
Ala Ala Met Phe Asn Ile Arg Asn Ile Gly Lys Thr Leu Val Thr Arg
1 5 10 15

Thr Gln Gly Thr Lys Ile Ala Ser Asp Gly Leu Lys Gly Arg Val Phe
20 25 30

Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Val Ala Phe Arg Lys
35 40 45

Phe Lys Leu Ile Thr Glu Asp Val Gln Gly Lys Asn Cys Leu Thr Asn
50 55 60

Phe His Gly Met Asp Leu Thr Arg Asp Lys Met Cys Ser Met Val Lys
65 70 75 80

Lys Trp Gln Thr Met Ile Glu Ala His Val Asp Val Lys Thr Thr Asp
85 90 95

Gly Tyr Leu Leu Arg Leu Phe Cys Val Gly Phe Thr Lys Lys Arg Asn
100 105 110

Asn Gln Ile Arg Lys Thr Ser Tyr Ala Gln His Gln Gln Val Arg Gln
115 120 125

Ile Arg Lys Lys Met Met Glu Ile Met Thr Arg Glu Val Gln Thr Asn
130 135 140

Asp Leu Lys Glu Val Val Asn Lys Leu Ile Xaa Asp Ala Leu Glu Lys
145 150 155 160

Thr

<210> 1567
<211> 113
<212> PRT
<213> Homo sapiens

<400> 1567
Pro Ser Leu Lys Gly Thr Lys Ala Gly Ala Pro Pro Arg Cys Gly Arg

```
 1               5                   10                  15

Ser Arg Thr Ser Gly Ser Pro Gly Leu Gln Glu Phe Gly Thr Ser Pro
            20                  25                  30

Gly Pro Arg Gln Ser Pro Ala Arg Leu Val Ala Met Pro Arg Lys Ile
        35                  40                  45

Glu Glu Ile Lys Asp Phe Leu Leu Thr Ala Arg Arg Lys Asp Ala Lys
    50                  55                  60

Ser Val Lys Ile Lys Lys Asn Lys Asp Asn Val Lys Phe Lys Val Arg
65                  70                  75                  80

Cys Ser Arg Tyr Leu Tyr Thr Leu Val Ile Thr Asp Lys Glu Lys Ala
                85                  90                  95

Glu Lys Leu Lys Gln Ser Leu Pro Pro Gly Leu Ala Val Lys Glu Leu
            100                 105                 110

Lys
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<210> 1568
<211> 48
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (24)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (33)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1568

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Gly Cys Asn Tyr Gly Lys Pro Xaa His His Gly Val Asn Gln Leu Lys
 1               5                   10                  15

Phe Ala Arg Ser Leu Gln Ser Xaa Ala Glu Glu Arg Ala Gly Arg His
            20                  25                  30
```

Xaa Gly Ala Leu Arg Val Leu Asn Ser Tyr Trp Val Gly Glu Asp Ser
35 40 45

<210> 1569
<211> 120
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (103)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (106)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1569
Gly Thr Ser Glu Arg Xaa Glu His Ala Met Lys Ala Ser Gly Thr Leu
1 5 10 15

Arg Glu Tyr Lys Val Val Gly Arg Cys Leu Pro Thr Pro Lys Cys His
20 25 30

Thr Pro Pro Leu Tyr Arg Met Arg Ile Phe Ala Pro Asn His Val Val
35 40 45

Ala Lys Ser Arg Phe Trp Tyr Phe Val Ser Gln Leu Lys Lys Met Lys
50 55 60

Lys Ser Ser Gly Glu Ile Val Tyr Cys Gly Gln Val Phe Glu Lys Ser
65 70 75 80

Pro Leu Arg Val Lys Asn Phe Gly Ile Trp Leu Arg Tyr Asp Ser Arg
85 90 95

Ser Gly Thr His Asn Met Xaa Arg Glu Xaa Arg Asp Leu Thr Asn Ala
100 105 110

Gly Ala Val Asn Gln Cys Asn Gly
        115   120

<210> 1570
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (61)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (78)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1570
Cys Pro Pro Leu Trp Gln Glu Glu Val Trp Leu Asp Pro Asn Glu Thr
  1   5   10   15

Asn Glu Ile Ala Asn Ala Asn Ser Arg Gln Gln Ile Arg Lys Leu Ile
             20   25   30

Lys Asp Gly Leu Ile Ile Arg Lys Pro Val Thr Val His Ser Arg Ala
         35   40   45

Arg Cys Arg Lys Asn Thr Leu Ala Arg Arg Lys Gly Xaa His Met Gly
     50   55   60

Ile Val Ser Gly Lys Val Gln Pro Met Pro Glu Cys Gln Xaa Arg Ser
 65   70   75   80

His Gly Leu Arg Lys
                 85

<210> 1571
<211> 135
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (134)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1571
Phe Ala Lys Met Thr Asn Thr Lys Gly Lys Arg Arg Gly Thr Arg Tyr
1 5 10 15

Met Phe Ser Arg Pro Phe Arg Lys His Gly Val Val Pro Leu Ala Thr
20 25 30

Tyr Met Arg Ile Tyr Lys Lys Gly Asp Ile Val Asp Ile Lys Gly Met
35 40 45

Gly Thr Val Gln Lys Gly Met Pro His Lys Cys Tyr His Gly Lys Thr
50 55 60

Gly Arg Val Tyr Asn Val Thr Gln His Ala Val Gly Ile Val Val Asn
65 70 75 80

Lys Gln Val Lys Gly Lys Ile Leu Ala Lys Arg Ile Asn Val Arg Ile
85 90 95

Glu His Ile Lys His Ser Lys Ser Arg Asp Ser Phe Leu Lys Arg Val
100 105 110

Lys Glu Asn Asp Gln Lys Lys Lys Glu Ala Lys Glu Lys Gly Thr Trp
115 120 125

Val Gln Leu Lys Arg Xaa Pro
130 135

<210> 1572
<211> 71
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (7)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (37)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (58)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (65)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (69)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1572
Thr Ala Thr Pro Ala Asn Xaa Xaa Leu Pro Trp Gly Xaa Lys Lys Xaa
1   5   10   15

Ala Arg Arg Ser Lys Ile Xaa Ser Phe Val Xaa Val Cys Xaa Tyr Asn
            20   25   30

His Leu Met Pro Xaa Arg Tyr Ser Val Xaa Tyr Ser Pro Trp Gly Lys
35 40 45

Ala Val Arg Ser Leu Gly Cys Leu Pro Xaa Phe Leu Ala Leu Lys Arg
50 55 60

Xaa Ala Arg Arg Xaa Pro Arg
65 70

<210> 1573
<211> 68
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (59)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (62)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1573
Ala Ala Ala Lys Gly Ala Ala Ala Met Ser Ala His Leu Gln Trp Met
1 5 10 15

Val Val Arg Asn Cys Ser Ser Phe Leu Ile Lys Arg Asn Lys Gln Thr
20 25 30

Tyr Ser Thr Glu Pro Asn Asn Leu Lys Ala Arg Asn Ser Phe Arg Tyr
35 40 45

Asn Gly Leu Ile His Arg Lys Thr Val Gly Xaa Glu Pro Xaa Ala Asp
50 55 60

Gly Lys Xaa Val
65

<210> 1574
<211> 127

<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1574
Gly Arg Met Xaa Pro Ala Lys Lys Gly Gly Glu Lys Lys Lys Gly Arg
1 5 10 15

Ser Ala Ile Asn Glu Val Val Thr Arg Glu Tyr Thr Ile Asn Ile His
20 25 30

Lys Arg Ile His Gly Val Gly Phe Lys Lys Arg Ala Pro Arg Ala Leu
35 40 45

Lys Glu Ile Arg Lys Phe Ala Met Lys Glu Met Gly Thr Pro Asp Val
50 55 60

Arg Ile Asp Thr Arg Leu Asn Lys Ala Val Trp Ala Lys Gly Ile Arg
65 70 75 80

Asn Val Pro Tyr Arg Ile Arg Val Arg Leu Ser Arg Lys Arg Asn Glu
85 90 95

Asp Glu Asp Ser Pro Asn Lys Leu Tyr Thr Leu Val Thr Tyr Val Pro
100 105 110

Val Thr Thr Phe Lys Asn Leu Gln Thr Val Asn Val Asp Glu Asn
115 120 125

<210> 1575
<211> 115
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (12)
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<220>
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<220>
<221> SITE
<222> (97)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1575
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Trp Phe Pro Arg Ala Ala Gly Phe Arg His Xaa Xaa Val Gln Ile Arg
  1               5                  10                  15

Ala Xaa Glu Arg Lys Gly Thr Ser Ser Phe Gly Lys Xaa Arg Asn Lys
             20                  25                  30

Thr His Thr Leu Cys Arg Arg Xaa Gly Ser Lys Ala Tyr His Leu Gln
         35                  40                  45

Xaa Ser Thr Cys Gly Lys Phe Gly Tyr Pro Ala Lys Arg Lys Arg Lys
     50                  55                  60

Xaa Asn Trp Ser Ala Lys Ala Lys Arg Arg Asn Thr Thr Gly Thr Gly
 65                  70                  75                  80

Arg Xaa Arg His Leu Lys Phe Val Tyr Arg Arg Phe Arg His Gly Phe
```

85 90 95

Xaa Glu Gly Thr Thr Pro Lys Pro Lys Arg Ala Ala Val Ala Ala Ser
100 105 110

Ser Ser Ser
115

<210> 1576
<211> 121
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (108)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (114)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (116)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1576
Gly Arg Arg Ser Glu Met Thr Lys Gly Thr Ser Ser Phe Gly Lys Arg
1 5 10 15

Arg Asn Lys Thr His Thr Leu Cys Arg Arg Cys Gly Ser Lys Ala Tyr
20 25 30

His Leu Gln Lys Ser Thr Cys Gly Lys Cys Gly Tyr Pro Ala Lys Arg
35 40 45

Lys Arg Lys Tyr Asn Trp Ser Ala Lys Ala Lys Arg Arg Asn Thr Thr
50 55 60

Gly Thr Gly Arg Met Arg His Leu Lys Ile Val Tyr Arg Arg Phe Arg
65 70 75 80

His Gly Phe Arg Glu Gly Thr Thr Pro Lys Pro Lys Arg Ala Ala Val
85 90 95

Ala Ala Phe Gln Phe Ile Phe Lys Asn Val Asn Xaa Phe Ser His Ala
100 105 110

Ile Xaa Cys Xaa Gly Val Leu Lys Asn
115 120

<210> 1577
<211> 61
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (57)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (59)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (61)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1577
Gly Ile Val Gly Lys Tyr Gly Thr Arg Tyr Gly Ala Ser Leu Arg Lys
1 5 10 15

Met Val Lys Lys Ile Glu Ile Ser Gln His Ala Lys Tyr Thr Cys Ser
20 25 30

Phe Cys Gly Lys Thr Lys Met Lys Arg Arg Ala Val Gly Ile Trp His
35 40 45

Cys Gly Ser Cys Met Lys Thr Val Xaa Gly Xaa Ala Xaa
50 55 60

<210> 1578
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (44)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (51)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (63)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1578
Glu Leu Gly Lys Gly Lys Met Glu Lys Pro Ser Pro Tyr Pro Ala Gln
1 5 10 15

Gly Pro Cys Ile Ile Tyr Asn Glu Asp Asn Gly Ile Ile Lys Ala Phe
20 25 30

Gln Lys His Pro Trp Asn Tyr Ser Ala Xaa Met Xaa Ser Lys Leu Lys
35 40 45

His Phe Xaa Ser Leu Leu Pro Gly Gly Ala Cys Gly Asp Val Xaa Gly
50 55 60

Ile Gly Xaa Glu Met Ala Phe Pro Gly Xaa
65 70

<210> 1579
<211> 98
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (81)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (87)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (91)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1579
Ser Xaa Met Ala Cys Ala Arg Pro Leu Ile Ser Val Tyr Ser Glu Lys
1 5 10 15

Gly Glu Ser Ser Gly Lys Asn Val Thr Leu Pro Ala Val Phe Lys Ala
20 25 30

Pro Ile Arg Pro Asp Ile Val Asn Phe Val His Thr Asn Leu Arg Lys
35 40 45

Asn Asn Arg Gln Pro Tyr Ala Val Ser Glu Leu Ala Gly His Gln Thr
50 55 60

Ser Ala Glu Ser Trp Gly Thr Gly Arg Ala Val Ala Arg Ile Pro Arg
65 70 75 80

Xaa Arg Gly Gly Gly Thr Xaa Arg Ser Gly Xaa Gly Ala Phe Gly Asn
85 90 95

Met Cys

<210> 1580
<211> 72
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (50)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (55)
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<220>
<221> SITE
<222> (64)
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<220>
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<222> (71)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1580
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Leu Ser Leu Xaa Gly Lys Lys Lys Lys Arg Leu Arg Val Asp Lys Trp
  1               5                  10                  15

Trp Gly Xaa Arg Lys Glu Leu Ala Thr Val Arg Thr Ile Cys Ser His
             20                  25                  30

Val Gln Asn Met Ile Lys Gly Val Thr Leu Gly Phe Arg Tyr Lys Met
         35                  40                  45

Arg Xaa Val Tyr Ala His Xaa Pro Ile Asn Val Val Ile Gln Glu Xaa
     50                  55                  60

Gly Ser Ile Val Glu Ile Xaa Xaa
 65                  70
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<210> 1581
<211> 153
<212> PRT

<213> Homo sapiens

<400> 1581
Ala Ile Met Gly Arg Met His Ala Pro Gly Lys Gly Leu Ser Gln Ser
1 5 10 15

Ala Leu Pro Tyr Arg Arg Ser Val Pro Thr Trp Leu Lys Leu Thr Ser
20 25 30

Asp Asp Val Lys Glu Gln Ile Tyr Lys Leu Ala Lys Lys Gly Leu Thr
35 40 45

Pro Ser Gln Ile Gly Val Ile Leu Arg Asp Ser His Gly Val Ala Gln
50 55 60

Val Arg Phe Val Thr Gly Asn Lys Ile Leu Arg Ile Leu Lys Ser Lys
65 70 75 80

Gly Leu Ala Pro Asp Leu Pro Glu Asp Leu Tyr His Leu Ile Lys Lys
85 90 95

Ala Val Ala Val Arg Lys His Leu Glu Arg Asn Arg Lys Asp Lys Asp
100 105 110

Ala Lys Phe Arg Leu Ile Leu Ile Glu Ser Arg Ile His Arg Leu Ala
115 120 125

Arg Tyr Tyr Lys Thr Lys Arg Val Leu Pro Pro Asn Trp Lys Tyr Glu
130 135 140

Ser Ser Thr Ala Ser Ala Leu Val Ala
145 150

<210> 1582
<211> 129
<212> PRT
<213> Homo sapiens

<400> 1582
Gly Pro Ala Asn Met Gly Arg Val Arg Thr Lys Thr Val Lys Lys Ala
1 5 10 15

Ala Arg Val Ile Ile Glu Lys Tyr Tyr Thr Arg Leu Gly Asn Asp Phe
20 25 30

His Thr Asn Lys Arg Val Cys Glu Glu Ile Ala Ile Ile Pro Ser Lys
35 40 45

Lys Leu Arg Asn Lys Ile Ala Gly Tyr Val Thr His Leu Met Lys Arg

50 55 60

Ile Gln Arg Gly Pro Val Arg Gly Ile Ser Ile Lys Leu Gln Glu Glu
65 70 75 80

Glu Arg Glu Arg Arg Asp Asn Tyr Val Pro Glu Val Ser Ala Leu Asp
85 90 95

Gln Glu Ile Ile Glu Val Asp Pro Asp Thr Lys Glu Met Leu Lys Leu
100 105 110

Leu Asp Phe Gly Ser Leu Ser Asn Leu Gln Ser Leu Ser Leu Gln Leu
115 120 125

Gly

<210> 1583
<211> 109
<212> PRT
<213> Homo sapiens

<400> 1583
Asn Asn Gly Arg Ala Lys Lys Gly Arg Gly His Val Gln Pro Ile Arg
1 5 10 15

Cys Thr Asn Cys Ala Arg Cys Val Pro Lys Asp Lys Ala Ile Lys Lys
20 25 30

Phe Val Ile Arg Asn Ile Val Glu Ala Ala Ala Val Arg Asp Ile Ser
35 40 45

Glu Ala Ser Val Phe Asp Ala Tyr Val Leu Pro Lys Leu Tyr Val Lys
50 55 60

Leu His Tyr Cys Val Thr Val Pro Ser Ile Ala Arg Leu Leu Gly Ile
65 70 75 80

Asp Pro Ala Lys Pro Gly Arg Thr Glu His Pro His His Asp Ser Asp
85 90 95

Leu Leu Ala Leu His Leu Arg Pro Pro Pro Lys Pro Met
100 105

<210> 1584
<211> 119
<212> PRT

<213> Homo sapiens

<220>
<221> SITE
<222> (60)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (99)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (118)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1584

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Val Gln Arg Phe Ile Lys Ile Asp Gly Lys Val Arg Thr Asp Ile Thr
  1               5                  10                  15

Tyr Pro Ala Gly Phe Met Asp Val Ile Ser Ile Asp Lys Thr Gly Glu
             20                  25                  30

Asn Phe Arg Leu Ile Tyr Asp Thr Lys Gly Arg Phe Ala Val His Arg
         35                  40                  45

Ile Thr Pro Glu Glu Ala Lys Tyr Lys Leu Cys Xaa Val Arg Lys Ile
     50                  55                  60

Phe Val Gly Thr Lys Gly Ile Pro His Leu Val Thr His Asp Ala Arg
 65                  70                  75                  80

Thr Ile Arg Tyr Pro Asp Pro Leu Ile Lys Val Asn Asp Pro Phe Ile
                 85                  90                  95

Leu Ile Xaa Arg Leu Ala Arg Leu Leu Ile Ser Ser Ile Ser Thr Leu
            100                 105                 110

Val Thr Cys Val Trp Xaa Leu
        115
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<210> 1585
<211> 81
<212> PRT
<213> Homo sapiens

<220>
<221> SITE

<222> (14)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

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<220>
<221> SITE
<222> (53)
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<220>
<221> SITE
<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (72)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (74)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1585
Gly Arg Tyr Ala Ala Lys Arg Phe Arg Lys Ala Gln Cys Xaa Ile Val
1 5 10 15

Glu Arg Leu Thr Asn Ser Met Met Met Xaa Gly Arg Asn Asn Gly Lys
20 25 30

Lys Leu Met Thr Val Arg Ile Val Xaa His Ala Phe Glu Ile Ile Arg
35 40 45

Leu Leu Thr Gly Xaa Glu Pro Ser Ala Gly Pro Gly Glu Arg His His
50 55 60

Gln His Xaa Ser Pro Gly Arg Xaa His Xaa His Trp Ala Arg Arg Asp
65 70 75 80

Cys

<210> 1586
<211> 111
<212> PRT
<213> Homo sapiens

<400> 1586
Lys Asn Cys Ile Val Leu Ile Asp Ser Thr Pro Tyr Arg Gln Trp Tyr
1 5 10 15

Glu Ser His Tyr Ala Leu Pro Leu Gly Arg Lys Lys Gly Ala Lys Leu
20 25 30

Thr Pro Glu Glu Glu Glu Ile Leu Asn Lys Lys Arg Ser Lys Lys Ile
35 40 45

Gln Lys Lys Tyr Asp Glu Arg Lys Lys Asn Ala Lys Ile Ser Ser Leu
50 55 60

Leu Glu Glu Gln Phe Gln Gln Gly Lys Leu Leu Ala Cys Ile Ala Ser
65 70 75 80

Arg Pro Gly Gln Cys Gly Arg Ala Asp Gly Tyr Val Leu Glu Gly Lys
85 90 95

Glu Leu Glu Phe Tyr Leu Arg Lys Ile Lys Ala Arg Lys Gly Lys
100 105 110

<210> 1587
<211> 125
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (105)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (117)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1587
Arg Thr Met Pro Gly Val Thr Val Lys Asp Val Asn Gln Gln Glu Phe
1 5 10 15

```
Val Arg Ala Leu Ala Ala Phe Leu Lys Lys Ser Gly Lys Leu Lys Val
            20                  25                  30

Pro Glu Trp Val Asp Thr Val Lys Leu Ala Lys His Lys Glu Leu Ala
        35                  40                  45

Pro Tyr Asp Glu Asn Trp Phe Tyr Thr Arg Ala Ala Ser Thr Ala Arg
    50                  55                  60

His Leu Tyr Leu Arg Gly Gly Ala Gly Val Gly Ser Met Thr Lys Ile
65                  70                  75                  80

Tyr Gly Gly Arg Gln Arg Asn Gly Val Met Pro Ser His Phe Ser Arg
                85                  90                  95

Gly Ser Lys Ser Val Ala Arg Arg Xaa Leu Gln Ala Leu Gly Gly Ala
            100                 105                 110

Glu Asn Gly Gly Xaa Gly Pro Arg Trp Arg Pro Ala Asn
        115                 120                 125


<210> 1588
<211> 38
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (29)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (33)
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1588
Cys Met Leu Xaa Leu Val Leu Xaa Leu Leu Ser Ser Ser Ser Ala Glu
1   5   10   15

Glu Tyr Xaa Gly Leu Ser Ala Asn Gln Cys Ala Val Xaa Ala Lys Asp
            20   25   30

Xaa Val Xaa Cys Gly Tyr
        35

<210> 1589
<211> 55
<212> PRT
<213> Homo sapiens

<400> 1589
Gly Thr Ala Thr Gln Gly Leu Ser Pro Val His Thr Pro Gly Asp Gly
1   5   10   15

Arg Leu His Lys Ala Val Ser Val Gly Pro Arg Val His Ile Ile Glu
            20   25   30

Glu Leu Gln Ile Phe Ser Ser Gly Gln Pro Val Ala Glu Ser Ala Pro
        35   40   45

Gly Thr Pro Thr Gly Gly Leu
    50   55

<210> 1590
<211> 92
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1590
Leu Glu Asp Gly Phe Gly Glu His Pro Phe Tyr His Cys Leu Xaa Ala

```
 1               5                   10                  15
Glu Val Pro Lys Glu His Trp Thr Pro Glu Gly His Ser Ile Val Gly
            20                  25                  30
Phe Ala Met Tyr Tyr Phe Thr Tyr Asp Pro Trp Ile Gly Lys Leu Leu
        35                  40                  45
Tyr Leu Glu Asp Phe Phe Val Met Ser Asp Tyr Arg Gly Phe Gly Ile
    50                  55                  60
Gly Ser Glu Ile Leu Lys Asn Leu Ser Gln Val Ala Met Arg Cys Arg
65                  70                  75                  80
Cys Ser Ser Met His Phe Phe Gly Ser Arg Met Glu
                85                  90
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<210> 1591
<211> 139
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (5)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (8)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (10)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (114)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (117)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (125)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (133)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1591
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Xaa Gly Gly Phe Xaa Ile Thr Xaa Gly Xaa Asp Glu Gly Lys Leu Val
  1               5                  10                  15

Thr Pro Ala Gly Asp Arg Ser Gly Ile Pro Gly Ser Thr His Ala Ser
             20                  25                  30

Gly Arg Asp Val Ser Gln Lys Val Leu Arg Ser Gln Thr Trp Val Pro
         35                  40                  45

Arg Leu Pro Ala Ser Glu Ala Xaa Ser Arg His Arg Gly Lys Val Lys
     50                  55                  60

Ser Phe Pro Lys Asp Asp Pro Ser Lys Pro Val His Leu Thr Ala Phe
 65                  70                  75                  80

Leu Gly Tyr Lys Ala Gly Met Thr His Ile Val Arg Glu Val Asp Arg
                 85                  90                  95

Pro Gly Ser Lys Val Asn Lys Lys Glu Gly Gly Gly Gly Cys Asp His
            100                 105                 110

Cys Xaa Asp Thr Xaa His Gly Gly Leu Trp Ala Leu Xaa Ala Thr Leu
        115                 120                 125

Glu Asn Pro Arg Xaa Leu Arg Asn Phe Lys Asn
    130                 135
```

<210> 1592
<211> 42
<212> PRT

<213> Homo sapiens

<400> 1592
Ala Glu His Gly Asp Gln Asp Tyr Ile Trp His Cys Ile Asp Leu Phe
1 5 10 15

Leu Asp Phe Ile Thr Val Phe Arg Lys Leu Met Met Ile Leu Ala Met
20 25 30

Asn Glu Lys Asp Lys Lys Lys Glu Lys Lys
35 40

<210> 1593
<211> 85
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (25)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (31)
<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE
<222> (33)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (47)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (56)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (60)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (62)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (79)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1593
Trp Ile Pro Arg Ala Ala Gly Ser Leu Ser Leu Ala Gln Arg Arg Gly
1 5 10 15

Xaa Thr Lys Thr Tyr Thr Val Gly Xaa Glu Glu Cys Thr Val Xaa Pro
20 25 30

Xaa Leu Ser Ile Pro Cys Lys Leu Gln Ser Gly Thr His Cys Xaa Trp
35 40 45

Thr Asp Gln Leu Leu Gln Gly Xaa Glu Lys Gly Xaa Gln Xaa Arg His
50 55 60

Leu Ala Cys Leu Pro Arg Glu Pro Gly Leu Gly Thr Trp Gln Xaa Leu
65 70 75 80

Arg Ser Gln Ile Ala
85

<210> 1594
<211> 183
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (80)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (107)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE

<222> (122)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (136)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (151)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (152)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (160)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1594
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Ala Ala Arg Gly Ala Gln Arg Asp Thr Arg Glu Pro Thr Met Ala Pro
  1               5                  10                  15

Phe Glu Pro Leu Ala Ser Gly Ile Leu Leu Leu Leu Trp Leu Ile Ala
             20                  25                  30

Pro Ser Arg Ala Cys Thr Cys Val Pro Pro His Pro Gln Thr Ala Phe
         35                  40                  45

Cys Asn Ser Asp Leu Val Ile Arg Ala Lys Phe Val Gly Thr Pro Glu
     50                  55                  60

Val Asn Gln Thr Thr Leu Tyr Gln Arg Tyr Glu Ile Lys Met Thr Xaa
 65                  70                  75                  80

Met Tyr Lys Gly Phe Gln Ala Leu Gly Asp Ala Ala Asp Ile Arg Phe
                 85                  90                  95

Val Tyr Thr Pro Ala Met Glu Ser Val Cys Xaa Tyr Phe His Arg Ser
            100                 105                 110

His Asn Arg Ser Glu Glu Phe Leu Ile Xaa Gly Lys Leu Gln Asp Gly
        115                 120                 125

Leu Leu His Ile Thr Thr Cys Xaa Phe Val Ala Pro Trp Asn Ser Leu
    130                 135                 140
```

Ser Leu Ala Gln Arg Arg Xaa Xaa Thr Lys Thr Tyr Thr Val Gly Xaa
145 150 155 160

Glu Glu Met His Lys Cys Phe Pro Val Tyr Pro Ser Pro Ala Asn Cys
165 170 175

Arg Val Gly Thr His Cys Leu
180

<210> 1595
<211> 153
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (143)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (151)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1595
Ser Thr Cys Pro Asp Glu Gln Cys Val Asn Ser Pro Gly Ser Tyr Gln
1 5 10 15

Cys Val Pro Cys Thr Glu Gly Phe Arg Gly Trp Asn Gly Gln Cys Leu
20 25 30

Asp Val Asp Glu Cys Leu Glu Pro Asn Val Cys Ala Asn Gly Asp Cys
35 40 45

Ser Asn Leu Glu Gly Ser Tyr Met Cys Ser Cys His Lys Gly Tyr Thr
50 55 60

Arg Thr Pro Asp His Lys His Cys Arg Asp Ile Asp Glu Cys Gln Gln
65 70 75 80

Gly Asn Leu Cys Val Asn Gly Gln Cys Lys Asn Thr Glu Gly Ser Phe
85 90 95

Arg Cys Thr Val Asp Arg Gly Tyr Gln Leu Ser Ala Ala Lys Asp Gln
100 105 110

Phe Glu Asp Ile Asp Glu Cys His Thr Val Ile Ser Val Ala His Gly
115 120 125

His Ala Arg Thr Leu Lys Leu Phe Ser Met Cys Phe Leu Thr Xaa Val
    130   135   140

Thr Glu His Leu Gly Leu Xaa Thr Leu
145   150

<210> 1596
<211> 111
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (102)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1596
Leu Gly Ser Ser Ala Met Ala Pro Ser Arg Lys Phe Phe Val Gly Gly
  1   5   10   15

Asn Trp Lys Met Asn Gly Arg Lys Gln Ser Leu Gly Glu Leu Ile Gly
             20   25   30

Thr Leu Asn Ala Ala Lys Val Pro Ala Asp Thr Glu Val Val Cys Ala
         35   40   45

Pro Pro Thr Ala Tyr Ile Asp Phe Ala Arg Gln Lys Leu Asp Pro Lys
     50   55   60

Ile Ala Val Ala Ala Gln Asn Cys Tyr Lys Val Thr Asn Gly Ala Phe
 65   70   75   80

Thr Gly Glu Ile Ser Pro Gly Met Ile Lys Asp Cys Gly Pro Arg Gly
                 85   90   95

Trp Ser Trp Gly Thr Xaa Arg Glu Ala Cys Leu Trp Gly Ile Arg
            100   105   110

<210> 1597
<211> 82
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (71)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (79)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (80)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1597
Ile Phe Glu Asp Ser Asp Ser Leu Arg Leu Arg Arg Asp Val Leu Pro
1 5 10 15

Ala Ala Xaa Val Gln Ala Ala Leu Pro Ala Thr Ser Cys Val Pro His
20 25 30

Ala Lys Val Pro Lys Ser His Val His Pro Arg Ser Ala Leu Ser Leu
35 40 45

Thr Cys Leu Leu Leu Val His Leu Ser Ile Ala His Leu His Leu Ala
50 55 60

Ser Ile Asn Ala Leu Leu Xaa Gln Pro Tyr His Pro Gly Ser Xaa Xaa
65 70 75 80

Ser Pro

<210> 1598
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (16)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (47)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1598
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Xaa Lys Xaa Gly Arg Asn Lys Ala Arg Pro Leu Thr Ser Leu Arg Xaa
  1               5                  10                  15

Thr Phe Xaa Ala Thr Phe Cys Pro Val Xaa Gly Thr Tyr Ile Leu Asn
             20                  25                  30

Asp Cys Pro Xaa Thr His Ser Gly Ile Phe Phe Phe Leu Lys Xaa Xaa
         35                  40                  45

Xaa Lys Ala Phe
     50
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<210> 1599
<211> 32
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (9)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1599
Ala Phe Asn Xaa Ser Tyr Arg Lys Xaa Val Xaa Ala Val Arg Xaa Glu
1 5 10 15

Phe Arg Val Thr Gln Arg Pro Gly Leu Xaa Xaa Leu Gly Leu Glu Phe
20 25 30

<210> 1600
<211> 19
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (12)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (13)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1600
Ala Arg Gly Phe Phe Phe Phe Phe Phe Phe Phe Xaa Xaa Phe Xaa Phe
1 5 10 15

Phe Lys Lys

<210> 1601
<211> 22
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (20)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1601
Arg Xaa Asn Arg Val Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe Phe
1 5 10 15

Phe Phe Phe Xaa Pro Xaa
20

<210> 1602
<211> 104
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (98)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1602
Asp Phe Gly Arg Ser Phe Leu Leu Trp Phe Ser Leu Phe Phe Leu Pro
1 5 10 15

Phe Tyr Ser Ala Arg Ile Ser Gly Gly Leu Met Val Gly Tyr Asn Val
20 25 30

Ser Val Leu Leu Gln Ile Gly Leu Lys Gly Tyr Pro Ala Glu Ser Pro
35 40 45

Ala Phe Leu Ser Ser Ile Tyr Phe Ser Gly Lys Leu Phe Phe Leu Phe
50 55 60

Phe Phe Lys Val Asn Leu Cys Ile Glu Leu Asn Cys Ile Ser Val Phe
65 70 75 80

Pro Ala Tyr Val Tyr Ile Ile Pro Met Ile Pro Asn Ser Tyr Leu Tyr
85 90 95

Phe Xaa Thr Asn Ser Gln Ser Glu
100

<210> 1603
<211> 86
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (30)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (45)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (62)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (63)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (73)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (80)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (81)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1603
```
Phe Leu Met Leu Ser Phe Met Gly Ile Val Thr Phe Leu Phe Ser Lys
  1               5                  10                  15

Ser His Cys Trp Asn His Gln Gly Cys Gly Met Ser Leu Xaa Val Leu
             20                  25                  30

Phe Met Gln Val Thr Val Thr Phe Ala Ile Met Ala Xaa Phe Glu Thr
        35                  40                  45

Leu Ile Met Cys Phe Tyr Phe Phe Ile Pro Val Lys Met Xaa Xaa Lys
    50                  55                  60

Arg Lys Lys Val Val Ile Ala Pro Xaa Ile Ser Gly Ser Lys Leu Xaa
 65                  70                  75                  80

Xaa Lys Phe Pro Lys Lys
                 85
```

<210> 1604
<211> 34
<212> PRT
<213> Homo sapiens

<400> 1604
Ser Asp Glu Ile Ile Tyr Asn Phe Ile Val Thr Ser Ser Val Phe Pro
1 5 10 15

Phe Glu Arg Cys Met Asn Ser Leu His Phe Tyr Ser Asn Val Leu Ser
20 25 30

Val Asp

<210> 1605
<211> 53
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (17)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (30)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (37)
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<400> 1605
Leu Leu Val Trp Ser Glu Tyr Asn Thr Ser Ile Ile Thr Tyr Asn Ser
1 5 10 15

Xaa Pro Gly Thr Gly Gly Tyr Lys Tyr Asn Phe Phe Lys Xaa Asn Ser
            20   25   30

Trp Leu Ser Thr Xaa Leu Gln Val Pro Leu Xaa Gly Xaa Leu Trp Xaa
        35   40   45

Ile Thr Leu Gly Lys
    50

<210> 1606
<211> 32
<212> PRT
<213> Homo sapiens

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<400> 1606
Asp Ala Trp Ala Asp Ala Trp Gly Lys Val Ser Ser Ser Leu Xaa Ser
1 5 10 15

Xaa Ile Cys Xaa Leu Xaa Xaa Arg Lys Val Arg Xaa Gly Gln Xaa Met
20 25 30

<210> 1607
<211> 31
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<400> 1607
Leu Ile Met Asp Thr Ile Leu Asn Lys Xaa Ile Gln Val Lys Pro Val
1 5 10 15

Lys Glu Lys Glu Ile Lys Val Ser Gly Ser Cys Xaa Ser Xaa Val
20 25 30

<210> 1608
<211> 107
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<213> Homo sapiens

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<400> 1608

```
Asp Pro Gln Gly Ile Arg His Pro His Ile Val Gln Leu Lys Asp Phe
  1               5                  10                  15

Gln Cys Glu Leu Gly Ala Gly Xaa Leu Pro Lys Gly Val Glu Lys Asp
             20                  25                  30

Ile Xaa Phe Arg Pro Xaa Leu Cys Leu Leu Lys Gln Gln Leu Gly Thr
         35                  40                  45

Val Glu Pro Ile Asn Leu Xaa Phe Asn Pro Leu Gly Ser Phe Phe Ala
     50                  55                  60

Gly Gln Gly Gly Gly Arg Lys Pro Trp Xaa Phe Xaa Xaa Phe Xaa Ser
 65                  70                  75                  80

Gln Leu Asn Pro Gly Gln Xaa Asn Phe Leu Gly Pro Leu Lys Glu Lys
                 85                  90                  95

Xaa Phe Gly Pro Xaa Xaa Xaa Xaa Leu Ser Xaa
            100                 105
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<210> 1609
<211> 72
<212> PRT
<213> Homo sapiens

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<400> 1609
Arg Gln Thr Ser Thr Ala Lys Leu Gln Lys Gly Gly Phe Cys Ser Arg
1 5 10 15

Arg Lys Glu Asp Val Tyr Leu Gln Gly Ala Lys Gln Gly Glu Leu Gly
20 25 30

Ser Ser Cys Leu Arg Pro Asn Leu His Asp Asp Leu Gln Ala Arg Val
35 40 45

Phe Lys Xaa Ser Gly Lys Phe Pro Gly Lys Pro Glu Val Lys Gly Gln
50 55 60

Asn Cys Lys Ser Val Glu Ile Gly
65 70

<210> 1610
<211> 77
<212> PRT
<213> Homo sapiens

<400> 1610
Leu Tyr Arg Gly Ser Val Gln Gly Arg Val Glu Leu Leu Ser Glu Gly
1 5 10 15

Ser Leu Gly Gly Pro Leu Arg Pro Gly Pro Asp Pro Val Leu Gln Gly
20 25 30

Leu Ser Gln Gly Gln Val His Gly Glu Thr Met Gly Cys Leu Ser Asp
35 40 45

Thr Asp Leu Ala Leu Leu Ser Pro Pro Ile Arg Leu Ser Phe Leu Cys
50 55 60

Ser Glu Cys Leu Gln Gly Leu Asp Pro Gly Lys Glu Phe
65 70 75

<210> 1611
<211> 72
<212> PRT
<213> Homo sapiens

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<400> 1611
Glu Asn Leu Pro Ser Gln Xaa Ala Pro Ala Gly Leu Pro Lys Xaa Xaa
1   5   10   15

Gln Pro Cys Leu Tyr Phe Tyr Gly Xaa Asn Gly His Lys Ile Ile Ile
20 25 30

Asn Leu Thr Lys Thr Xaa Leu Phe Ser Xaa Phe Leu Glu Leu Ser Trp
35 40 45

Ser Phe Leu Ile Leu Xaa Phe Gly Asn Xaa Arg Leu Phe Leu Lys Cys
50 55 60

Phe Xaa Asp Val Lys Ile Xaa Tyr
65 70

<210> 1612
<211> 63
<212> PRT
<213> Homo sapiens

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<400> 1612
Arg Glu Ser Glu Met Leu Cys Asn Leu Leu Xaa Gln Leu Lys His Xaa
1   5   10   15

Met Leu Arg Gly Arg Asn Tyr Lys Xaa Cys Ser Asn Leu Phe Trp Val
            20   25   30

Ile Xaa Met Tyr Leu Trp Val Gln Ala Leu Phe Gly Gly Phe Xaa Phe
        35   40   45

Gln Arg Asn Xaa Xaa Lys Val Xaa Leu Leu Ile Lys Lys Arg Lys
    50   55   60

<210> 1613
<211> 22
<212> PRT
<213> Homo sapiens

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<220>
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<220>
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<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (12)
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<400> 1613
Lys Ser Xaa Ser Xaa Thr Ala Gly Asp Arg Xaa Xaa Thr Ser Gly Ser

1 5 10 15

Pro Gly Leu Gln Glu Phe
20

<210> 1614
<211> 85
<212> PRT
<213> Homo sapiens

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<400> 1614
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Asp Gly Gly Phe Xaa Xaa Phe Phe Phe Phe Phe Phe Phe Xaa Xaa Phe
  1               5                  10                  15

Phe Phe Tyr Xaa Trp Val Ile Ser Thr Cys Phe Ile Pro Ala Ile Lys
             20                  25                  30

Ile Ile Lys Asn Ile Ser Asn Tyr Tyr Thr His Thr Lys Xaa Val Gln
         35                  40                  45

Ser Leu Xaa Leu Pro Pro Thr Pro Arg Gly Lys Asn Cys Phe Xaa Leu
     50                  55                  60

Trp Glu Val Val Ser Glu Thr Arg Gly Gln Xaa Thr Gln Xaa Arg Leu
 65                  70                  75                  80

Gly Gly Xaa Arg Xaa
                 85
```

<210> 1615
<211> 85
<212> PRT
<213> Homo sapiens

<400> 1615
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Tyr Ala Val Pro Cys Ser Gly Ile Gln Gly Arg Phe Ser Pro Leu Ser
  1               5                  10                  15
```

Phe Leu Leu Ala Gly Asp Ser Cys Thr Cys Ala Gly Ser Cys Lys Cys
            20   25   30

Lys Glu Cys Lys Cys Thr Ser Cys Lys Lys Ser Lys Trp Asp Pro Leu
        35   40   45

Phe Pro Leu Pro Leu Pro Val Leu Gln Pro Val Pro Ser Ser Pro Ser
    50   55   60

Ser Gly Glu Leu Lys Gln Val Trp Gly Cys Pro Ile Ala Pro Gly Asn
65   70   75   80

Trp Trp Pro Pro Gln
                85

<210> 1616
<211> 29
<212> PRT
<213> Homo sapiens

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<400> 1616
Ala Glu Gly Asn Ile Arg Xaa Ala Lys Lys Lys Lys Lys Lys Lys Lys
1   5   10   15

Lys Lys Lys Lys Lys Lys Lys Lys Xaa Xaa Lys Xaa Xaa
20 25

<210> 1617
<211> 37
<212> PRT
<213> Homo sapiens

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<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (36)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1617
Gly Pro Ala Xaa Trp Arg Glu Thr Pro Pro Xaa Leu Tyr Lys Glu Phe
1 5 10 15

Pro Gly Val Xaa Gly Ser Phe Ser Leu Xaa Ser Glu Trp Gly Ala Gln
20 25 30

Ile Trp Ala Xaa Cys
35

<210> 1618
<211> 22
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (22)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1618
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Gly Xaa Gly Phe Xaa Pro Ser Pro Ser Cys Phe Pro Gln Cys Leu Lys
 1               5                  10                  15

Xaa Leu Asp Gly Leu Xaa
            20
```

<210> 1619
<211> 52
<212> PRT
<213> Homo sapiens

<400> 1619
```
Gln Ser Ile Ser Leu Asn Arg Asp Gly Val Glu Glu Leu Lys Val Gly
 1               5                  10                  15

Ile Cys Ser Leu Met Thr Thr Met Phe Thr Ile Cys Cys Gly Leu Val
            20                  25                  30

Gly Ala Leu Arg Gln Glu Asn His Val Glu Pro Thr Gly Ser Arg Pro
        35                  40                  45

Ala Trp Glu Thr
    50
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<210> 1620

<211> 52
<212> PRT
<213> Homo sapiens

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<400> 1620
Pro Thr Glu Gln Val Thr Leu Gly Ile Thr Ala Gln Ser Tyr Ser Arg
1 5 10 15

Val His Ile Asn Asn Arg Val Tyr Asp Leu Asp Xaa Gly Ser Gly His
20 25 30

Pro Asp Xaa Ala Ala Ala Ile Lys Gly Ser Phe Val Gln Arg Leu Lys
35 40 45

Ser Tyr Val Ile
50

<210> 1621
<211> 113
<212> PRT
<213> Homo sapiens

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<400> 1621
Leu Phe Pro Ala Pro Ala Pro Pro Pro Ala Pro Ala Phe Ala Pro Pro

```
  1               5                   10                  15

Pro Lys Val Pro Ser Pro Glu Arg Ser Ala Pro Arg Val Pro Leu Pro
            20                  25                  30

Ser Pro Gln Pro Ser Tyr Pro Phe Arg Pro Ala Ala Ser Gly Gly Thr
        35                  40                  45

Pro Pro Pro Ala Cys Leu Pro Pro Ala Gln Pro Cys Gln Val Pro Pro
    50                  55                  60

Ala Met Asn Leu Phe Arg Phe Leu Gly Lys Leu Ser Gln Leu Leu Ala
 65                 70                  75                  80

Ile Ile Leu Leu Leu Leu Xaa Ile Trp Asn Ser Arg Ser Cys Ala Glu
                85                  90                  95

Ile Gln Glu Lys Asn Ser Pro Val Trp Cys Gly Xaa Phe Asn Gly Xaa
            100                 105                 110

Ile


<210> 1622
<211> 21
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1622
Val Phe Lys Thr Met Xaa Gln Val Ser Asn Asp Glu Ile Lys His Leu
  1               5                   10                  15

Phe Val Leu Tyr Gln
            20


<210> 1623
<211> 40
<212> PRT
<213> Homo sapiens

<220>
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<222> (7)
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<222> (39)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (40)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1623
Leu Arg Thr Ser Cys Phe Xaa Leu Asn Xaa Met Ile His Phe Ile Lys
1   5   10   15

Val Pro Val Ile Lys Tyr Xaa Val Lys Tyr Leu Leu Xaa Trp Thr Ile
            20   25   30

Xaa Cys Lys Leu Pro Phe Xaa Xaa
        35   40

<210> 1624
<211> 95
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (95)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1624
Ile His Pro Xaa Leu Ala Ser Gln Val Ala Gly His Tyr Arg Arg Glu
1 5 10 15

His Ser Arg Pro Arg Leu Lys Xaa Ala Tyr Ser Lys Lys Gln Phe Gln
20 25 30

Phe Leu Ser Lys Leu Cys Xaa Xaa Arg Gly Ser Thr Asp Phe Leu Gly
35 40 45

Pro Val Asn Leu Asn Gln Ser Leu Arg Phe Cys Gln Glu Ser Ser Leu
50 55 60

Leu Ser Lys Trp Val Phe Pro Asn Gly His Asn Gly Lys Xaa Xaa Arg
65 70 75 80

Gly Xaa Asn Ile Lys Lys Xaa Lys Lys Asn Leu Gly Gly Gly Xaa
85 90 95

<210> 1625
<211> 40
<212> PRT
<213> Homo sapiens

<220>
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<222> (16)
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<220>
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<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1625
Ala Arg Ala Thr Met Ala Leu Trp Thr Xaa Val Ser Phe Ala Glu Xaa
1 5 10 15

Leu Glu Arg Gly Ser Asp Glu Lys Val Xaa Leu Lys Arg Leu Ala Arg
20 25 30

Leu Leu Gly Leu Ile Thr Ala Pro
35 40

<210> 1626
<211> 26
<212> PRT
<213> Homo sapiens

<220>
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<220>
<221> SITE
<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1626
```
Ala Arg Ala Gly Ile Val Pro Xaa His Ser Ser Leu Gly Asp Arg Ala
  1               5                  10                  15

Arg Leu His Leu Lys Lys Lys Lys Lys Xaa
             20                  25
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<210> 1627
<211> 171
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1627
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Glu Leu Gln Ala Ser Glu Asn Gln Pro Cys Ser Arg His Ala Arg Pro
  1               5                  10                  15

Arg Leu Pro Ser Ser Leu Phe Pro Leu Pro Ala Gln Pro Ser Leu Pro
             20                  25                  30

Ser Ser Ala Gly Lys Ala Gly Thr His Ser Gly Cys Leu Pro Pro Gly
         35                  40                  45

Gly Lys Glu Arg Glu Gly Gly Trp Val Gly Xaa Gly Leu Pro Pro Gly
     50                  55                  60

Asn Val Thr Leu Pro Gly Pro Arg Ile Ala Pro Gly Pro Lys Pro Lys
 65                  70                  75                  80

Ala Gln Pro Gly Thr Lys Leu Arg Xaa Ser Ala Gly Arg Ser Tyr Phe
                 85                  90                  95

Tyr Leu Pro Pro Pro Leu Leu Val Pro Pro Pro Gly Arg Leu Ala Ala
            100                 105                 110

Glu Ser Asp Thr Gly Xaa Xaa Lys Xaa Xaa Xaa Glu Pro Trp Tyr Pro
        115                 120                 125

Ile Leu Gly Pro Gly Pro Xaa Leu Gly Pro Asn Pro Ser Ser Val Asp
    130                 135                 140

Asn Gly Val Trp Asn Lys Cys Cys Leu Ser Xaa Gln Gln Lys Lys Lys
145                 150                 155                 160

Lys Arg Gly Gly Arg Phe Arg Gly Phe Lys Ala
                165                 170
```

<210> 1628
<211> 120
<212> PRT
<213> Homo sapiens

<220>
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<400> 1628
```
Arg Pro Ala Arg Ser Pro Ala Glu Val Gly Ser Arg Gly Leu Ser Ser
  1               5                  10                  15

Pro Pro Arg Ala His His Arg Pro Val Ser Pro Ala Ala Pro Gly Arg
             20                  25                  30

Trp Ser Thr Ser Ala Arg Val Arg Thr Arg Lys Met Val Asn Tyr Ala
         35                  40                  45

Trp Ala Gly Arg Xaa Arg Arg Lys Leu Trp Trp Arg Ser Val Ala Val
     50                  55                  60

Leu Thr Cys Lys Ser Val Val Arg Pro Gly Tyr Arg Gly Glu Arg Leu
 65                  70                  75                  80

Asn Arg Thr Ile Leu Val Ser Trp Phe Pro Ser Glu Xaa Phe Pro Gln
                 85                  90                  95
```

Asp Lys Leu Gly Ala Leu Ala Arg Pro Arg Arg Asn Pro Xaa Xaa Gly
100 105 110

Ile Phe Ile Arg Xaa Lys Arg Ile
115 120

<210> 1629
<211> 86
<212> PRT
<213> Homo sapiens

<400> 1629
Asn Leu Val Pro Gly Ser Ser Ala Thr Tyr Ile Ser Leu Ser Ser Cys
1 5 10 15

Cys Phe Val Lys Arg Lys Arg Lys Lys Lys Pro Lys Leu Val Arg Val
20 25 30

Ile Ser Asn Tyr Leu Ile Phe Cys Arg Ser Val Ile Lys Asn Leu Val
35 40 45

Ile Pro Ser Thr Ser Tyr Cys Glu Glu Gln Thr Leu Gly Pro Thr Leu
50 55 60

Lys Ser Pro Leu Val Thr His Ser His Pro Pro Gly Ser Cys Leu Pro
65 70 75 80

Gly Arg Gly Cys Arg Lys
85

<210> 1630
<211> 35
<212> PRT
<213> Homo sapiens

<220>
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<400> 1630
Leu Lys Lys Lys Phe Pro Glu Glu Glu Lys Lys Thr Thr Lys Asn Lys
1 5 10 15

Thr Leu Lys Val Asp Ile Leu Cys Gly Xaa Thr Phe Glu Leu Asn Ser
20 25 30

Glu Phe Phe
35

<210> 1631
<211> 40
<212> PRT
<213> Homo sapiens

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<400> 1631
His Glu Gln Pro Thr Ala Ala Cys Ile Cys Ile Xaa Arg Gln Val Pro
1 5 10 15

Pro Val Pro Ala Ala Arg Xaa Pro Gln Ser Arg Thr Xaa Ser Xaa Gln
20 25 30

Ala Lys Leu Ala Leu Thr Met Pro
35 40

<210> 1632
<211> 97
<212> PRT
<213> Homo sapiens

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<222> (91)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (95)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1632
Xaa Ser Gly Ser Pro Gly Pro Ala Gly Pro Arg Gly Pro Val Gly Pro
1   5   10   15

Xaa Gly Pro Pro Gly Lys Asp Gly Thr Xaa Gly His Pro Gly Ala Ile
            20   25   30

Gly Pro Pro Gly Pro Arg Gly Asn Xaa Gly Glu Xaa Gly Ser Xaa Gly
        35   40   45

Ser Pro Gly Pro Xaa Arg Ala Thr Arg Ala Leu Leu Xaa Pro Pro Gly
    50   55   60

Ala Pro Gly Pro Cys Cys Gly Gly Val Xaa Ala Ala Ala Ile Ala Gly
65   70   75   80

Ile Gly Arg Leu Lys Lys Leu Gly Arg Phe Xaa Pro Arg Val Xaa Trp
                85   90   95

Gly

<210> 1633
<211> 43
<212> PRT
<213> Homo sapiens

<220>
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<222> (31)
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<222> (39)
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<221> SITE
<222> (40)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1633
Glu Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1 5 10 15

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Gly Arg Pro Phe Xaa Arg
20 25 30

Ile Gln Xaa Tyr Val Xaa Xaa Xaa Ala Thr Ser
35 40

<210> 1634
<211> 88
<212> PRT
<213> Homo sapiens

<220>
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<222> (82)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (88)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1634
Ala Arg Ala Ala Leu Ser Ala Thr Lys Thr Cys Arg Pro Ala Phe Arg
1 5 10 15

Gly Ala Ser Ala Ala Pro Arg Gly Gly Gly Pro Ala Arg Ser Pro Gly
20 25 30

Arg Val Leu Gly Arg His Ala Ala Gly Ser Leu Ala Arg Leu Val Gly
35 40 45

Arg Ser Arg Gly Phe Trp Leu Leu Gly Gly Glu Val Lys Ser Phe Cys
50 55 60

Arg Cys Trp Gly Arg Arg Thr Arg Arg Glu Arg Lys Lys Lys Lys Lys
65 70 75 80

Lys Xaa Leu Gly Lys Tyr Phe Xaa
85

<210> 1635
<211> 105
<212> PRT
<213> Homo sapiens

<220>
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<222> (70)
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<222> (102)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1635
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Tyr Ser His Ser Gly Phe Cys Ser Pro Thr Asp Glu Asp Arg Cys Thr
  1               5                  10                  15

Asn Glu Ala Asp Gly Asn His Pro Val Glu Val His Leu Arg Ser Asp
             20                  25                  30

Pro Asp Asp Ala Arg Ala Met Thr Gly Pro Ala Gly Val Ala Pro Arg
         35                  40                  45

Gly Asp Gln Pro Trp Ser Ser His Arg Arg Lys Pro Leu Arg Ser Gly
     50                  55                  60

Lys Arg Arg Arg Lys Xaa Lys Trp Gln Lys Gln Lys Glu Pro Gln Ser
 65                  70                  75                  80

Ser Ile Gly Asp His Ser Met His Phe Leu Pro Ala Ala Thr Gln Thr
                 85                  90                  95

Leu Pro Glu Leu Leu Xaa Asn Leu Met
            100                 105
```

<210> 1636
<211> 47
<212> PRT
<213> Homo sapiens

<220>
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<222> (6)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (46)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1636
Gln Arg Pro Arg Xaa Xaa Gly Thr Gly Ser Gly Pro Pro Gly Pro Gly
1 5 10 15

Lys Ala Ser His Gly Gly Gly Ala Pro Val Ser Arg Ser Gly Thr Gly
20 25 30

Ser Glu Asp Gly Arg Glu Ser Arg Ala Thr Val Val Val Xaa Cys
35 40 45

<210> 1637
<211> 55
<212> PRT
<213> Homo sapiens

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<222> (50)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (55)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1637
```
Gly Asp Pro Pro Glu Gly Pro Ala Thr Ser Pro Leu Thr Asn Ser Xaa
  1               5                  10                  15

His Pro Xaa Ser Xaa Gly Thr Ala Ala Ala Thr Gln Arg Arg Xaa Ser
             20                  25                  30

Glu Gln Gly Gly Arg Xaa Thr Cys Gly Pro Ala Gly Ala Gly Ser Pro
         35                  40                  45

Xaa Xaa Pro Pro Arg Ala Xaa
     50                  55
```

<210> 1638
<211> 55
<212> PRT
<213> Homo sapiens

<220>
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<222> (3)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (44)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1638
```
Ile Arg Xaa His Ala Thr Xaa Tyr Arg Gly Xaa Phe Cys Xaa Arg Arg
 1               5                  10                  15

Thr Xaa Xaa Xaa Leu His Ser Ala Asn Val Thr Thr Xaa Xaa Leu Leu
            20                  25                  30

Leu Xaa Xaa Phe Tyr Xaa Xaa Arg Xaa Xaa Ala Xaa Val Asn Ile Ser
        35                  40                  45

Xaa Val Pro His Cys Pro Ile
    50                  55
```

<210> 1639
<211> 58
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (15)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (54)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1639
```
Ile Cys Pro Gln Asn Pro Leu Asn Pro Leu Val Asn Leu Thr Xaa Ser
 1               5                  10                  15
```

Pro Lys Arg Asn Ser Ser Leu Asp Thr Arg Lys Lys Pro Cys Arg Glu
20 25 30

Ser Lys Lys Phe Asn Thr His Ser Arg Pro Lys Ser Ser His Gln Leu
35 40 45

Arg Lys Arg Ser Ser Xaa Thr Pro Thr Thr
50 55

<210> 1640
<211> 37
<212> PRT
<213> Homo sapiens

<220>
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<222> (30)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1640
Met Cys Val Asp Cys Met Asn Asp Leu Glu Lys Lys Lys Lys Lys Lys
1 5 10 15

Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Xaa Pro Xaa
20 25 30

Gly Xaa Pro Xaa Pro
35

<210> 1641
<211> 41

<212> PRT
<213> Homo sapiens

<400> 1641
Tyr Val Trp Leu Gly His Phe Val Ala Lys Val Arg Thr Cys Leu Trp
1 5 10 15

Lys Thr Ser Leu Trp Leu Gly Glu Ser Val Trp Pro Ala Ala Ser Asp
20 25 30

Leu Cys Arg Val Leu Thr Cys Gln Gly
35 40

<210> 1642
<211> 99
<212> PRT
<213> Homo sapiens

<220>
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<222> (1)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (18)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (19)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (20)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (40)
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<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (51)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (95)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1642

```
Xaa Pro Ala Ala Ser Tyr Leu Met Thr Leu Met Glu Pro Leu Ser Leu
  1               5                  10                  15

Ile Xaa Xaa Xaa Leu Ser Pro Pro Leu Xaa Xaa Ser Lys Glu Asn His
             20                  25                  30

Phe Asp Ala Arg Ser Cys Leu Xaa Ser Xaa Pro Lys Cys Ser Cys Ser
         35                  40                  45

Xaa Pro Xaa Pro Gly Ile Ser Leu Pro Arg Asp Lys Ser Ala Ser Glu
     50                  55                  60

Ile Leu His Asp Ser Leu Cys Phe Gln Asn Pro Gly Leu Phe Cys Ile
 65                  70                  75                  80

Ser Ser Phe Leu Gly Pro Ala Ser Cys Val Pro Leu Lys Gly Xaa Trp
                 85                  90                  95

Ala Lys Thr
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<210> 1643
<211> 42
<212> PRT

<213> Homo sapiens

<220>
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<222> (2)
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<220>
<221> SITE
<222> (4)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1643
Lys Xaa Pro Xaa Asn Leu Gly Lys Ala Arg Leu Gln Val Pro Val Arg
1 5 10 15

Asn Ser Arg Val Asp Leu Arg Val Phe Ile Tyr Ile Asp Ile Tyr Ile
20 25 30

Asp Ile Tyr Arg Tyr Ile Tyr Arg Tyr Ile
35 40

<210> 1644
<211> 46
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (26)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (35)
<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE
<222> (40)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (42)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (43)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1644
Arg Val Gly Val Arg Leu Ala Gln Val Pro Xaa His Leu Thr Ser Arg
1 5 10 15

Ser His His Pro His Pro Val Phe His Xaa Arg Leu Lys Ala Thr Met
20 25 30

Arg Met Xaa His Thr Glu Ala Xaa Met Xaa Xaa Asn His Leu
35 40 45

<210> 1645
<211> 69
<212> PRT
<213> Homo sapiens

<400> 1645
His Val Arg Leu Lys Pro Ile Phe Ser Pro Phe Phe Leu Leu Phe Ser
1 5 10 15

Leu Ala Ala His Ile Val Pro Leu Phe Tyr Glu Pro Gln Phe Ser Gly
20 25 30

Leu Ser Leu Lys Lys Lys Ser Ser Leu Asn Ile Ala Phe Arg Lys Leu
35 40 45

Leu Phe Leu Asp Lys Lys Ser Tyr Thr Leu Lys Lys Lys Lys Thr Phe
50 55 60

Ser Arg Lys Ile Tyr
65

<210> 1646
<211> 78
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (42)

<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (54)
<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (77)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1646

```
Ile Ile Cys Phe Val Leu Ser Phe Ile Tyr His Phe Phe Leu Tyr Lys
  1               5                  10                  15

Ser Ile Ile Ser Arg Phe Leu Tyr Tyr Met Ile Asp Ile Asn Trp Val
             20                  25                  30

Ile Ser Ser Arg Gln Phe Val Phe Ser Xaa Xaa Pro Pro Ser Thr Val
         35                  40                  45

Ser Gln Arg Pro Asp Xaa Val Gly Lys Val Phe Phe Leu Arg Ile Val
     50                  55                  60

Lys Gly Ser Xaa Gln Leu Gly Leu Ile Lys Ala Xaa Xaa Pro
 65                  70                  75
```

<210> 1647
<211> 58
<212> PRT
<213> Homo sapiens

<400> 1647

Ile Cys Pro Gln Asn Pro Leu Asn Pro Leu Val Asn Leu Thr Val Ser
1 5 10 15

Pro Lys Arg Asn Ser Ser Leu Asp Thr Arg Lys Lys Pro Cys Arg Glu
20 25 30

Ser Lys Lys Phe Asn Thr His Ser Arg Pro Lys Ser Ser His Gln Leu
35 40 45

Arg Lys Arg Ser Ser Ser Thr Pro Thr Thr
50 55

<210> 1648
<211> 59
<212> PRT
<213> Homo sapiens

<400> 1648
Cys Leu Phe Leu Leu Pro Val Met Leu Leu Gln Ile His Ile Ser Arg
1 5 10 15

Ser Thr Val Asn Val Ser Thr Ser Arg Gly Thr Pro Pro Ser Thr Leu
20 25 30

Ser Val Lys Gly Gln Asn Glu Thr Val Arg Val Lys Gly Thr Gly Arg
35 40 45

Lys Phe Ala Cys Leu Gln Val Thr Arg Ile Arg
50 55

<210> 1649
<211> 110
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (54)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (71)
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<220>
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<222> (88)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (94)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1649
```
Val Pro Pro Pro Val Pro Trp Gly Gly Pro Xaa Arg Glu Gly Glu Val
  1               5                  10                  15

Ser His Thr Lys Ala Asp Ala Pro Leu Val Gly Gly Xaa Trp Pro Gly
             20                  25                  30

Lys Ile Glu Gly Cys Ala Gly Leu Pro Leu Arg Ala Ala Gln Thr Ala
         35                  40                  45

Leu Met Cys Gly Gly Xaa Ala Arg Trp Val Arg Ala Gln Glu Val Ala
     50                  55                  60

Pro Xaa Thr Val Ala Asp Xaa Leu Pro Arg Val Pro Gly Ser Ser Leu
 65                  70                  75                  80

Tyr Pro Trp Tyr Ala Xaa Asn Xaa Trp Phe Pro His Pro Xaa Ala Ala
                 85                  90                  95

Lys Ser Leu Phe Pro Trp Ile Ser Gln Ala Lys Leu Gly Leu
            100                 105                 110
```

<210> 1650
<211> 74
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (11)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (28)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1650
```
Ser Pro Glu Gly Leu Ser Leu Leu Ala Pro Xaa Pro Gly Arg Ala Pro
  1               5                  10                  15

Ala Gly Pro Thr Pro Leu Arg Gly Gln Cys Gln Xaa Gly Ser Leu Thr
             20                  25                  30

Gly Ala Val His Leu Ser Asn Gly Asn Ala Gly Val Leu Arg Arg Ala
         35                  40                  45

Gln Gly Gly Gln Lys Pro Pro Val Glu Gln Lys Gly Lys Ser Ser Leu
     50                  55                  60

Asp Leu His Phe Gln Tyr Glu Tyr Arg Pro
 65                  70
```

<210> 1651
<211> 83
<212> PRT
<213> Homo sapiens

<220>
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<222> (30)
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<221> SITE

<222> (49)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (51)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (52)
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<222> (62)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (64)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (65)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (67)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1651
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Asn Lys Gly Gly Gly Arg Met Met Thr Tyr Pro Glu Val Leu Pro Leu
  1               5                  10                  15

Thr Ala Arg Thr Gly Ala Cys Ser Val Pro Trp Glu His Xaa Ala Gln
             20                  25                  30

Leu Ser Gly Val Gln Ala Val Gly Ser Phe Pro Asn Xaa Ser Ile Ser
         35                  40                  45

Xaa Pro Xaa Xaa Leu Lys Pro Val Gly Gln Ile Ser Lys Xaa Leu Xaa
     50                  55                  60

Xaa Arg Xaa Pro Phe Thr Asn Pro Arg Phe Cys Gly Gln Cys Pro Lys
 65                  70                  75                  80

Gly Val Gly
```

<210> 1652
<211> 90
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (11)
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<220>
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<222> (41)
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<222> (54)
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<222> (55)
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<222> (76)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (89)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1652
Phe Phe Phe Phe Leu Asp Val Lys Gly Ile Xaa Phe Gln Arg Leu Leu
1 5 10 15

Glu Ser Leu Val Tyr Thr Asp Glu Gly Val Arg Cys Cys Phe Pro Ser
20 25 30

Glu Ser Ser Ala Ser Thr Glu Ile Xaa Leu Xaa Leu Ile Phe Asp Ile
35 40 45

Leu His Cys Leu Leu Xaa Xaa Xaa Arg Ser Phe Leu Pro Phe Thr Ser
50 55 60

Pro Ser Asn Tyr Val Gln Met Cys Arg Leu Leu Xaa Ser Gly Leu Ser
65 70 75 80

Pro Lys Ala Leu Thr Leu Gly Leu Xaa Phe
85 90

<210> 1653
<211> 55
<212> PRT
<213> Homo sapiens

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<400> 1653
Lys Leu Trp Phe Val Phe Val Phe Cys Leu Phe His Leu Phe Pro Ser
1 5 10 15

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Gln Pro Gln Thr Phe Cys Ser Leu Arg Glu Leu Thr Phe Pro Phe Phe
            20                  25                  30

Phe Leu Phe Phe Phe Phe Gly Xaa Leu Xaa Val Xaa Asn Lys Ile Xaa
        35                  40                  45

Xaa Ala Ile Lys Lys Lys Lys
    50                  55
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<210> 1654
<211> 61
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1654
Val Xaa Ala Thr Asn Leu Pro Ser Leu Val Ile Ala Xaa Cys Ser Xaa
1 5 10 15

Ile Glu Ser Leu Val Pro Leu Leu Ile Trp Pro Gln Lys Pro Pro Asn
20 25 30

Ser Pro Trp Leu Ile Leu Thr Val Xaa Pro Lys Lys Gly Thr Xaa Ser
35 40 45

Leu Gly Pro Leu Xaa Lys Lys Thr Leu Xaa Lys Xaa Asn
50 55 60

<210> 1655
<211> 20
<212> PRT
<213> Homo sapiens

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<400> 1655
Ala Ala Val Leu Gln Thr Ala Arg Arg Ala Arg Ser Ala Cys Arg Leu
1 5 10 15

Xaa Xaa Xaa Xaa

20

<210> 1656
<211> 24
<212> PRT
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<400> 1656
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Ala Asp Ile Gln Thr Glu Arg Ala Tyr Gln Lys Xaa Xaa Thr Ile Phe
  1               5                  10                  15

Xaa Asn Xaa Lys Arg Val Leu Leu
             20
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<210> 1657
<211> 34
<212> PRT
<213> Homo sapiens

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<400> 1657
Ala Ala Ala Cys Leu Pro Ala Thr Glu Xaa Ser Gln His His Glu Gly
1 5 10 15

Leu Asp Leu Leu Ser Pro Leu Pro Gly Arg Glu Gly Leu Gly Xaa Pro
20 25 30

Ser Xaa

<210> 1658
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1658
Cys Lys Gln Tyr Leu Thr Asn Pro Gln Val Leu Asn Tyr Gln Thr Cys
1 5 10 15

Ile Lys Asn Phe Gly Trp Gly Asp Leu Gly Ala Glu Pro Asn Leu Arg
20 25 30

Ala Val His Ala Lys Thr Ser Pro Val Lys Ala Asn Tyr Tyr Thr Gln
35 40 45

Leu Ile Gln
50

<210> 1659
<211> 166
<212> PRT
<213> Homo sapiens

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<400> 1659
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Ser Thr His Ala Ser Gly His Ser His Ser Gln Ala Ser Leu Ala Gly
  1               5                  10                  15

Ser Arg Val Ala Arg Val Arg Cys Leu Leu Gln Leu Gln Asp Asp Arg
             20                  25                  30

Pro Glu Asp Ala Leu Leu Leu Phe Leu Pro Gln Pro Arg Gln Glu Ala
         35                  40                  45

Thr Xaa Pro Gln Xaa Pro Ser Arg Pro Ser Arg Gly Pro Xaa Trp Leu
     50                  55                  60

Gly Leu Leu Lys Lys Ala Glu Xaa Gly Gly His Pro Ser Gln Glu Xaa
 65                  70                  75                  80

Pro Gly Trp Xaa Gly Glu Xaa Xaa Glu Arg Arg Pro Pro Trp Xaa Leu
                 85                  90                  95

Asn Xaa Arg Thr Phe Trp Asn Arg Ile Pro Glu Glu Gln Arg Ala Arg
            100                 105                 110

Gly Pro Xaa Leu Xaa Xaa Arg Gly Pro Xaa Xaa Val Xaa Pro Trp Gly
        115                 120                 125

Phe Leu Glu Xaa Xaa Pro Gly Lys Glu Ser Xaa Leu Arg Gly Gly Xaa
    130                 135                 140

Phe Arg Gly Lys Xaa Leu Phe Leu Ile Lys Ala Lys Leu Gly Ile Xaa
145                 150                 155                 160

Phe Xaa Lys Arg Lys Gly
                165
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<210> 1660
<211> 68
<212> PRT
<213> Homo sapiens

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<222> (20)
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<222> (66)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1660
Ser Pro Gly Leu Gln Glu Phe Gly Xaa Arg Gly Xaa Arg Asn Arg Leu
1   5   10   15

Asn Tyr Ala Xaa Xaa His His Xaa Xaa Pro His Arg Xaa Ser Ile Pro
            20   25   30

Thr His Ala Leu His Ser Xaa Arg Gly Asp Asp Ala Xaa Leu Thr Ile
        35   40   45

Lys Ile Xaa Xaa Pro Pro Met Val Leu Glu Pro Thr Ser Thr Pro Asp
    50   55   60

His Xaa Val Asp
65

<210> 1661
<211> 61
<212> PRT
<213> Homo sapiens

<220>
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<220>
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<222> (48)
<223> Xaa equals any of the naturally occurring L-amino acids

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<222> (54)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1661
Leu Asn Ala Asp Thr Leu Met Asn Asp Gln Gln Gln Leu Ser Ala Leu
1   5   10   15

Lys Lys Thr Leu Ile Phe Glu Phe Thr Cys Trp Val Pro Gly Ser Asn
            20   25   30

Gly Gly Lys Arg Pro Leu Phe Ile Lys Arg Gly Pro Pro Phe Xaa Xaa

35 40 45

Pro Lys Asp Phe Leu Xaa Phe Gln Ile Gly Lys Gly Thr
50 55 60

<210> 1662
<211> 54
<212> PRT
<213> Homo sapiens

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<222> (3)
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<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (47)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1662
Thr Val Xaa Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Asn Leu
1 5 10 15

Glu Val Xaa Gly Ile Xaa Asn Leu Asp Ile Xaa Phe Gly Thr Ser Asn
20 25 30

Pro His Ser Pro Thr His Ala Gly Gly Cys Ala Cys Arg Thr Xaa Leu
35 40 45

Thr Asp Trp Trp Ile Leu
50

<210> 1663
<211> 95
<212> PRT
<213> Homo sapiens

<400> 1663
Ala Arg Glu Lys Leu Cys Val Arg Gly Arg Gly Leu Phe Arg Cys Arg
1 5 10 15

Val Ser Ser Ser Cys Thr Leu Phe Lys Ser Leu His Trp Arg Asn Ser
20 25 30

Ala Ile Thr Ser Ser Leu Val Ala Glu Gly Arg Gly Asn Ile His Leu
35 40 45

Phe Met Pro Val Cys Cys Met Gln Ala Phe Trp Leu Pro Thr Leu Gln
50 55 60

Gln Asn Asn Cys Thr Asn Ser Leu Val Pro Ile Pro Pro Thr Glu Ser
65 70 75 80

Pro Gly Ala Thr Val Phe Phe Ala Leu His Cys Lys Glu Arg Asp
85 90 95

<210> 1664
<211> 100
<212> PRT
<213> Homo sapiens

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<222> (91)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1664
Val Asn Gln Glu Thr Thr Pro Val Asp Cys Gly Ala Leu Glu Gly Leu
1   5   10   15

Val Gly Val Asn Leu Pro Thr Pro Tyr Asn Cys Gly Arg Ile Gln Lys
            20   25   30

Ser Leu Ser Phe Tyr Ile His Ser Leu Asp Val Ile Gly Pro Leu Pro
        35   40   45

Pro Ile Ser Leu Arg Cys His Ala Ser Met Gly Ser Gly Val Val Arg
    50   55   60

Lys Asn Lys Arg Arg Xaa Asp Ser Leu Val Met Asp Lys Ile Leu Thr
65   70   75   80

Thr Val Phe Pro Xaa Gly Ile Pro Tyr Xaa Xaa Phe Asn Phe Phe Phe
                85   90   95

Ser Leu Lys Asn
            100

<210> 1665
<211> 33
<212> PRT
<213> Homo sapiens

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<221> SITE
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1665
Ser Ala Pro Gly Gly Ser Cys Tyr Ser Gly Xaa Pro Arg Val Pro Lys
1 5 10 15

Cys Xaa Ile Gln Xaa Asp Pro Xaa Ser Xaa Pro Pro Cys Leu Gln Leu
20 25 30

Val

<210> 1666
<211> 47
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (26)
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<400> 1666
Gly Arg Val Gly Gly Arg Val Gly Gly Arg Val Gly Arg Glu Pro Gln
1 5 10 15

Val Tyr Thr Leu Pro Pro Ser Arg Glu Xaa Met Thr Lys Lys Gln Ser
20 25 30

Ala Glu Leu Pro Xaa Ser Xaa Gly Phe Tyr Pro Thr Lys Ser Pro
35 40 45

<210> 1667
<211> 34
<212> PRT

<213> Homo sapiens

<220>
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<400> 1667
Leu Glu Ile Thr Leu Gln Gly Glu Pro Lys Leu Arg Pro Pro Lys Pro
1 5 10 15

Glu Arg Ala Thr Leu Glu Gln Leu Lys Glu His Thr Pro Leu Phe Leu
20 25 30

Pro Xaa

<210> 1668
<211> 41
<212> PRT
<213> Homo sapiens

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<400> 1668
Ile Cys Pro Gln Asn Pro Leu Asn Pro Leu Val Asn Leu Thr Val Xaa

1 5 10 15

Pro Lys Arg Asn Lys Leu Phe Gly His Xaa Glu Lys Thr Leu Tyr Arg
20 25 30

Glu Glu Xaa Xaa Phe Xaa Asn Pro Tyr
35 40

<210> 1669
<211> 96
<212> PRT
<213> Homo sapiens

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (88)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1669
Gly Arg Ala Leu Pro Gly Arg Val Arg Ala Ala Thr Gly Glu Gly Arg
1 5 10 15

Thr Phe Val Xaa Asn Gly Thr Val Leu Leu Ala Pro Pro Arg Gly Gly
20 25 30

Pro Leu Val Ser Pro Leu Pro Ala Arg Arg Arg Cys Val Trp Glu Gly
35 40 45

Val Gly Cys Gly Pro Arg Pro Asp Leu Ala Val Pro Pro Ala Ala Phe
50 55 60

Cys Val Ala Gly Ala Gly Arg Arg Gly Pro Leu Thr Xaa Gln Thr Ala
65 70 75 80

Leu Ala Val Xaa Ser Ser Gly Xaa Arg Leu Ala Gly Gly Thr Pro Thr
85 90 95

<210> 1670
<211> 140
<212> PRT
<213> Homo sapiens

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<400> 1670
Gly Ser Thr His Ala Ser Gly Ser Thr Glu Lys Glu Gly Leu Leu His
1 5 10 15

Glu Ala Thr Leu Ser Val His Gln Gly Leu Gly Leu Arg Gly Pro Trp
20 25 30

Ser Ser Cys Ser Ser Pro Ala Pro Pro Trp Met His Cys Cys Arg Ala
35 40 45

Glu Xaa Pro Leu Pro Gly Pro Ala Leu Gly Phe Leu Glu Thr Ser Phe
50 55 60

Ser Phe Ala Ile Phe Phe Lys Trp Glu Lys Gly Gly Gln Leu Ser Leu
65 70 75 80

Gly Lys Arg Gly Pro Ala Thr Cys Pro Ala Trp Ala Pro Glu Pro Ser
85 90 95

Ser Leu Thr Gly Gln Ser Leu Val Gly Lys Ala Ala Ser Trp Pro Xaa
100 105 110

Ser Leu Leu Met Phe Leu Val Ser Arg Val Gln Ser Gln Leu Phe Xaa
115 120 125

Phe Leu Val Val Pro Val Xaa Glu Ala Phe Gln Asn
130 135 140

<210> 1671
<211> 34
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (2)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (20)
<223> Xaa equals any of the naturally occurring L-amino acids

<220>
<221> SITE
<222> (27)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1671
His Xaa Xaa Met Glu Ser Asp Lys Met Val Thr Gly Ser Trp Gly Pro
1 5 10 15

Arg Leu Ser Xaa His Glu Gly Cys Ser Ala Xaa Cys Ile Ser Val Tyr
20 25 30

Val Val

<210> 1672
<211> 113

<212> PRT
<213> Homo sapiens

<220>
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<223> Xaa equals any of the naturally occurring L-amino acids

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<223> Xaa equals any of the naturally occurring L-amino acids

<220>
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<222> (12)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1672
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Arg Xaa Leu Leu Thr Ile Xaa Glu Ser Trp Tyr Xaa Cys Arg Tyr Arg
  1               5                  10                  15

Ser Gly Ile Pro Gly Gly Ile Pro Leu Ser Pro Arg Asp Pro Thr Leu
             20                  25                  30

Ala Ser Trp Pro Thr Arg Ser Arg Glu Ser Leu Arg Glu Arg Arg Arg
         35                  40                  45

Ser Arg Ala Ala Ser Gly Leu Gly Ile Arg Pro Leu Gly Pro Pro Leu
     50                  55                  60

Val Ser Arg Val Gly Arg Asn Arg Arg Leu Ala His Leu Ala Trp Val
 65                  70                  75                  80

Cys Pro His Val Val Ile Val Gln Ile Asn Ala His Ser Glu Leu Ala
                 85                  90                  95

Val Tyr Phe Leu Lys Phe Asn Ile Val Phe Val Ile Leu Lys Tyr Leu
            100                 105                 110

Leu
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<210> 1673
<211> 86
<212> PRT
<213> Homo sapiens

<220>

<221> SITE
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<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1673
Pro Ala Phe Asn Phe Asp Pro Leu Phe Phe Leu Phe Val Arg Cys Thr
1 5 10 15

Arg Leu Pro Ser Cys Phe Ser Leu Leu Ser Cys His Gln Pro Phe Leu
20 25 30

Leu Gly Gly His Val Leu Gly Lys Arg Pro His Asp Leu Ser Gly Ser
35 40 45

Thr Gln Cys Leu Arg His Pro Ala Ser Phe Ala Cys Ile Pro Gln Thr
50 55 60

Ile Ser Leu Ile Leu Phe Thr Ala Ala Asn Leu Ser Leu Val Asp Glu
65 70 75 80

Thr Val Phe Ile Xaa Leu
85

<210> 1674
<211> 56
<212> PRT
<213> Homo sapiens

<400> 1674
Ser Asp Tyr Glu Leu Leu Phe Lys Arg Lys Met Leu Phe Ile His Ala
1 5 10 15

Glu Val Ile Gln Phe Pro Pro Ser Tyr Arg Ser Ile Leu Ile His Pro
20 25 30

Thr Leu Glu Met Gln His Leu Cys Gly Arg Leu Phe His Lys Pro Pro
35 40 45

Arg Leu Leu Arg Leu Gly Arg Tyr
50 55

<210> 1675
<211> 65
<212> PRT
<213> Homo sapiens

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<400> 1675
Leu Val Cys Ile Leu Pro Lys Val Arg Xaa Pro Thr Leu Gly Ile Thr
1 5 10 15

Leu Leu Ile Val Ile Leu Val Xaa Ile Leu Pro Gly Val Met Tyr Ser
20 25 30

Leu Lys Ala Leu Asn Val Cys Ile Ala Thr Xaa His Gln Ile Leu Asn
35 40 45

Gly Leu Ser Phe Gly Trp Asn Tyr Lys Leu Lys Lys Cys Phe Ser Gly
50 55 60

Lys
65

<210> 1676
<211> 52
<212> PRT
<213> Homo sapiens

<220>
<221> SITE
<222> (44)
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<400> 1676
Pro Thr Glu Gln Val Thr Leu Gly Ile Thr Ala Gln Ser Tyr Ser Arg
1 5 10 15

Val His Ile Asn Asn Arg Val Tyr Asp Leu Asp Val Gly Ser Gly His
20 25 30

Pro Asp Gly Ala Ala Ala Ile Lys Gly Ser Phe Xaa Gln Arg Leu Lys
35 40 45

Ser Tyr Val Ile
     50

<210> 1677
<211> 40
<212> PRT
<213> Homo sapiens

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<220>
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<222> (37)
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<220>
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<222> (39)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1677
Xaa Xaa Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Xaa Lys Lys
 1   5   10   15

Lys Lys Lys Lys Lys Lys Gly Gly Arg Xaa Lys Gly Ser Lys Leu Thr

20 25 30

Tyr Xaa Cys Met Xaa Arg Xaa Ser
35 40

<210> 1678
<211> 49
<212> PRT
<213> Homo sapiens

<400> 1678
Thr Ala Ala Met Ser Ile Phe Thr Pro Thr Asn Gln Ile Arg Leu Thr
1 5 10 15

Asn Val Ala Val Val Arg Met Lys Arg Ala Arg Lys Arg Phe Glu Ile
20 25 30

Ala Cys Tyr Arg Asn Lys Ser Ser Ala Gly Gly Gly Leu Trp Lys Lys
35 40 45

Thr

<210> 1679
<211> 51
<212> PRT
<213> Homo sapiens

<400> 1679
Ala Ala Ala Gln Gln Val Val Asp Gln Ala Thr Glu Ala Gly Gln Lys
1 5 10 15

Ala Met Asp Gln Leu Ala Lys Thr Thr Gln Glu Thr Ile Asp Lys Thr
20 25 30

Ala Asn Gln Ala Ser Asp Thr Phe Ser Gly Ile Gly Lys Lys Phe Gly
35 40 45

Leu Leu Lys
50

<210> 1680
<211> 41
<212> PRT
<213> Homo sapiens

<400> 1680
Ala Phe Asn Arg Ser Gln Arg Gly Ser Cys Ser Ala Thr Tyr Glu Thr
1 5 10 15

Pro Thr Gln Lys Gln Val Val Tyr Glu Trp Phe Ser Ala Arg Phe Pro
20 25 30

Thr Asn Val Arg Cys Val Thr Gly Glu
35 40

<210> 1681
<211> 34
<212> PRT
<213> Homo sapiens

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<400> 1681
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1 5 10 15

His Pro Asn Pro Leu Pro Lys Gly Arg Arg Gly Pro Val Thr Gln Phe
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Ala Leu

<210> 1682
<211> 85
<212> PRT
<213> Homo sapiens

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<400> 1682
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Gln Thr Ile Ser Tyr Glu Val Thr Leu Ala Ile Ile Pro Thr Ile Asn
20 25 30

Ile Thr Asn Xaa Leu Ala Pro Leu Thr Ser Pro Pro Leu Ser Gln His
35 40 45

Lys Asn Thr Pro Glu Tyr Pro Ala Ile Ile Thr Leu Trp Pro Tyr Xaa
50 55 60

Ile Ile Phe His Thr Arg Xaa Asn Asn Glu Pro Pro Ser Xaa Leu Xaa
65 70 75 80

Lys Gly Asn Phe Xaa
85

<210> 1683
<211> 53
<212> PRT
<213> Homo sapiens

<400> 1683
Val Gly Leu Glu Ile Asn Met Leu Ala Phe Ile Pro Val Leu Thr Lys
1 5 10 15

Lys Ile Asn Pro Arg Ser Thr Glu Ala Ala Ile Lys Tyr Phe Leu Thr
20 25 30

Gln Ala Thr Ala Ser Ile Ile Leu Leu Ile Ala Ile Leu Phe Asn Asn
35 40 45

Ile Leu Ser Gly Gln
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<210> 1684
<211> 169
<212> PRT
<213> Homo sapiens

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<221> SITE
<222> (146)
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<222> (156)
<223> Xaa equals any of the naturally occurring L-amino acids

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<221> SITE
<222> (161)
<223> Xaa equals any of the naturally occurring L-amino acids

<400> 1684
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1 5 10 15

Asp Gly Arg Val Ser Val Ser Ala Arg Ile Asp Arg Lys Gly Phe Cys
20 25 30

Glu Gly Asp Glu Ile Ser Ile His Ala Asp Phe Glu Asn Thr Cys Ser
35 40 45

Arg Ile Val Val Pro Lys Ala Ala Ile Val Ala Arg His Thr Tyr Leu
50 55 60

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Ala Asn Gly Gln Thr Lys Val Leu Thr Gln Lys Leu Ser Ser Val Arg
 65                 70                  75                  80

Gly Asn His Ile Ile Ser Gly Thr Cys Ala Ser Trp Arg Gly Lys Ser
                85                  90                  95

Leu Arg Val Gln Lys Ile Arg Pro Ser Ile Leu Gly Cys Asn Ile Leu
            100                 105                 110

Arg Val Glu Tyr Ser Leu Leu Ile Tyr Val Ser Val Pro Gly Ser Lys
        115                 120                 125

Lys Val Ile Leu Asp Leu Pro Leu Val Ile Gly Ser Arg Ser Gly Leu
    130                 135                 140

Ser Xaa Arg Thr Ser Ser Trp Xaa Ala Xaa Thr Xaa Ser Glu Asp Glu
145                 150                 155                 160

Xaa Gly Arg Ser Glu His Pro Asp Thr
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<212> DNA
<213> Homo sapiens

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aattcgaggg tgcaccgtca gtcttcctct tccccccaaa acccaaggac accctcatga 120
tctcccggac tcctgaggtc acatgcgtgg tggtggacgt aagccacgaa gaccctgagg 180
tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca aagccgcggg 240
aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg caccaggact 300
ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca acccccatcg 360
agaaaaccat ctccaaagcc aaagggcagc cccgagaacc acaggtgtac accctgcccc 420
catcccggga tgagctgacc aagaaccagg tcagcctgac ctgcctggtc aaaggcttct 480
atccaagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac aactacaaga 540
ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctacagcaag ctcaccgtgg 600
acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat gaggctctgc 660
acaaccacta cacgcagaag agcctctccc tgtctccggg taaatgagtg cgacggccgc 720
gactctagag gat                                                     733

<210> 1686
<211> 5
<212> PRT
<213> Homo sapiens
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<220>
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<400> 1686
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1 5

<210> 1687
<211> 86
<212> DNA
<213> Homo sapiens

<400> 1687
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cccgaaatat ctgccatctc aattag 86

<210> 1688
<211> 27
<212> DNA
<213> Homo sapiens

<400> 1688
gcggcaagct ttttgcaaag cctaggc 27

<210> 1689
<211> 271
<212> DNA
<213> Homo sapiens

<400> 1689
ctcgagattt ccccgaaatc tagatttccc cgaaatgatt tccccgaaat gatttccccg 60
aaatatctgc catctcaatt agtcagcaac catagtcccg cccctaactc cgcccatccc 120
gcccctaact ccgcccagtt ccgcccattc tccgccccat ggctgactaa ttttttttat 180
ttatgcagag gccgaggccg cctcggcctc tgagctattc cagaagtagt gaggaggctt 240
ttttggaggc ctaggctttt gcaaaaagct t 271

<210> 1690
<211> 32
<212> DNA
<213> Homo sapiens

<400> 1690
gcgctcgagg gatgacagcg atagaacccc gg 32

<210> 1691
<211> 31
<212> DNA
<213> Homo sapiens

<400> 1691
gcgaagcttc gcgactcccc ggatccgcct c 31

<210> 1692
<211> 12
<212> DNA
<213> Homo sapiens

<400> 1692
ggggactttc cc 12

<210> 1693
<211> 73
<212> DNA
<213> Homo sapiens

<400> 1693
gcggcctcga ggggactttc ccggggactt tccggggact ttccgggact ttccatcctg 60
ccatctcaat tag 73

<210> 1694
<211> 256
<212> DNA
<213> Homo sapiens

<400> 1694
ctcgagggga ctttcccggg gactttccgg ggactttccg ggactttcca tctgccatct 60
caattagtca gcaaccatag tcccgcccct aactccgccc atcccgcccc taactccgcc 120
cagttccgcc cattctccgc cccatggctg actaattttt tttatttatg cagaggccga 180
ggccgcctcg gcctctgagc tattccagaa gtagtgagga ggcttttttg gaggcctagg 240
cttttgcaaa aagctt 256

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/05882

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12P 19/34
US CL : 435/91.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 435/91.1

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
MEDLINE, SCISEARCH, GenEmbl Database

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Database GenEmbl on STN. KELKER, W. 'Sequence of human E-cadherin cDNA', GenEmbl Database, Aceesion Z18923.1, Version Z18923.1 GI:31074, 04 December, 1992 (04.12.1992), see nucleotide position 456-1007.	1-12, 14-16, and 21 for SEQ ID NO:1
Y	BANERJI, J. A gene pair from the human major histocompatibility complex encodes large proline-rich proteins with multiple repeated motifs and a single ubiquitin-like domain, Proc. Natl. Acad. Sci. USA, 1990, Vol 87, pages 2374-2378, see entire document.	1-12, 14-16, and 21 for SEQ ID NO:2
Y	Database GenEmbl on STN. SKUCE, C. 'Homo sapiens chromosome 20 clone RP4-661I20 map q11.23-12', GenEmbl Database, Aceesion AL031669, Version AL031669.18 GI:6983365, 11 FEBRUARY, 2000 (04.02.2000), see nucleotide position 63147-63482.	1-12, 14-16, and 21 for SEQ ID NO:3
Y	Database GenEmbl on STN. RAKER, V.A. 'Human SnRNP core protein Sm D2 mRNA, complete cds'., GenEmbl Database, Accession U15008, Version U15008.1 GI:600747, 10 December, 1994 (10.12.1994), see nucelotide position 23-479	1-12, 14-16, and 21 for SEQ ID NO:4
Y	Database GenEmbl on STN. ELLER et al. 'Cellular retinoic acid-binding protein [human, skin, mRNA, 735 nt]', GenEmbl Database, Accession S74445, Version S74445.1, GI:241541, 7 May, 1993 (07.05.1993), see nucleotide position 7-733.	1-12, 14-16 and 21 for SEQ ID NO:6

☒ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
03 May 2000 (03.05.2000)	26 JUL 2000
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Box PCT Washington, D.C. 20231 Facsimile No. (703)305-3230	Authorized officer Michael Woodward Telephone No. (703) 308-0196

Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/05882

C (Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Database GenEmbl on STN. SHARMA et al 'Human class III alcohol dehydrogenase (ADH5) chi subunit mRNA, complete cds.', GenEmbl Database, Accession M30471, Version M30471.1 GI:178133, 5 October, 1995 (05.10.1997), see nucleotide position 2-2277.	1-12, 14-16, and 21 for SEQ ID NO:8
Y	Database GenEmbl on STN. ABEDINIA, M. 'Human transketolase (TKT) mRNA, complete cds.', GenEmbl, Accession U55017 M86521, Version U55017.1 GI:1297296, 6 May, 1996 (06.05.1996), see nucleotide position 687-2038.	1-12, 14-16, and 21 for SEQ ID NO:10

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US00/05882

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:

3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:
Please See Continuation Sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:

4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: 1-12, 14-16, and 21 for the first 10 sequences in Table 1

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

BOX II. OBSERVATIONS WHERE UNITY OF INVENTION IS LACKING This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1.

Group 1, claims 1-12, 14-16, and 21 in so far as they are drawn to the first ten polynucleotides of Table 1 (pages 12-118), protein, vector, gene, method of making host cell, recombinant host cell, method of producing the protein of SEQ ID NO:61.
Groups 2-209, claims 1-12, 14-16, in so far as they are drawn to the next 208 polynucleotide groups (any four sequences constitute a single group) and encoded proteins listed in Table 1.
Groups 210-418, claim 13, in so far as they are drawn to isolated antibodies that bind to any one group of the next 208 polypeptide sequence groups listed in Table 1.
Groups 419-627, claims 15-16, in so far as they are drawn to a method of making any one group of the next 208 polypeptide sequence groups listed in Table 1.
Groups 628-836, claim 17, in so far as they are drawn to a method of treatment by administration any one group of the next 208 polypeptide sequence groups listed in Table 1.
Groups 837-1045, claim 18, in so far as they are drawn to a method of diagnosing a pathological condition by determining a presence or absence of a mutation in any one group of the next 208 polypeptide sequence groups listed in Table 1.
Groups 1046-1255, claim 19, in so far as they are drawn to a method of diagnosing a pathological condition by determining the presence or amount of any one group of the next 208 polypeptide sequence groups listed in Table 1.
Groups 1256-1465, claims 20 and 23, in so far as they are drawn to a method of identifying any one group of the next 208 polypeptide sequence groups listed in Table 1, and the product produce by the same method.
Group 1466-1675, claim 22, in so far as they are drawn to a method of identifying an activity in a biological assay by expression of any one group of the next 208 polypeptide sequence groups listed in Table 1.

The inventions not elected, do not relate to a single inventive concept under PCT Rule 13.1 because, under PCT rule 13.2, the non-elected groups lack the same or corresponding technical features for the following reasons: Group 1 corresponds to the first invention wherein the first product is the polynucleotide, and the first method of use is the method of using the polynucleotide to make the protein, and the protein. Note, there is no method of making the polynucleotide. Each of groups 2-1675 does not share the same or corresponding special technical feature because, each group is drawn to different polynucleotide or encoded protein. Additionally, each of groups 210-1675 does not share the same or corresponding technical feature because, each group is drawn to different compounds or methods of using any of the fifty polynucleotides and encoded proteins listed in Table 1. The Authority therefore considers that the several inventions do not share a special technical feature within the meaning of PCT Rule 13.2 and thus do not relate to a single general inventive concept within the meaning of PCT Rule 13.1.